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(54) Title: SYNTHETIC PEPTIDES AND USES THEREFORE

(57) Abstract: A synthetic polypeptide is disclosed, which comprises a plurality of different segments of at least one parent polypep-
tide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide
to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide. Synthetic polynucleotides are
also disclosed that code for the synthetic polypeptides of the invention as well as expression constructs comprising the synthetic
polynucleotides. Also disclosed are methods for constructing the aforementioned molecules and immunopotentiating compositions
and methods for treating and/or preventing a disease or condition.

WO 01/090197 A1

SYNTHETIC PEPTIDES AND USES THEREFORE

FIELD OF THE INVENTION

THIS INVENTION relates generally to agents for modulating immune responses. More particularly, the present invention relates to a synthetic polypeptide comprising a plurality of different segments of a parent polypeptide, wherein the segments are linked to each other such that one or more functions of the parent polypeptide are impeded, abrogated or otherwise altered and such that the synthetic polypeptide, when introduced into a suitable host, can elicit an immune response against the parent polypeptide. The invention also relates to synthetic polynucleotides encoding the synthetic polypeptides and to synthetic constructs comprising these polynucleotides. The invention further relates to the use of the polypeptides and polynucleotides of the invention in compositions for modulating immune responses. The invention also extends to methods of using such compositions for prophylactic and/or therapeutic purposes.

Bibliographic details of various publications referred to in this specification are collected at the end of the description.

BACKGROUND OF THE INVENTION

The modern reductionist approach to vaccine and therapy development has been pursued for a number of decades and attempts to focus only on those parts of pathogens or of cancer proteins which are relevant to the immune system. To date the performance of this approach has been relatively poor considering the vigorous research carried out and the number of effective vaccines and therapies that it has produced. This approach is still being actively pursued, however, despite its poor performance because vaccines developed using this approach are often extremely safe and because only by completely understanding the immune system can new vaccine strategies be developed.

One area that has benefited greatly from research efforts is knowledge about how the adaptive immune system operates and more specifically how T and B cells learn to recognise specific parts of pathogens and cancers. T cells are mainly involved in cell-mediated immunity whereas B cells are involved in the generation of antibody-mediated immunity. The two most important types of T cells involved in adaptive cellular immunity

- 2 -

are $\alpha\beta$ CD8⁺ cytotoxic T lymphocytes (CTL) and CD4⁺ T helper lymphocytes. CTL are important mediators of cellular immunity against many viruses, tumours, some bacteria and some parasites because they are able to kill infected cells directly and secrete various factors which can have powerful effects on the spread of infectious organisms. CTLs
5 recognise epitopes derived from foreign intracellular proteins, which are 8-10 amino acids long and which are presented by class I major histocompatibility complex (MHC) molecules (in humans called human lymphocyte antigens - HLAs) (Jardetzky *et al.*, 1991; Fremont *et al.*, 1992; Rotzschke *et al.*, 1990). T helper cells enhance and regulate CTL responses and are necessary for the establishment of long-lived memory CTL. They also
10 inhibit infectious organisms by secreting cytokines such as IFN- γ . T helper cells recognise epitopes derived mostly from extracellular proteins which are 12-25 amino acids long and which are presented by class II MHC molecules (Chicz *et al.*, 1993; Newcomb *et al.*, 1993). B cells, or more specifically the antibodies they secrete, are important mediators in the control and clearance of mostly extracellular organisms. Antibodies recognise mainly
15 conformational determinants on the surface of organisms, for example, although sometimes they may recognise short linear determinants.

Despite significant advances towards understanding how T and linear B cell epitopes are processed and presented to the immune system, the full potential of epitope-based vaccines has not been fully exploited. The main reason for this is the large number
20 of different T cell epitopes, which have to be included into such vaccines to cover the extreme HLA polymorphism in the human population. The human HLA diversity is one of the main reasons why whole pathogen vaccines frequently provide better population coverage than subunit or peptide-based vaccine strategies. There is a range of epitope-based strategies though which have tried to solve this problem, *e.g.*, peptide blends, peptide
25 conjugates and polyepitope vaccines (ie comprising strings of multiple epitopes) (Dyall *et al.*, 1995; Thomson *et al.*, 1996; Thomson *et al.*, 1998; Thomson *et al.*, 1998). These approaches however will always be sub optimal not only because of the slow pace of epitope characterisation but also, because it is virtually impossible for them to cover every existing HLA polymorphism in the population. A number of strategies have sought to
30 avoid both problems by not identifying epitopes and instead incorporating larger amounts of sequence information *e.g.*, approaches using whole genes or proteins and approaches that mix multiple protein or gene sequences together. The proteins used by these strategies

- 3 -

however sometimes still function and therefore can compromise vaccine safety *e.g.*, whole cancer proteins. Alternative strategies have tried to improve the safety of vaccines by fragmenting the genes and expressing them either separately or as complex mixtures *e.g.*, library DNA immunisation or by ligating such fragments back together. These approaches
5 are still sub-optimal because they are too complex, generate poor levels of immunity, cannot guarantee that all proteins no longer function and/or that all fragments are present, which compromises substantially complete immunological coverage.

The lack of a safe and efficient vaccine strategy that can provide substantially complete immunological coverage is an important problem, especially when trying to
10 develop vaccines against rapidly mutating and persistent viruses such as HIV and hepatitis C virus, because partial population coverage could allow vaccine-resistant pathogens to re-emerge in the future. Human immunodeficiency virus (HIV) is an RNA lentivirus virus approximately 9 kb in length, which infects CD4⁺ T cells, causing T cell decline and AIDS typically 3-8 years after infection. It is currently the most serious human viral infection,
15 evidenced by the number of people currently infected with HIV or who have died from AIDS, estimated by the World Health Organisation (WHO) and UNAIDS in their AIDS epidemic update (December 1999) to be 33.6 and 16.3 million people, respectively. The spread of HIV is also now increasing fastest in areas of the world where over half of the human population reside, hence an effective vaccine is desperately needed to curb the
20 spread of this epidemic. Despite the urgency, an effective vaccine for HIV is still some way off because of delays in defining the correlates of immune protection, lack of a suitable animal model, existence of up to 8 different subtypes of HIV and a high HIV mutation rate.

A significant amount of research has been carried out to try and develop a vaccine
25 capable of generating neutralising antibody responses that can protect against field isolates of HIV. Despite these efforts, it is now clear that the variability, instability and inaccessibility of critical determinants on the HIV envelope protein will make it extremely difficult and perhaps impossible to develop such a vaccine (Kwong *et al.*, 1998). The limited ability of antibodies to block HIV infection is also supported by the observation
30 that development of AIDS correlates primarily with a reduction in CTL responsiveness to HIV and not to altered antibody levels (Ogg *et al.*, 1998). Hence CTL-mediated and not antibody-mediated responses appear to be critical for maintaining the asymptomatic state

- 4 -

in vivo. There is also some evidence to suggest that pre-existing HIV-specific CTL responses can block the establishment of a latent HIV infection. This evidence comes from a number of cases where individuals have generated HIV-specific CTL responses without becoming infected and appear to be protected from establishing latent HIV infections despite repeated virus exposure (Rowland-Jones *et al.*, 1995; Parmiani 1998). Taken together, these observations suggest that a vaccine capable of generating a broad range of strong CTL responses may be able to stop individuals from becoming latently infected with HIV or at least allow infected individuals to remain asymptomatic for life. Virtually all of the candidate HIV vaccines developed to date have been derived from subtype B HIV proteins (western world subtype) whereas the majority of the HIV infections worldwide are caused by subtypes A/E or C (E and A are similar except in the envelop protein)(referred to as developing world subtypes). Hence existing candidate vaccines may not be suitable for the more common HIV subtypes. Recently, there has been some evidence that B subtype vaccines may be partially effective against other common HIV subtypes (Rowland-Jones *et al.*, 1998). Accordingly, the desirability of a vaccine still remains, whose effectiveness is substantially complete against all isolates of all strains of HIV.

SUMMARY OF THE INVENTION

The present invention is predicated in part on a novel strategy for enhancing the efficacy of an immunopotentiating composition. This strategy involves utilising the sequence information of a parent polypeptide to produce a synthetic polypeptide that
5 comprises a plurality of different segments of the parent polypeptide, which are linked sequentially together in a different arrangement relative to that of the parent polypeptide. As a result of this change in relationship, the sequence of the linked segments in the synthetic polypeptide is different to a sequence contained within the parent polypeptide. As more fully described hereinafter, the present strategy is used advantageously to cause
10 significant disruption to the structure and/or function of the parent polypeptide while minimising the destruction of potentially useful epitopes encoded by the parent polypeptide.

Thus, in one aspect of the present invention, there is provided a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide,
15 wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide.

In one embodiment, the synthetic polypeptide consists essentially of different segments of a single parent polypeptide.

In an alternate embodiment, the synthetic polypeptide consists essentially of
20 different segments of a plurality of different parent polypeptides.

Suitably, said segments in said synthetic polypeptide are linked sequentially in a different order or arrangement relative to that of corresponding segments in said at least one parent polypeptide.

Preferably, at least one of said segments comprises partial sequence identity or
25 homology to one or more other said segments. The sequence identity or homology is preferably contained at one or both ends of said at least one segment.

In another aspect, the invention resides in a synthetic polynucleotide encoding the synthetic polypeptide as broadly described above.

- 6 -

According to yet another aspect, the invention contemplates a synthetic construct comprising a said polynucleotide as broadly described above that is operably linked to a regulatory polynucleotide.

In a further aspect of the invention, there is provided a method for producing a
5 synthetic polynucleotide as broadly described above, comprising:

- linking together in the same reading frame a plurality of nucleic acid sequences encoding different segments of at least one parent polypeptide to form a synthetic polynucleotide whose sequence encodes said segments linked together in a different relationship relative to their linkage in the at least one parent polypeptide.

10 Preferably, the method further comprises fragmenting the sequence of a respective parent polypeptide into fragments and linking said fragments together in a different relationship relative to their linkage in said parent polypeptide sequence. In a preferred embodiment of this type, the fragments are randomly linked together.

Suitably, the method further comprises reverse translating the sequence of a
15 respective parent polypeptide or a segment thereof to provide a nucleic acid sequence encoding said parent polypeptide or said segment. In a preferred embodiment of this type, an amino acid of said parent polypeptide sequence is reverse translated to provide a codon, which has higher translational efficiency than other synonymous codons in a cell of interest. Suitably, an amino acid of said parent polypeptide sequence is reverse translated
20 to provide a codon which, in the context of adjacent or local sequence elements, has a lower propensity of forming an undesirable sequence (e.g., a palindromic sequence or a duplicated sequence) that is refractory to the execution of a task (e.g., cloning or sequencing).

In another aspect, the invention encompasses a computer program product for
25 designing the sequence of a synthetic polypeptide as broadly described above, comprising:

- code that receives as input the sequence of at least one parent polypeptide;
- code that fragments the sequence of a respective parent polypeptide into fragments;

- 7 -

- code that links together said fragments in a different relationship relative to their linkage in said parent polypeptide sequence; and
- a computer readable medium that stores the codes.

In yet another aspect, the invention provides a computer program product for
5 designing the sequence of a synthetic polynucleotide as broadly described above, comprising:

- code that receives as input the sequence of at least one parent polypeptide;
- code that fragments the sequence of a respective parent polypeptide into fragments;
- 10 - code that reverse translates the sequence of a respective fragment to provide a nucleic acid sequence encoding said fragment;
- code that links together in the same reading frame each said nucleic acid sequence to provide a polynucleotide sequence that codes for a polypeptide sequence in which said fragments are linked together in a different relationship relative to their
15 linkage in the at least one parent polypeptide sequence; and
- a computer readable medium that stores the codes.

In still yet another aspect, the invention provides a computer for designing the sequence of a synthetic polypeptide as broadly described above, wherein said computer comprises:

- 20 (a) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said machine-readable data comprise the sequence of at least one parent polypeptide;
- (b) a working memory for storing instructions for processing said machine-readable data;
- 25 (c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium, for processing said machine readable data to provide said synthetic polypeptide sequence; and
- (d) an output hardware coupled to said central processing unit, for receiving said synthetic polypeptide sequence.

- 8 -

In a preferred embodiment, the processing of said machine readable data comprises fragmenting the sequence of a respective parent polypeptide into fragments and linking together said fragments in a different relationship relative to their linkage in the sequence of said parent polypeptide.

5 In still yet another aspect, the invention resides in a computer for designing the sequence of a synthetic polynucleotide as broadly described above, wherein said computer comprises:

(a) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said machine-readable data comprise the
10 sequence of at least one parent polypeptide;

(b) a working memory for storing instructions for processing said machine-readable data;

(c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium, for processing said machine readable data to provide said
15 synthetic polynucleotide sequence; and

(d) an output hardware coupled to said central processing unit, for receiving said synthetic polynucleotide sequence.

In a preferred embodiment, the processing of said machine readable data comprises fragmenting the sequence of a respective parent polypeptide into fragments,
20 reverse translating the sequence of a respective fragment to provide a nucleic acid sequence encoding said fragment and linking together in the same reading frame each said nucleic acid sequence to provide a polynucleotide sequence that codes for a polypeptide sequence in which said fragments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide sequence.

25 According to another aspect, the invention contemplates a composition, comprising an immunopotentiating agent selected from the group consisting of a synthetic polypeptide as broadly described above, a synthetic polynucleotide as broadly described above and a synthetic construct as broadly described above, together with a pharmaceutically acceptable carrier.

- 9 -

The composition may optionally comprise an adjuvant.

In a further aspect, the invention encompasses a method for modulating an immune response, which response is preferably directed against a pathogen or a cancer, comprising administering to a patient in need of such treatment an effective amount of an immunopotentiating agent selected from the group consisting of a synthetic polypeptide as broadly described above, a synthetic polynucleotide as broadly described above and a synthetic construct as broadly described above, or a composition as broadly described above.

According to still a further aspect of the invention, there is provided a method for treatment and/or prophylaxis of a disease or condition, comprising administering to a patient in need of such treatment an effective amount of an immunopotentiating agent selected from the group consisting of a synthetic polypeptide as broadly described above, a synthetic polynucleotide as broadly described above and a synthetic construct as broadly described above, or a composition as broadly described above.

The invention also encompasses the use of the synthetic polypeptide, the synthetic polynucleotide and the synthetic construct as broadly described above in the study, and modulation of immune responses.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is a diagrammatic representation showing the number of people living with AIDS in 1998 in various parts of the world and most prevalent HIV clades in these regions. Estimates generated by UNAIDS.

- 5 Figure 2 is a graphical representation showing trends in the incidence of the common HIV clades and estimates for the future. Graph from the International Aids Vaccine Initiative (IAVI).

- Figure 3 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV gag [SEQ ID NO: 1] used for the construction of an
10 embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV gag protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

- 15 Figure 4 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV pol [SEQ ID NO: 2] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV pol protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton
20 Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR98-485.

- Figure 5 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV vif [SEQ ID NO: 3] used for the construction of an
25 embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV vif protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR98-485.

- 11 -

Figure 6 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV vpr [SEQ ID NO: 4] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV vpr protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

Figure 7 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV tat [SEQ ID NO: 5] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV tat protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

Figure 8 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV rev [SEQ ID NO: 6] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV rev protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

Figure 9 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV vpu [SEQ ID NO: 7] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV vpu protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

Figure 10 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV env [SEQ ID NO: 8] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade

- 12 -

consensus sequences for the HIV env protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

- 5 Figure 11 is a diagrammatic representation showing overlapping segments of a parent polypeptide sequence for HIV nef [SEQ ID NO: 9] used for the construction of an embodiment of an HIV Savine. Also shown are the alignments of common HIV clade consensus sequences for the HIV nef protein from the HIV Molecular Immunology Database 1997, Editors Bette Korber, John Moore, Cristian Brander, Richard Koup, Barton
10 Haynes and Bruce Walker. Publisher, Los Alamos National Laboratory, Theoretical Biology and Biophysics, Los Alamos, New Mexico, Pub LAUR 98-485.

- Figure 12 is a diagrammatic representation depicting the systematic segmentation of the designed degenerate consensus sequences for each HIV protein and the reverse translation of each segment into a DNA sequence. Also shown is the number of segments
15 used during random rearrangement and amino acids that were removed. Amino acids surrounded by an open square were removed from the design, because degenerate codons to cater for the desired amino acid combination required too many degenerate bases to comply with the incorporation of degenerate sequence rules outlined in the description of the invention herein. Amino acids surrounded by an open circle were removed only in the
20 segment concerned mainly because they were coded for in an oligonucleotide overlap region. Amino acids marked with an asterisk were designed differently in one fragment compared to the corresponding overlap region (see tat gene)

- Figure 13 is a diagrammatic representation showing the first and second most frequently used codons in mammals used to reverse translate HIV protein segments. Also
25 shown are all first and second most frequently used degenerate codons for two amino acids where only one base is varied. Codons used where more than one base was varied were worked out in each case by comparing all the codons for each amino acid. The IUPAC codes for degenerate bases are also shown.

- Figure 14 illustrates the construction plan for the HIV Savine showing the
30 approximate sizes of the subcassettes, cassettes and full-length Savine cDNA and the restriction sites involved in joining them together. Also shown are the extra sequences

- 13 -

added onto each subcassette during their design and a brief description of how the subcassettes, cassettes and full length cDNA were constructed and transferred into appropriate DNA plasmids. *Description of full length construction:* pA was cleaved with *XhoI/SalI* and cloned into *XhoI* arms of the B cassette; pAB was cleaved with *XhoI* and
 5 cloned into *XhoI* arms of the C cassette; full length construct is excisable with either *XbaI/BamHI* at the 5' end or *BglIII* at the 3' end. *Options for excising cassettes:* A) *XbaI/BamHI* at the 5' end, *BglIII/XhoI* at the 3' end; B) *XbaI/BamHI* at the 5' end, *BglIII/SalI* at the 3' end; C) *XbaI/BamHI* at the 5' end, *BglIII/SalI* at the 3' end. *Cleaving plasmid vectors:* pDNAVacc is cleavable with *XbaI/XhoI* (DNA vaccination); pBCB07 or
 10 pTK7.5 vectors are cleavable with *BamHI/SalI* (Recombinant Vaccinia); pAvipox vector pAF09 is cleavable with *BamHI/SalI* (Recombinant Avipox).

Figure 15 shows the full length DNA (17253 bp) and protein sequence (5742 aas) of the HIV Savine construct. Fragment boundaries are shown, together with the position of each fragment in each designed HIV protein, fragment number (in brackets), spacer
 15 residues (two alanine residues) and which fragment the spacer was for (open boxes and arrows). The location of residual restriction site joining sequences corresponding to subcassette or cassette boundaries (shaded boxes) are also shown, along with start and stop codons, Kozak sequence, the location of the murine influenza virus CTL epitope sequence (near the 3' end), important restriction sites at each end and the position of each degenerate
 20 amino acid (indicated by 'X').

Figure 16 depicts the layout and position of oligonucleotides in the designed DNA sequence for subcassette A1. The sequences which anneal to the short amplification oligonucleotides are indicated by hatched boxes and the position of oligonucleotide overlap regions are dark shaded.

25 Figure 17: Panel (a) depicts the stepwise asymmetric PCR of the two halves of subcassette A1 (lanes 2-5 and 7-9, respectively) and final splicing together by SOEing (lane 10). DNA standards in lane 1 are pUC18 digested with *Sau3AI*. Panel (b) shows the stepwise ligation-mediated joining and PCR amplification of each cassette as indicated. DNA standards in lane 1 are SPP1 cut with *EcoRI*.

30 Figure 18: Panel (a) shows summary of the construction of the DNA vaccine plasmids that express one HIV Savine cassette. Panel (b) shows a summary of the

- 14 -

construction of the plasmids used for marker rescue recombination to generate Vaccinia viruses expressing one HIV Savine cassette. Panel (c) shows a summary of the construction of the DNA vaccine plasmids which each express a version of the full-length HIV Savine cDNA

5 Figure 19 shows restimulation of HIV specific polyclonal CTL responses from three HIV-infected patients by the HIV Savine constructs. PBMCs from three different patients were restimulated for 7 days by infection with Vaccinia virus pools expressing the HIV Savine cassettes: Pool 1 included VV-AC1 and VV-BC1; Pool 2 included VV-AC2, VV-BC2 and VV-CC2. The restimulated PBMCs were then mixed with autologous LCLs
10 (effector to target ratio of 50:1), which were either uninfected or infected with either Vaccinia viruses expressing the HIV proteins gag (VV-gag), env (VV-env) or pol (VV-pol), VV- HIV Savine pools 1 (light bars) or 2 (dark bars) or a control Vaccinia virus (VV-Lac) and the amount of ^{51}Cr released used to determine percent specific lysis. K562 cells were used to determine the level of NK cell-mediated killing in their stimulated culture.

15 Figure 20 is a diagrammatic representation showing CD4+ proliferation of PBMCs from HIV-1 infected patients restimulated with either Pool1 or Pool2 of the HIV-1 Savine. Briefly PBMCs were stained with CFSE and culture for 6 days with or without VVs encoding either pool1 or pool2 of the HIV-1 Savine. Restimulated Cells were then labelled with antibodies and analysed by FACS.

20 Figure 21 is a graphical representation showing the CTL response in mice vaccinated with the HIV Savine. C57BL6 mice were immunised with the HIV-1 Savine DNA vaccine comprising the six plasmids described in Figure 18a (100 μg total DNA was given as 50 $\mu\text{g}/\text{leg}$ i.m.). One week later Poxviruses (1×10^7 pfu) comprising Pool 1 of the HIV-1 Savine were used to boost the immune responses. Three weeks later splenocytes
25 from these mice were restimulated with VV-Pool 1 or VV-Pool 2 for 5 days and the resultant effectors used in a ^{51}Cr release cytotoxicity assay against targets infected with CTRVV, VV-pools or VV expressing the natural antigens from HIV-1.

Figure 22 shows immune responses of HIV Immune Macaques (vaccinated with recombinant FPV expressing gag-pol and challenged with HIV-1 2 years prior to
30 experiment). Monkeys 1 and 2 were immunised once at day 0 with VV Savine pool 1 (Three VVs which together express the entire HIV Savine). Monkey 3 was immunised

- 15 -

twice with FPV-gag-pol *i.e.*, Day 0 is 3 weeks after first FPV-gag-pol immunisation. A) IFN- γ detection by ELISPOT of whole blood (0.5 mL, venous blood heparin-anticoagulated) stimulated with Aldrithiol-2 inactivated whole HIV-1 (20 hours, 20 $\mu\text{g/mL}$). Plasma samples were then centrifuged (1000xg) and assayed in duplicate for
5 antigen-specific IFN using capture ELISA. B) Flow cytometric detection of HIV-1 specific CD69+/CD8+ T cells. Freshly isolated PBMCs were stimulated with inactivated HIV-1 as above for 16 hours, washed and labelled with the antibodies. Cells were then analysed using a FACScalibur™ flow cytometer and data. analysed using Cell-Quest software. C) Flow cytometric detection of HIV-1 specific CD69+/CD4+ T cells carried out as in B).

10 Figure 23 shows a diagram of a system used to carry out the instructions encoded by the storage medium of Figures 28 and 29.

Figure 24 depicts a flow diagram showing an embodiment of a method for designing synthetic polynucleotide and synthetic polypeptides of the invention.

15 Figure 25 shows an algorithm, which *inter alia* utilises the steps of the method shown in Figure 24.

Figure 26 shows an example of applying the algorithm of Figure 25 to an input consensus polyprotein sequence of Hepatitis C 1a to execute the segmentation of the polyprotein sequence, the rearrangement of the segments, the linkage of the rearranged segments and the outputting of synthetic polynucleotide and polypeptide sequences for the
20 preparation of Savines for treating and/or preventing Hepatitis C infection.

Figure 27 illustrates an example of applying the algorithm of Figure 25 to input consensus melanocyte differentiation antigens (gp100, MART, TRP-1, Tyros, Trp-2, MC1R, MUC1F and MUC1R) and to consensus melanoma specific antigens (BAGE, GAGE-1, gp100In4, MAGE-1, MAGE-3, PRAME, TRP2IN2, NYNSO1a, NYNSO1b and
25 LAGE1) to facilitate segmentation of those sequences, to rearrange the segments, to link the rearranged segments and to synthetic polynucleotide and polypeptide sequences for the preparation of Savines for treating and/or preventing melanoma.

Figure 28 shows a cross section of a magnetic storage medium.

Figure 29 shows a cross section of an optically readable data storage medium.

- 16 -

Figure 30 shows six HIV Savine cassette sequences (A1 [SEQ ID NO: 393], A2 [SEQ ID NO: 399], B1[SEQ ID NO: 395], B2 [SEQ ID NO: 401], C1 [SEQ ID NO: 397] and C2 [SEQ ID NO: 403]). A1, B1 and C1 can be joined together using, for example, convenient restriction enzyme sites provided at the ends of each cassette to construct an embodiment of a full length HIV Savine [SEQ ID NO: 405]. A2, B2 and C2 can also be joined together to provide another embodiment of a full length HIV Savine with 350 aa mutations common in major HIV clades. The cassettes A/B/C can be joined into single constructs using specific restriction enzyme sites incorporated after the start codon or before the stop codon in the cassettes

BRIEF DESCRIPTION OF THE SEQUENCES: SUMMARY TABLE**TABLE A**

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1	GAG consensus polypeptide	499 aa
SEQ ID NO: 2	POL consensus polypeptide	995 aa
SEQ ID NO: 3	VIF consensus polypeptide	192 aa
SEQ ID NO: 4	VPR consensus polypeptide	96 aa
SEQ ID NO: 5	TAT consensus polypeptide	102 aa
SEQ ID NO: 6	REV consensus polypeptide	123 aa
SEQ ID NO: 7	VPU consensus polypeptide	81 aa
SEQ ID NO: 8	ENV consensus polypeptide	651 aa
SEQ ID NO: 9	NEF consensus polypeptide	206 aa
SEQ ID NO: 10	GAG segment 1	90 nts
SEQ ID NO: 11	Polypeptide encoded by SEQ ID NO: 10	30 aa
SEQ ID NO: 12	GAG segment 2	90 nts
SEQ ID NO: 13	Polypeptide encoded by SEQ ID NO: 12	30 aa
SEQ ID NO: 14	GAG segment 3	90 nts
SEQ ID NO: 15	Polypeptide encoded by SEQ ID NO: 14	30 aa
SEQ ID NO: 16	GAG segment 4	90 nts
SEQ ID NO: 17	Polypeptide encoded by SEQ ID NO: 16	30 aa
SEQ ID NO: 18	GAG segment 5	90 nts
SEQ ID NO: 19	Polypeptide encoded by SEQ ID NO: 18	30 aa
SEQ ID NO: 20	GAG segment 6	90 nts
SEQ ID NO: 21	Polypeptide encoded by SEQ ID NO: 20	30 aa
SEQ ID NO: 22	GAG segment 7	90 nts

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 23	Polypeptide encoded by SEQ ID NO: 22	30 aa
SEQ ID NO: 24	GAG segment 8	90 nts
SEQ ID NO: 25	Polypeptide encoded by SEQ ID NO: 24	30 aa
SEQ ID NO: 26	GAG segment 9	90 nts
SEQ ID NO: 27	Polypeptide encoded by SEQ ID NO: 26	30 aa
SEQ ID NO: 28	GAG segment 10	90 nts
SEQ ID NO: 29	Polypeptide encoded by SEQ ID NO: 28	30 aa
SEQ ID NO: 30	GAG segment 11	90 nts
SEQ ID NO: 31	Polypeptide encoded by SEQ ID NO: 30	30 aa
SEQ ID NO: 32	GAG segment 12	90 nts
SEQ ID NO: 33	Polypeptide encoded by SEQ ID NO: 32	30 aa
SEQ ID NO: 34	GAG segment 13	90 nts
SEQ ID NO: 35	Polypeptide encoded by SEQ ID NO: 34	30 aa
SEQ ID NO: 36	GAG segment 14	90 nts
SEQ ID NO: 37	Polypeptide encoded by SEQ ID NO: 36	30 aa
SEQ ID NO: 38	GAG segment 15	90 nts
SEQ ID NO: 39	Polypeptide encoded by SEQ ID NO: 38	30 aa
SEQ ID NO: 40	GAG segment 16	90 nts
SEQ ID NO: 41	Polypeptide encoded by SEQ ID NO: 40	30 aa
SEQ ID NO: 42	GAG segment 17	90 nts
SEQ ID NO: 43	Polypeptide encoded by SEQ ID NO: 42	30 aa
SEQ ID NO: 44	GAG segment 18	90 nts
SEQ ID NO: 45	Polypeptide encoded by SEQ ID NO: 44	30 aa
SEQ ID NO: 46	GAG segment 19	90 nts

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 47	Polypeptide encoded by SEQ ID NO: 46	30 aa
SEQ ID NO: 48	GAG segment 20	90 nts
SEQ ID NO: 49	Polypeptide encoded by SEQ ID NO: 48	30 aa
SEQ ID NO: 50	GAG segment 21	90 nts
SEQ ID NO: 51	Polypeptide encoded by SEQ ID NO: 50	30 aa
SEQ ID NO: 52	GAG segment 22	90 nts
SEQ ID NO: 53	Polypeptide encoded by SEQ ID NO: 52	30 aa
SEQ ID NO: 54	GAG segment 23	90 nts
SEQ ID NO: 55	Polypeptide encoded by SEQ ID NO: 54	30 aa
SEQ ID NO: 56	GAG segment 24	90 nts
SEQ ID NO: 57	Polypeptide encoded by SEQ ID NO: 56	30 aa
SEQ ID NO: 58	GAG segment 25	90 nts
SEQ ID NO: 59	Polypeptide encoded by SEQ ID NO: 58	30 aa
SEQ ID NO: 60	GAG segment 26	90 nts
SEQ ID NO: 61	Polypeptide encoded by SEQ ID NO: 60	30 aa
SEQ ID NO: 62	GAG segment 27	90 nts
SEQ ID NO: 63	Polypeptide encoded by SEQ ID NO: 62	30 aa
SEQ ID NO: 64	GAG segment 28	90 nts
SEQ ID NO: 65	Polypeptide encoded by SEQ ID NO: 64	30 aa
SEQ ID NO: 66	GAG segment 29	90 nts
SEQ ID NO: 67	Polypeptide encoded by SEQ ID NO: 66	30 aa
SEQ ID NO: 68	GAG segment 30	90 nts
SEQ ID NO: 69	Polypeptide encoded by SEQ ID NO: 68	30 aa
SEQ ID NO: 70	GAG segment 31	90 nts

- 20 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 71	Polypeptide encoded by SEQ ID NO: 70	30 aa
SEQ ID NO: 72	GAG segment 32	90 nts
SEQ ID NO: 73	Polypeptide encoded by SEQ ID NO: 72	30 aa
SEQ ID NO: 74	GAG segment 33	57 nts
SEQ ID NO: 75	Polypeptide encoded by SEQ ID NO: 74	19 aa
SEQ ID NO: 76	POL segment 1	90 nts
SEQ ID NO: 77	Polypeptide encoded by SEQ ID NO: 76	30 aa
SEQ ID NO: 78	POL segment 2	90 nts
SEQ ID NO: 79	Polypeptide encoded by SEQ ID NO: 78	30 aa
SEQ ID NO: 80	POL segment 3	90 nts
SEQ ID NO: 81	Polypeptide encoded by SEQ ID NO: 80	30 aa
SEQ ID NO: 82	POL segment 4	90 nts
SEQ ID NO: 83	Polypeptide encoded by SEQ ID NO: 82	30 aa
SEQ ID NO: 84	POL segment 5	90 nts
SEQ ID NO: 85	Polypeptide encoded by SEQ ID NO: 84	30 aa
SEQ ID NO: 86	POL segment 6	90 nts
SEQ ID NO: 87	Polypeptide encoded by SEQ ID NO: 86	30 aa
SEQ ID NO: 88	POL segment 7	90 nts
SEQ ID NO: 89	Polypeptide encoded by SEQ ID NO: 88	30 aa
SEQ ID NO: 90	POL segment 8	90 nts
SEQ ID NO: 91	Polypeptide encoded by SEQ ID NO: 90	30 aa
SEQ ID NO: 92	POL segment 9	90 nts
SEQ ID NO: 93	Polypeptide encoded by SEQ ID NO: 92	30 aa
SEQ ID NO: 94	POL segment 10	90 nts

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 95	Polypeptide encoded by SEQ ID NO: 94	30 aa
SEQ ID NO: 96	POL segment 11	90 nts
SEQ ID NO: 97	Polypeptide encoded by SEQ ID NO: 96	30 aa
SEQ ID NO: 98	POL segment 12	90 nts
SEQ ID NO: 99	Polypeptide encoded by SEQ ID NO: 98	30 aa
SEQ ID NO: 100	POL segment 13	90 nts
SEQ ID NO: 101	Polypeptide encoded by SEQ ID NO: 100	30 aa
SEQ ID NO: 102	POL segment 14	90 nts
SEQ ID NO: 103	Polypeptide encoded by SEQ ID NO: 102	30 aa
SEQ ID NO: 104	POL segment 15	90 nts
SEQ ID NO: 105	Polypeptide encoded by SEQ ID NO: 104	30 aa
SEQ ID NO: 106	POL segment 16	90 nts
SEQ ID NO: 107	Polypeptide encoded by SEQ ID NO: 106	30 aa
SEQ ID NO: 108	POL segment 17	90 nts
SEQ ID NO: 109	Polypeptide encoded by SEQ ID NO: 108	30 aa
SEQ ID NO: 110	POL segment 18	90 nts
SEQ ID NO: 111	Polypeptide encoded by SEQ ID NO: 110	30 aa
SEQ ID NO: 112	POL segment 19	90 nts
SEQ ID NO: 113	Polypeptide encoded by SEQ ID NO: 112	30 aa
SEQ ID NO: 114	POL segment 20	90 nts
SEQ ID NO: 115	Polypeptide encoded by SEQ ID NO: 114	30 aa
SEQ ID NO: 116	POL segment 21	90 nts
SEQ ID NO: 117	Polypeptide encoded by SEQ ID NO: 116	30 aa
SEQ ID NO: 118	POL segment 22	90 nts

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 119	Polypeptide encoded by SEQ ID NO: 118	30 aa
SEQ ID NO: 120	POL segment 23	90 nts
SEQ ID NO: 121	Polypeptide encoded by SEQ ID NO: 120	30 aa
SEQ ID NO: 122	POL segment 24	90 nts
SEQ ID NO: 123	Polypeptide encoded by SEQ ID NO: 122	30 aa
SEQ ID NO: 124	POL segment 25	90 nts
SEQ ID NO: 125	Polypeptide encoded by SEQ ID NO: 124	30 aa
SEQ ID NO: 126	POL segment 26	90 nts
SEQ ID NO: 127	Polypeptide encoded by SEQ ID NO: 126	30 aa
SEQ ID NO: 128	POL segment 27	90 nts
SEQ ID NO: 129	Polypeptide encoded by SEQ ID NO: 128	30 aa
SEQ ID NO: 130	POL segment 28	90 nts
SEQ ID NO: 131	Polypeptide encoded by SEQ ID NO: 130	30 aa
SEQ ID NO: 132	POL segment 29	90 nts
SEQ ID NO: 133	Polypeptide encoded by SEQ ID NO: 132	30 aa
SEQ ID NO: 134	POL segment 30	90 nts
SEQ ID NO: 135	Polypeptide encoded by SEQ ID NO: 134	30 aa
SEQ ID NO: 136	POL segment 31	90 nts
SEQ ID NO: 137	Polypeptide encoded by SEQ ID NO: 136	30 aa
SEQ ID NO: 138	POL segment 32	90 nts
SEQ ID NO: 139	Polypeptide encoded by SEQ ID NO: 138	30 aa
SEQ ID NO: 140	POL segment 33	90 nts
SEQ ID NO: 141	Polypeptide encoded by SEQ ID NO: 140	30 aa
SEQ ID NO: 142	POL segment 34	90 nts

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 143	Polypeptide encoded by SEQ ID NO: 142	30 aa
SEQ ID NO: 144	POL segment 35	90 nts
SEQ ID NO: 145	Polypeptide encoded by SEQ ID NO: 144	30 aa
SEQ ID NO: 146	POL segment 36	90 nts
SEQ ID NO: 147	Polypeptide encoded by SEQ ID NO: 146	30 aa
SEQ ID NO: 148	POL segment 37	90 nts
SEQ ID NO: 149	Polypeptide encoded by SEQ ID NO: 148	30 aa
SEQ ID NO: 150	POL segment 38	90 nts
SEQ ID NO: 151	Polypeptide encoded by SEQ ID NO: 150	30 aa
SEQ ID NO: 152	POL segment 39	90 nts
SEQ ID NO: 153	Polypeptide encoded by SEQ ID NO: 152	30 aa
SEQ ID NO: 154	POL segment 40	90 nts
SEQ ID NO: 155	Polypeptide encoded by SEQ ID NO: 154	30 aa
SEQ ID NO: 156	POL segment 41	90 nts
SEQ ID NO: 157	Polypeptide encoded by SEQ ID NO: 156	30 aa
SEQ ID NO: 158	POL segment 42	90 nts
SEQ ID NO: 159	Polypeptide encoded by SEQ ID NO: 158	30 aa
SEQ ID NO: 160	POL segment 43	90 nts
SEQ ID NO: 161	Polypeptide encoded by SEQ ID NO: 160	30 aa
SEQ ID NO: 162	POL segment 44	90 nts
SEQ ID NO: 163	Polypeptide encoded by SEQ ID NO: 162	30 aa
SEQ ID NO: 164	POL segment 45	90 nts
SEQ ID NO: 165	Polypeptide encoded by SEQ ID NO: 164	30 aa
SEQ ID NO: 166	POL segment 46	90 nts

- 24 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 167	Polypeptide encoded by SEQ ID NO: 166	30 aa
SEQ ID NO: 168	POL segment 47	90 nts
SEQ ID NO: 169	Polypeptide encoded by SEQ ID NO: 168	30 aa
SEQ ID NO: 170	POL segment 48	90 nts
SEQ ID NO: 171	Polypeptide encoded by SEQ ID NO: 170	30 aa
SEQ ID NO: 172	POL segment 49	90 nts
SEQ ID NO: 173	Polypeptide encoded by SEQ ID NO: 172	30 aa
SEQ ID NO: 174	POL segment 50	90 nts
SEQ ID NO: 175	Polypeptide encoded by SEQ ID NO: 174	30 aa
SEQ ID NO: 176	POL segment 51	90 nts
SEQ ID NO: 177	Polypeptide encoded by SEQ ID NO: 176	30 aa
SEQ ID NO: 178	POL segment 52	90 nts
SEQ ID NO: 179	Polypeptide encoded by SEQ ID NO: 178	30 aa
SEQ ID NO: 180	POL segment 53	90 nts
SEQ ID NO: 181	Polypeptide encoded by SEQ ID NO: 180	30 aa
SEQ ID NO: 182	POL segment 54	90 nts
SEQ ID NO: 183	Polypeptide encoded by SEQ ID NO: 182	30 aa
SEQ ID NO: 184	POL segment 55	90 nts
SEQ ID NO: 185	Polypeptide encoded by SEQ ID NO: 184	30 aa
SEQ ID NO: 186	POL segment 56	90 nts
SEQ ID NO: 187	Polypeptide encoded by SEQ ID NO: 186	30 aa
SEQ ID NO: 188	POL segment 57	90 nts
SEQ ID NO: 189	Polypeptide encoded by SEQ ID NO: 188	30 aa
SEQ ID NO: 190	POL segment 58	90 nts

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 191	Polypeptide encoded by SEQ ID NO: 190	30 aa
SEQ ID NO: 192	POL segment 59	90 nts
SEQ ID NO: 193	Polypeptide encoded by SEQ ID NO: 192	30 aa
SEQ ID NO: 194	POL segment 60	90 nts
SEQ ID NO: 195	Polypeptide encoded by SEQ ID NO: 194	30 aa
SEQ ID NO: 196	POL segment 61	90 nts
SEQ ID NO: 197	Polypeptide encoded by SEQ ID NO: 196	30 aa
SEQ ID NO: 198	POL segment 62	90 nts
SEQ ID NO: 199	Polypeptide encoded by SEQ ID NO: 198	30 aa
SEQ ID NO: 200	POL segment 63	90 nts
SEQ ID NO: 201	Polypeptide encoded by SEQ ID NO: 200	30 aa
SEQ ID NO: 202	POL segment 64	90 nts
SEQ ID NO: 203	Polypeptide encoded by SEQ ID NO: 202	30 aa
SEQ ID NO: 204	POL segment 65	90 nts
SEQ ID NO: 205	Polypeptide encoded by SEQ ID NO: 204	30 aa
SEQ ID NO: 206	POL segment 66	60 nts
SEQ ID NO: 207	Polypeptide encoded by SEQ ID NO: 206	20 aa
SEQ ID NO: 208	VIF segment 1	90 nts
SEQ ID NO: 209	Polypeptide encoded by SEQ ID NO: 208	30 aa
SEQ ID NO: 210	VIF segment 2	90 nts
SEQ ID NO: 211	Polypeptide encoded by SEQ ID NO: 210	30 aa
SEQ ID NO: 212	VIF segment 3	90 nts
SEQ ID NO: 213	Polypeptide encoded by SEQ ID NO: 212	30 aa
SEQ ID NO: 214	VIF segment 4	90 nts

- 26 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 215	Polypeptide encoded by SEQ ID NO: 214	30 aa
SEQ ID NO: 216	VIF segment 5	90 nts
SEQ ID NO: 217	Polypeptide encoded by SEQ ID NO: 216	30 aa
SEQ ID NO: 218	VIF segment 6	90 nts
SEQ ID NO: 219	Polypeptide encoded by SEQ ID NO: 218	30 aa
SEQ ID NO: 220	VIF segment 7	90 nts
SEQ ID NO: 221	Polypeptide encoded by SEQ ID NO: 220	30 aa
SEQ ID NO: 222	VIF segment 8	90 nts
SEQ ID NO: 223	Polypeptide encoded by SEQ ID NO: 222	30 aa
SEQ ID NO: 224	VIF segment 9	90 nts
SEQ ID NO: 225	Polypeptide encoded by SEQ ID NO: 224	30 aa
SEQ ID NO: 226	VIF segment 10	90 nts
SEQ ID NO: 227	Polypeptide encoded by SEQ ID NO: 226	30 aa
SEQ ID NO: 228	VIF segment 11	90 nts
SEQ ID NO: 229	Polypeptide encoded by SEQ ID NO: 228	30 aa
SEQ ID NO: 230	VIF segment 12	81 nts
SEQ ID NO: 231	Polypeptide encoded by SEQ ID NO: 230	27 aa
SEQ ID NO: 232	VPR segment 1	90 nts
SEQ ID NO: 233	Polypeptide encoded by SEQ ID NO: 232	30 aa
SEQ ID NO: 234	VPR segment 2	90 nts
SEQ ID NO: 235	Polypeptide encoded by SEQ ID NO: 234	30 aa
SEQ ID NO: 236	VPR segment 3	90 nts
SEQ ID NO: 237	Polypeptide encoded by SEQ ID NO: 236	30 aa
SEQ ID NO: 238	VPR segment 4	90 nts

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 239	Polypeptide encoded by SEQ ID NO: 238	30 aa
SEQ ID NO: 240	VPR segment 5	90 nts
SEQ ID NO: 241	Polypeptide encoded by SEQ ID NO: 240	30 aa
SEQ ID NO: 242	VPR segment 6	63 nts
SEQ ID NO: 243	Polypeptide encoded by SEQ ID NO: 242	21 aa
SEQ ID NO: 244	TAT segment 1	90 nts
SEQ ID NO: 245	Polypeptide encoded by SEQ ID NO: 244	30 aa
SEQ ID NO: 246	TAT segment 2	90 nts
SEQ ID NO: 247	Polypeptide encoded by SEQ ID NO: 246	30 aa
SEQ ID NO: 248	TAT segment 3	90 nts
SEQ ID NO: 249	Polypeptide encoded by SEQ ID NO: 248	30 aa
SEQ ID NO: 250	TAT segment 4	90 nts
SEQ ID NO: 251	Polypeptide encoded by SEQ ID NO: 250	30 aa
SEQ ID NO: 252	TAT segment 5	90 nts
SEQ ID NO: 253	Polypeptide encoded by SEQ ID NO: 252	30 aa
SEQ ID NO: 254	TAT segment 6	81 nts
SEQ ID NO: 255	Polypeptide encoded by SEQ ID NO: 254	27 aa
SEQ ID NO: 256	REV segment 1	90 nts
SEQ ID NO: 257	Polypeptide encoded by SEQ ID NO: 256	30 aa
SEQ ID NO: 258	REV segment 2	90 nts
SEQ ID NO: 259	Polypeptide encoded by SEQ ID NO: 258	30 aa
SEQ ID NO: 260	REV segment 3	90 nts
SEQ ID NO: 261	Polypeptide encoded by SEQ ID NO: 260	30 aa
SEQ ID NO: 262	REV segment 4	90 nts

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 263	Polypeptide encoded by SEQ ID NO: 262	30 aa
SEQ ID NO: 264	REV segment 5	90 nts
SEQ ID NO: 265	Polypeptide encoded by SEQ ID NO: 264	30 aa
SEQ ID NO: 266	REV segment 6	90 nts
SEQ ID NO: 267	Polypeptide encoded by SEQ ID NO: 266	30 aa
SEQ ID NO: 268	REV segment 7	90 nts
SEQ ID NO: 269	Polypeptide encoded by SEQ ID NO: 268	30 aa
SEQ ID NO: 270	REV segment 8	54 nts
SEQ ID NO: 271	Polypeptide encoded by SEQ ID NO: 270	18 aa
SEQ ID NO: 272	VPU segment 1	90 nts
SEQ ID NO: 273	Polypeptide encoded by SEQ ID NO: 272	30 aa
SEQ ID NO: 274	VPU segment 2	90 nts
SEQ ID NO: 275	Polypeptide encoded by SEQ ID NO: 274	30 aa
SEQ ID NO: 276	VPU segment 3	90 nts
SEQ ID NO: 277	Polypeptide encoded by SEQ ID NO: 276	30 aa
SEQ ID NO: 278	VPU segment 4	90 nts
SEQ ID NO: 279	Polypeptide encoded by SEQ ID NO: 278	30 aa
SEQ ID NO: 280	VPU segment 5	63 nts
SEQ ID NO: 281	Polypeptide encoded by SEQ ID NO: 280	21 aa
SEQ ID NO: 282	ENV segment 1	90 nts
SEQ ID NO: 283	Polypeptide encoded by SEQ ID NO: 282	30 aa
SEQ ID NO: 284	ENV segment 2	90 nts
SEQ ID NO: 285	Polypeptide encoded by SEQ ID NO: 284	30 aa
SEQ ID NO: 286	ENV segment 3	90 nts

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 287	Polypeptide encoded by SEQ ID NO: 286	30 aa
SEQ ID NO: 288	ENV segment 4	90 nts
SEQ ID NO: 289	Polypeptide encoded by SEQ ID NO: 288	30 aa
SEQ ID NO: 290	ENV segment 5	90 nts
SEQ ID NO: 291	Polypeptide encoded by SEQ ID NO: 290	30 aa
SEQ ID NO: 292	ENV segment 6	90 nts
SEQ ID NO: 293	Polypeptide encoded by SEQ ID NO: 292	30 aa
SEQ ID NO: 294	ENV segment 7	90 nts
SEQ ID NO: 295	Polypeptide encoded by SEQ ID NO: 294	30 aa
SEQ ID NO: 296	ENV segment 8	90 nts
SEQ ID NO: 297	Polypeptide encoded by SEQ ID NO: 296	30 aa
SEQ ID NO: 298	ENV segment 9	57 nts
SEQ ID NO: 299	Polypeptide encoded by SEQ ID NO: 298	19 aa
SEQ ID NO: 300	GAP A segment 1	90 nts
SEQ ID NO: 301	Polypeptide encoded by SEQ ID NO: 300	30 aa
SEQ ID NO: 302	GAP A segment 2	90 nts
SEQ ID NO: 303	Polypeptide encoded by SEQ ID NO: 302	30 aa
SEQ ID NO: 304	GAP A segment 3	90 nts
SEQ ID NO: 305	Polypeptide encoded by SEQ ID NO: 304	30 aa
SEQ ID NO: 306	GAP A segment 4	90 nts
SEQ ID NO: 307	Polypeptide encoded by SEQ ID NO: 306	30 aa
SEQ ID NO: 308	GAP A segment 5	90 nts
SEQ ID NO: 309	Polypeptide encoded by SEQ ID NO: 308	30 aa
SEQ ID NO: 310	GAP A segment 6	90 nts

- 30 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 311	Polypeptide encoded by SEQ ID NO: 310	30 aa
SEQ ID NO: 312	GAP A segment 7	75 nts
SEQ ID NO: 313	Polypeptide encoded by SEQ ID NO: 312	25 nts
SEQ ID NO: 314	GAP B segment 1	90 nts
SEQ ID NO: 315	Polypeptide encoded by SEQ ID NO: 314	30 aa
SEQ ID NO: 316	GAP B segment 2	90 nts
SEQ ID NO: 317	Polypeptide encoded by SEQ ID NO: 316	30 aa
SEQ ID NO: 318	GAP B segment 3	90 nts
SEQ ID NO: 319	Polypeptide encoded by SEQ ID NO: 318	30 aa
SEQ ID NO: 320	GAP B segment 4	90 nts
SEQ ID NO: 321	Polypeptide encoded by SEQ ID NO: 320	30 aa
SEQ ID NO: 322	GAP B segment 5	90 nts
SEQ ID NO: 323	Polypeptide encoded by SEQ ID NO: 322	30 aa
SEQ ID NO: 324	GAP B segment 6	90 nts
SEQ ID NO: 325	Polypeptide encoded by SEQ ID NO: 324	30 aa
SEQ ID NO: 326	GAP B segment 7	90 nts
SEQ ID NO: 327	Polypeptide encoded by SEQ ID NO: 326	30 aa
SEQ ID NO: 328	GAP B segment 8	90 nts
SEQ ID NO: 329	Polypeptide encoded by SEQ ID NO: 328	30 aa
SEQ ID NO: 330	GAP B segment 9	90 nts
SEQ ID NO: 331	Polypeptide encoded by SEQ ID NO: 330	30 aa
SEQ ID NO: 332	GAP B segment 10	90 nts
SEQ ID NO: 333	Polypeptide encoded by SEQ ID NO: 332	30 aa
SEQ ID NO: 334	GAP B segment 11	90 nts

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 335	Polypeptide encoded by SEQ ID NO: 334	30 aa
SEQ ID NO: 336	GAP B segment 12	90 nts
SEQ ID NO: 337	Polypeptide encoded by SEQ ID NO: 336	30 aa
SEQ ID NO: 338	GAP B segment 13	90 nts
SEQ ID NO: 339	Polypeptide encoded by SEQ ID NO: 338	30 aa
SEQ ID NO: 340	GAP B segment 14	90 nts
SEQ ID NO: 341	Polypeptide encoded by SEQ ID NO: 340	30 aa
SEQ ID NO: 342	GAP B segment 15	90 nts
SEQ ID NO: 343	Polypeptide encoded by SEQ ID NO: 342	30 aa
SEQ ID NO: 344	GAP B segment 16	90 nts
SEQ ID NO: 345	Polypeptide encoded by SEQ ID NO: 344	30 aa
SEQ ID NO: 346	GAP B segment 17	90 nts
SEQ ID NO: 347	Polypeptide encoded by SEQ ID NO: 346	30 aa
SEQ ID NO: 348	GAP B segment 18	90 nts
SEQ ID NO: 349	Polypeptide encoded by SEQ ID NO: 348	30 aa
SEQ ID NO: 350	GAP B segment 19	90 nts
SEQ ID NO: 351	Polypeptide encoded by SEQ ID NO: 350	30 aa
SEQ ID NO: 352	GAP B segment 20	90 nts
SEQ ID NO: 353	Polypeptide encoded by SEQ ID NO: 352	30 aa
SEQ ID NO: 354	GAP B segment 21	90 nts
SEQ ID NO: 355	Polypeptide encoded by SEQ ID NO: 354	30 aa
SEQ ID NO: 356	GAP B segment 22	90 nts
SEQ ID NO: 357	Polypeptide encoded by SEQ ID NO: 356	30 aa
SEQ ID NO: 358	GAP B segment 23	90 nts

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 359	Polypeptide encoded by SEQ ID NO: 358	30 aa
SEQ ID NO: 360	GAP B segment 24	90 nts
SEQ ID NO: 361	Polypeptide encoded by SEQ ID NO: 360	30 aa
SEQ ID NO: 362	GAP B segment 25	90 nts
SEQ ID NO: 363	Polypeptide encoded by SEQ ID NO: 362	30 aa
SEQ ID NO: 364	GAP B segment 26	66 nts
SEQ ID NO: 365	Polypeptide encoded by SEQ ID NO: 364	22 aa
SEQ ID NO: 366	NEF segment 1	90 nts
SEQ ID NO: 367	Polypeptide encoded by SEQ ID NO: 366	30 aa
SEQ ID NO: 368	NEF segment 2	90 nts
SEQ ID NO: 369	Polypeptide encoded by SEQ ID NO: 368	30 aa
SEQ ID NO: 370	NEF segment 3	90 nts
SEQ ID NO: 371	Polypeptide encoded by SEQ ID NO: 370	30 aa
SEQ ID NO: 372	NEF segment 4	90 nts
SEQ ID NO: 373	Polypeptide encoded by SEQ ID NO: 372	30 aa
SEQ ID NO: 374	NEF segment 5	90 nts
SEQ ID NO: 375	Polypeptide encoded by SEQ ID NO: 374	30 aa
SEQ ID NO: 376	NEF segment 6	90 nts
SEQ ID NO: 377	Polypeptide encoded by SEQ ID NO: 376	30 aa
SEQ ID NO: 378	NEF segment 7	90 nts
SEQ ID NO: 379	Polypeptide encoded by SEQ ID NO: 378	30 aa
SEQ ID NO: 380	NEF segment 8	90 nts
SEQ ID NO: 381	Polypeptide encoded by SEQ ID NO: 380	30 aa
SEQ ID NO: 382	NEF segment 9	90 nts

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 383	Polypeptide encoded by SEQ ID NO: 382	30 aa
SEQ ID NO: 384	NEF segment 10	90 nts
SEQ ID NO: 385	Polypeptide encoded by SEQ ID NO: 384	30 aa
SEQ ID NO: 386	NEF segment 11	90 nts
SEQ ID NO: 387	Polypeptide encoded by SEQ ID NO: 386	30 aa
SEQ ID NO: 388	NEF segment 12	90 nts
SEQ ID NO: 389	Polypeptide encoded by SEQ ID NO: 388	30 aa
SEQ ID NO: 390	NEF segment 13	78 nts
SEQ ID NO: 391	Polypeptide encoded by SEQ ID NO: 390	26 aa
SEQ ID NO: 392	HIV Cassette A1	5703 nts
SEQ ID NO: 393	Polypeptide encoded by SEQ ID NO: 392	1896 aa
SEQ ID NO: 394	HIV Cassette B1	5685 nts
SEQ ID NO: 395	Polypeptide encoded by SEQ ID NO: 394	1890 aa
SEQ ID NO: 396	HIV Cassette C1	5925 nts
SEQ ID NO: 397	Polypeptide encoded by SEQ ID NO: 396	1967 aa
SEQ ID NO: 398	HIV Cassette A2	5703 nts
SEQ ID NO: 399	Polypeptide encoded by SEQ ID NO: 398	1896 aa
SEQ ID NO: 400	HIV Cassette B2	5685 nts
SEQ ID NO: 401	Polypeptide encoded by SEQ ID NO: 400	1890 aa
SEQ ID NO: 402	HIV Cassette C2	5925 nts
SEQ ID NO: 403	Polypeptide encoded by SEQ ID NO: 402	1967 aa
SEQ ID NO: 404	HIV complete Savine	17244 nts
SEQ ID NO: 405	Polypeptide encoded by SEQ ID NO: 404	5747 aa
SEQ ID NO: 406	HepC1a consensus polyprotein sequence	3011 aa

- 34 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 407	HepC1a segment 1	90 nts
SEQ ID NO: 408	Polypeptide encoded by SEQ ID NO: 407	30 aa
SEQ ID NO: 409	HepC1a segment 2	90 nts
SEQ ID NO: 410	Polypeptide encoded by SEQ ID NO: 409	30 aa
SEQ ID NO: 411	HepC1a segment 3	90 nts
SEQ ID NO: 412	Polypeptide encoded by SEQ ID NO: 411	30 aa
SEQ ID NO: 413	HepC1a segment 4	90 nts
SEQ ID NO: 414	Polypeptide encoded by SEQ ID NO: 413	30 aa
SEQ ID NO: 415	HepC1a segment 5	90 nts
SEQ ID NO: 416	Polypeptide encoded by SEQ ID NO: 415	30 aa
SEQ ID NO: 417	HepC1a segment 6	90 nts
SEQ ID NO: 418	Polypeptide encoded by SEQ ID NO: 417	30 aa
SEQ ID NO: 419	HepC1a segment 7	90 nts
SEQ ID NO: 420	Polypeptide encoded by SEQ ID NO: 419	30 aa
SEQ ID NO: 421	HepC1a segment 8	90 nts
SEQ ID NO: 422	Polypeptide encoded by SEQ ID NO: 421	30 aa
SEQ ID NO: 423	HepC1a segment 9	90 nts
SEQ ID NO: 424	Polypeptide encoded by SEQ ID NO: 423	30 aa
SEQ ID NO: 425	HepC1a segment 10	90 nts
SEQ ID NO: 426	Polypeptide encoded by SEQ ID NO: 425	30 aa
SEQ ID NO: 427	HepC1a segment 11	90 nts
SEQ ID NO: 428	Polypeptide encoded by SEQ ID NO: 427	30 aa
SEQ ID NO: 429	HepC1a segment 12	90 nts
SEQ ID NO: 430	Polypeptide encoded by SEQ ID NO: 429	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 431	HepC1a segment 13	90 nts
SEQ ID NO: 432	Polypeptide encoded by SEQ ID NO: 431	30 aa
SEQ ID NO: 433	HepC1a segment 14	90 nts
SEQ ID NO: 434	Polypeptide encoded by SEQ ID NO: 433	30 aa
SEQ ID NO: 435	HepC1a segment 15	90 nts
SEQ ID NO: 436	Polypeptide encoded by SEQ ID NO: 435	30 aa
SEQ ID NO: 437	HepC1a segment 16	90 nts
SEQ ID NO: 438	Polypeptide encoded by SEQ ID NO: 437	30 aa
SEQ ID NO: 439	HepC1a segment 17	90 nts
SEQ ID NO: 440	Polypeptide encoded by SEQ ID NO: 439	30 aa
SEQ ID NO: 441	HepC1a segment 18	90 nts
SEQ ID NO: 442	Polypeptide encoded by SEQ ID NO: 441	30 aa
SEQ ID NO: 443	HepC1a segment 19	90 nts
SEQ ID NO: 444	Polypeptide encoded by SEQ ID NO: 443	30 aa
SEQ ID NO: 445	HepC1a segment 20	90 nts
SEQ ID NO: 446	Polypeptide encoded by SEQ ID NO: 445	30 aa
SEQ ID NO: 447	HepC1a segment 21	90 nts
SEQ ID NO: 448	Polypeptide encoded by SEQ ID NO: 447	30 aa
SEQ ID NO: 449	HepC1a segment 22	90 nts
SEQ ID NO: 450	Polypeptide encoded by SEQ ID NO: 449	30 aa
SEQ ID NO: 451	HepC1a segment 23	90 nts
SEQ ID NO: 452	Polypeptide encoded by SEQ ID NO: 451	30 aa
SEQ ID NO: 453	HepC1a segment 24	90 nts
SEQ ID NO: 454	Polypeptide encoded by SEQ ID NO: 453	30 aa

- 36 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 455	HepC1a segment 25	90 nts
SEQ ID NO: 456	Polypeptide encoded by SEQ ID NO: 455	30 aa
SEQ ID NO: 457	HepC1a segment 26	90 nts
SEQ ID NO: 458	Polypeptide encoded by SEQ ID NO: 457	30 aa
SEQ ID NO: 459	HepC1a segment 27	90 nts
SEQ ID NO: 460	Polypeptide encoded by SEQ ID NO: 459	30 aa
SEQ ID NO: 461	HepC1a segment 28	90 nts
SEQ ID NO: 462	Polypeptide encoded by SEQ ID NO: 461	30 aa
SEQ ID NO: 463	HepC1a segment 29	90 nts
SEQ ID NO: 464	Polypeptide encoded by SEQ ID NO: 463	30 aa
SEQ ID NO: 465	HepC1a segment 30	90 nts
SEQ ID NO: 466	Polypeptide encoded by SEQ ID NO: 465	30 aa
SEQ ID NO: 467	HepC1a segment 31	90 nts
SEQ ID NO: 468	Polypeptide encoded by SEQ ID NO: 467	30 aa
SEQ ID NO: 469	HepC1a segment 32	90 nts
SEQ ID NO: 470	Polypeptide encoded by SEQ ID NO: 469	30 aa
SEQ ID NO: 471	HepC1a segment 33	90 nts
SEQ ID NO: 472	Polypeptide encoded by SEQ ID NO: 471	30 aa
SEQ ID NO: 473	HepC1a segment 34	90 nts
SEQ ID NO: 474	Polypeptide encoded by SEQ ID NO: 473	30 aa
SEQ ID NO: 475	HepC1a segment 35	90 nts
SEQ ID NO: 476	Polypeptide encoded by SEQ ID NO: 475	30 aa
SEQ ID NO: 477	HepC1a segment 36	90 nts
SEQ ID NO: 478	Polypeptide encoded by SEQ ID NO: 477	30 aa

- 37 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 479	HepC1a segment 37	90 nts
SEQ ID NO: 480	Polypeptide encoded by SEQ ID NO: 479	30 aa
SEQ ID NO: 481	HepC1a segment 38	90 nts
SEQ ID NO: 482	Polypeptide encoded by SEQ ID NO: 481	30 aa
SEQ ID NO: 483	HepC1a segment 39	90 nts
SEQ ID NO: 484	Polypeptide encoded by SEQ ID NO: 483	30 aa
SEQ ID NO: 485	HepC1a segment 40	90 nts
SEQ ID NO: 486	Polypeptide encoded by SEQ ID NO: 485	30 aa
SEQ ID NO: 487	HepC1a segment 41	90 nts
SEQ ID NO: 488	Polypeptide encoded by SEQ ID NO: 487	30 aa
SEQ ID NO: 489	HepC1a segment 42	90 nts
SEQ ID NO: 490	Polypeptide encoded by SEQ ID NO: 489	30 aa
SEQ ID NO: 491	HepC1a segment 43	90 nts
SEQ ID NO: 492	Polypeptide encoded by SEQ ID NO: 491	30 aa
SEQ ID NO: 493	HepC1a segment 44	90 nts
SEQ ID NO: 494	Polypeptide encoded by SEQ ID NO: 493	30 aa
SEQ ID NO: 495	HepC1a segment 45	90 nts
SEQ ID NO: 496	Polypeptide encoded by SEQ ID NO: 495	30 aa
SEQ ID NO: 497	HepC1a segment 46	90 nts
SEQ ID NO: 498	Polypeptide encoded by SEQ ID NO: 497	30 aa
SEQ ID NO: 499	HepC1a segment 47	90 nts
SEQ ID NO: 500	Polypeptide encoded by SEQ ID NO: 499	30 aa
SEQ ID NO: 501	HepC1a segment 48	90 nts
SEQ ID NO: 502	Polypeptide encoded by SEQ ID NO: 501	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 503	HepC1a segment 49	90 nts
SEQ ID NO: 504	Polypeptide encoded by SEQ ID NO: 503	30 aa
SEQ ID NO: 505	HepC1a segment 50	90 nts
SEQ ID NO: 506	Polypeptide encoded by SEQ ID NO: 505	30 aa
SEQ ID NO: 507	HepC1a segment 51	90 nts
SEQ ID NO: 508	Polypeptide encoded by SEQ ID NO: 507	30 aa
SEQ ID NO: 509	HepC1a segment 52	90 nts
SEQ ID NO: 510	Polypeptide encoded by SEQ ID NO: 509	30 aa
SEQ ID NO: 511	HepC1a segment 53	90 nts
SEQ ID NO: 512	Polypeptide encoded by SEQ ID NO: 511	30 aa
SEQ ID NO: 513	HepC1a segment 54	90 nts
SEQ ID NO: 514	Polypeptide encoded by SEQ ID NO: 513	30 aa
SEQ ID NO: 515	HepC1a segment 55	90 nts
SEQ ID NO: 516	Polypeptide encoded by SEQ ID NO: 515	30 aa
SEQ ID NO: 517	HepC1a segment 56	90 nts
SEQ ID NO: 518	Polypeptide encoded by SEQ ID NO: 517	30 aa
SEQ ID NO: 519	HepC1a segment 57	90 nts
SEQ ID NO: 520	Polypeptide encoded by SEQ ID NO: 519	30 aa
SEQ ID NO: 521	HepC1a segment 58	90 nts
SEQ ID NO: 522	Polypeptide encoded by SEQ ID NO: 521	30 aa
SEQ ID NO: 523	HepC1a segment 59	90 nts
SEQ ID NO: 524	Polypeptide encoded by SEQ ID NO: 523	30 aa
SEQ ID NO: 525	HepC1a segment 60	90 nts
SEQ ID NO: 526	Polypeptide encoded by SEQ ID NO: 525	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 527	HepC1a segment 61	90 nts
SEQ ID NO: 528	Polypeptide encoded by SEQ ID NO: 527	30 aa
SEQ ID NO: 529	HepC1a segment 62	90 nts
SEQ ID NO: 530	Polypeptide encoded by SEQ ID NO: 529	30 aa
SEQ ID NO: 531	HepC1a segment 63	90 nts
SEQ ID NO: 532	Polypeptide encoded by SEQ ID NO: 531	30 aa
SEQ ID NO: 533	HepC1a segment 64	90 nts
SEQ ID NO: 534	Polypeptide encoded by SEQ ID NO: 533	30 aa
SEQ ID NO: 535	HepC1a segment 65	90 nts
SEQ ID NO: 536	Polypeptide encoded by SEQ ID NO: 535	30 aa
SEQ ID NO: 537	HepC1a segment 66	90 nts
SEQ ID NO: 538	Polypeptide encoded by SEQ ID NO: 537	30 aa
SEQ ID NO: 539	HepC1a segment 67	90 nts
SEQ ID NO: 540	Polypeptide encoded by SEQ ID NO: 539	30 aa
SEQ ID NO: 541	HepC1a segment 68	90 nts
SEQ ID NO: 542	Polypeptide encoded by SEQ ID NO: 541	30 aa
SEQ ID NO: 543	HepC1a segment 69	90 nts
SEQ ID NO: 544	Polypeptide encoded by SEQ ID NO: 543	30 aa
SEQ ID NO: 545	HepC1a segment 70	90 nts
SEQ ID NO: 546	Polypeptide encoded by SEQ ID NO: 545	30 aa
SEQ ID NO: 547	HepC1a segment 71	90 nts
SEQ ID NO: 548	Polypeptide encoded by SEQ ID NO: 547	30 aa
SEQ ID NO: 549	HepC1a segment 72	90 nts
SEQ ID NO: 550	Polypeptide encoded by SEQ ID NO: 549	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 551	HepC1a segment 73	90 nts
SEQ ID NO: 552	Polypeptide encoded by SEQ ID NO: 551	30 aa
SEQ ID NO: 553	HepC1a segment 74	90 nts
SEQ ID NO: 554	Polypeptide encoded by SEQ ID NO: 553	30 aa
SEQ ID NO: 555	HepC1a segment 75	90 nts
SEQ ID NO: 556	Polypeptide encoded by SEQ ID NO: 555	30 aa
SEQ ID NO: 557	HepC1a segment 76	90 nts
SEQ ID NO: 558	Polypeptide encoded by SEQ ID NO: 557	30 aa
SEQ ID NO: 559	HepC1a segment 77	90 nts
SEQ ID NO: 560	Polypeptide encoded by SEQ ID NO: 559	30 aa
SEQ ID NO: 561	HepC1a segment 78	90 nts
SEQ ID NO: 562	Polypeptide encoded by SEQ ID NO: 561	30 aa
SEQ ID NO: 563	HepC1a segment 79	90 nts
SEQ ID NO: 564	Polypeptide encoded by SEQ ID NO: 563	30 aa
SEQ ID NO: 565	HepC1a segment 80	90 nts
SEQ ID NO: 566	Polypeptide encoded by SEQ ID NO: 565	30 aa
SEQ ID NO: 567	HepC1a segment 81	90 nts
SEQ ID NO: 568	Polypeptide encoded by SEQ ID NO: 567	30 aa
SEQ ID NO: 569	HepC1a segment 82	90 nts
SEQ ID NO: 570	Polypeptide encoded by SEQ ID NO: 569	30 aa
SEQ ID NO: 571	HepC1a segment 83	90 nts
SEQ ID NO: 572	Polypeptide encoded by SEQ ID NO: 571	30 aa
SEQ ID NO: 573	HepC1a segment 84	90 nts
SEQ ID NO: 574	Polypeptide encoded by SEQ ID NO: 573	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 575	HepC1a segment 85	90 nts
SEQ ID NO: 576	Polypeptide encoded by SEQ ID NO: 575	30 aa
SEQ ID NO: 577	HepC1a segment 86	90 nts
SEQ ID NO: 578	Polypeptide encoded by SEQ ID NO: 577	30 aa
SEQ ID NO: 579	HepC1a segment 87	90 nts
SEQ ID NO: 580	Polypeptide encoded by SEQ ID NO: 579	30 aa
SEQ ID NO: 581	HepC1a segment 88	90 nts
SEQ ID NO: 582	Polypeptide encoded by SEQ ID NO: 581	30 aa
SEQ ID NO: 583	HepC1a segment 89	90 nts
SEQ ID NO: 584	Polypeptide encoded by SEQ ID NO: 583	30 aa
SEQ ID NO: 585	HepC1a segment 90	90 nts
SEQ ID NO: 586	Polypeptide encoded by SEQ ID NO: 585	30 aa
SEQ ID NO: 587	HepC1a segment 91	90 nts
SEQ ID NO: 588	Polypeptide encoded by SEQ ID NO: 587	30 aa
SEQ ID NO: 589	HepC1a segment 92	90 nts
SEQ ID NO: 590	Polypeptide encoded by SEQ ID NO: 589	30 aa
SEQ ID NO: 591	HepC1a segment 93	90 nts
SEQ ID NO: 592	Polypeptide encoded by SEQ ID NO: 591	30 aa
SEQ ID NO: 593	HepC1a segment 94	90 nts
SEQ ID NO: 594	Polypeptide encoded by SEQ ID NO: 593	30 aa
SEQ ID NO: 595	HepC1a segment 95	90 nts
SEQ ID NO: 596	Polypeptide encoded by SEQ ID NO: 595	30 aa
SEQ ID NO: 597	HepC1a segment 96	90 nts
SEQ ID NO: 598	Polypeptide encoded by SEQ ID NO: 597	30 aa

- 42 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 599	HepC1a segment 97	90 nts
SEQ ID NO: 600	Polypeptide encoded by SEQ ID NO: 599	30 aa
SEQ ID NO: 601	HepC1a segment 98	90 nts
SEQ ID NO: 602	Polypeptide encoded by SEQ ID NO: 601	30 aa
SEQ ID NO: 603	HepC1a segment 99	90 nts
SEQ ID NO: 604	Polypeptide encoded by SEQ ID NO: 603	30 aa
SEQ ID NO: 605	HepC1a segment 100	90 nts
SEQ ID NO: 606	Polypeptide encoded by SEQ ID NO: 605	30 aa
SEQ ID NO: 607	HepC1a segment 101	90 nts
SEQ ID NO: 608	Polypeptide encoded by SEQ ID NO: 607	30 aa
SEQ ID NO: 609	HepC1a segment 102	90 nts
SEQ ID NO: 610	Polypeptide encoded by SEQ ID NO: 609	30 aa
SEQ ID NO: 611	HepC1a segment 103	90 nts
SEQ ID NO: 612	Polypeptide encoded by SEQ ID NO: 611	30 aa
SEQ ID NO: 613	HepC1a segment 104	90 nts
SEQ ID NO: 614	Polypeptide encoded by SEQ ID NO: 613	30 aa
SEQ ID NO: 615	HepC1a segment 105	90 nts
SEQ ID NO: 616	Polypeptide encoded by SEQ ID NO: 615	30 aa
SEQ ID NO: 617	HepC1a segment 106	90 nts
SEQ ID NO: 618	Polypeptide encoded by SEQ ID NO: 617	30 aa
SEQ ID NO: 619	HepC1a segment 107	90 nts
SEQ ID NO: 620	Polypeptide encoded by SEQ ID NO: 619	30 aa
SEQ ID NO: 621	HepC1a segment 108	90 nts
SEQ ID NO: 622	Polypeptide encoded by SEQ ID NO: 621	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 623	HepC1a segment 109	90 nts
SEQ ID NO: 624	Polypeptide encoded by SEQ ID NO: 623	30 aa
SEQ ID NO: 625	HepC1a segment 110	90 nts
SEQ ID NO: 626	Polypeptide encoded by SEQ ID NO: 625	30 aa
SEQ ID NO: 627	HepC1a segment 111	90 nts
SEQ ID NO: 628	Polypeptide encoded by SEQ ID NO: 627	30 aa
SEQ ID NO: 629	HepC1a segment 112	90 nts
SEQ ID NO: 630	Polypeptide encoded by SEQ ID NO: 629	30 aa
SEQ ID NO: 631	HepC1a segment 113	90 nts
SEQ ID NO: 632	Polypeptide encoded by SEQ ID NO: 631	30 aa
SEQ ID NO: 633	HepC1a segment 114	90 nts
SEQ ID NO: 634	Polypeptide encoded by SEQ ID NO: 633	30 aa
SEQ ID NO: 635	HepC1a segment 115	90 nts
SEQ ID NO: 636	Polypeptide encoded by SEQ ID NO: 635	30 aa
SEQ ID NO: 637	HepC1a segment 116	90 nts
SEQ ID NO: 638	Polypeptide encoded by SEQ ID NO: 637	30 aa
SEQ ID NO: 639	HepC1a segment 117	90 nts
SEQ ID NO: 640	Polypeptide encoded by SEQ ID NO: 639	30 aa
SEQ ID NO: 641	HepC1a segment 118	90 nts
SEQ ID NO: 642	Polypeptide encoded by SEQ ID NO: 641	30 aa
SEQ ID NO: 643	HepC1a segment 119	90 nts
SEQ ID NO: 644	Polypeptide encoded by SEQ ID NO: 643	30 aa
SEQ ID NO: 645	HepC1a segment 120	90 nts
SEQ ID NO: 646	Polypeptide encoded by SEQ ID NO: 645	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 647	HepC1a segment 121	90 nts
SEQ ID NO: 648	Polypeptide encoded by SEQ ID NO: 647	30 aa
SEQ ID NO: 649	HepC1a segment 122	90 nts
SEQ ID NO: 650	Polypeptide encoded by SEQ ID NO: 649	30 aa
SEQ ID NO: 651	HepC1a segment 123	90 nts
SEQ ID NO: 652	Polypeptide encoded by SEQ ID NO: 651	30 aa
SEQ ID NO: 653	HepC1a segment 124	90 nts
SEQ ID NO: 654	Polypeptide encoded by SEQ ID NO: 653	30 aa
SEQ ID NO: 655	HepC1a segment 125	90 nts
SEQ ID NO: 656	Polypeptide encoded by SEQ ID NO: 655	30 aa
SEQ ID NO: 657	HepC1a segment 126	90 nts
SEQ ID NO: 658	Polypeptide encoded by SEQ ID NO: 657	30 aa
SEQ ID NO: 659	HepC1a segment 127	90 nts
SEQ ID NO: 660	Polypeptide encoded by SEQ ID NO: 659	30 aa
SEQ ID NO: 661	HepC1a segment 128	90 nts
SEQ ID NO: 662	Polypeptide encoded by SEQ ID NO: 661	30 aa
SEQ ID NO: 663	HepC1a segment 129	90 nts
SEQ ID NO: 664	Polypeptide encoded by SEQ ID NO: 663	30 aa
SEQ ID NO: 665	HepC1a segment 130	90 nts
SEQ ID NO: 666	Polypeptide encoded by SEQ ID NO: 665	30 aa
SEQ ID NO: 667	HepC1a segment 131	90 nts
SEQ ID NO: 668	Polypeptide encoded by SEQ ID NO: 667	30 aa
SEQ ID NO: 669	HepC1a segment 132	90 nts
SEQ ID NO: 670	Polypeptide encoded by SEQ ID NO: 669	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 671	HepC1a segment 133	90 nts
SEQ ID NO: 672	Polypeptide encoded by SEQ ID NO: 671	30 aa
SEQ ID NO: 673	HepC1a segment 134	90 nts
SEQ ID NO: 674	Polypeptide encoded by SEQ ID NO: 673	30 aa
SEQ ID NO: 675	HepC1a segment 135	90 nts
SEQ ID NO: 676	Polypeptide encoded by SEQ ID NO: 675	30 aa
SEQ ID NO: 677	HepC1a segment 136	90 nts
SEQ ID NO: 678	Polypeptide encoded by SEQ ID NO: 677	30 aa
SEQ ID NO: 679	HepC1a segment 137	90 nts
SEQ ID NO: 680	Polypeptide encoded by SEQ ID NO: 679	30 aa
SEQ ID NO: 681	HepC1a segment 138	90 nts
SEQ ID NO: 682	Polypeptide encoded by SEQ ID NO: 681	30 aa
SEQ ID NO: 683	HepC1a segment 139	90 nts
SEQ ID NO: 684	Polypeptide encoded by SEQ ID NO: 683	30 aa
SEQ ID NO: 685	HepC1a segment 140	90 nts
SEQ ID NO: 686	Polypeptide encoded by SEQ ID NO: 685	30 aa
SEQ ID NO: 687	HepC1a segment 141	90 nts
SEQ ID NO: 688	Polypeptide encoded by SEQ ID NO: 687	30 aa
SEQ ID NO: 689	HepC1a segment 142	90 nts
SEQ ID NO: 690	Polypeptide encoded by SEQ ID NO: 689	30 aa
SEQ ID NO: 691	HepC1a segment 143	90 nts
SEQ ID NO: 692	Polypeptide encoded by SEQ ID NO: 691	30 aa
SEQ ID NO: 693	HepC1a segment 144	90 nts
SEQ ID NO: 694	Polypeptide encoded by SEQ ID NO: 693	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 695	HepC1a segment 145	90 nts
SEQ ID NO: 696	Polypeptide encoded by SEQ ID NO: 695	30 aa
SEQ ID NO: 697	HepC1a segment 146	90 nts
SEQ ID NO: 698	Polypeptide encoded by SEQ ID NO: 697	30 aa
SEQ ID NO: 699	HepC1a segment 147	90 nts
SEQ ID NO: 700	Polypeptide encoded by SEQ ID NO: 699	30 aa
SEQ ID NO: 701	HepC1a segment 148	90 nts
SEQ ID NO: 702	Polypeptide encoded by SEQ ID NO: 701	30 aa
SEQ ID NO: 703	HepC1a segment 149	90 nts
SEQ ID NO: 704	Polypeptide encoded by SEQ ID NO: 703	30 aa
SEQ ID NO: 705	HepC1a segment 150	90 nts
SEQ ID NO: 706	Polypeptide encoded by SEQ ID NO: 705	30 aa
SEQ ID NO: 707	HepC1a segment 151	90 nts
SEQ ID NO: 708	Polypeptide encoded by SEQ ID NO: 707	30 aa
SEQ ID NO: 709	HepC1a segment 152	90 nts
SEQ ID NO: 710	Polypeptide encoded by SEQ ID NO: 709	30 aa
SEQ ID NO: 711	HepC1a segment 153	90 nts
SEQ ID NO: 712	Polypeptide encoded by SEQ ID NO: 711	30 aa
SEQ ID NO: 713	HepC1a segment 154	90 nts
SEQ ID NO: 714	Polypeptide encoded by SEQ ID NO: 713	30 aa
SEQ ID NO: 715	HepC1a segment 155	90 nts
SEQ ID NO: 716	Polypeptide encoded by SEQ ID NO: 715	30 aa
SEQ ID NO: 717	HepC1a segment 156	90 nts
SEQ ID NO: 718	Polypeptide encoded by SEQ ID NO: 717	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 719	HepC1a segment 157	90 nts
SEQ ID NO: 720	Polypeptide encoded by SEQ ID NO: 719	30 aa
SEQ ID NO: 721	HepC1a segment 158	90 nts
SEQ ID NO: 722	Polypeptide encoded by SEQ ID NO: 721	30 aa
SEQ ID NO: 723	HepC1a segment 159	90 nts
SEQ ID NO: 724	Polypeptide encoded by SEQ ID NO: 723	30 aa
SEQ ID NO: 725	HepC1a segment 160	90 nts
SEQ ID NO: 726	Polypeptide encoded by SEQ ID NO: 725	30 aa
SEQ ID NO: 727	HepC1a segment 161	90 nts
SEQ ID NO: 728	Polypeptide encoded by SEQ ID NO: 727	30 aa
SEQ ID NO: 729	HepC1a segment 162	90 nts
SEQ ID NO: 730	Polypeptide encoded by SEQ ID NO: 729	30 aa
SEQ ID NO: 731	HepC1a segment 163	90 nts
SEQ ID NO: 732	Polypeptide encoded by SEQ ID NO: 731	30 aa
SEQ ID NO: 733	HepC1a segment 164	90 nts
SEQ ID NO: 734	Polypeptide encoded by SEQ ID NO: 733	30 aa
SEQ ID NO: 735	HepC1a segment 165	90 nts
SEQ ID NO: 736	Polypeptide encoded by SEQ ID NO: 735	30 aa
SEQ ID NO: 737	HepC1a segment 166	90 nts
SEQ ID NO: 738	Polypeptide encoded by SEQ ID NO: 737	30 aa
SEQ ID NO: 739	HepC1a segment 167	90 nts
SEQ ID NO: 740	Polypeptide encoded by SEQ ID NO: 739	30 aa
SEQ ID NO: 741	HepC1a segment 168	90 nts
SEQ ID NO: 742	Polypeptide encoded by SEQ ID NO: 741	30 aa

- 48 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 743	HepC1a segment 169	90 nts
SEQ ID NO: 744	Polypeptide encoded by SEQ ID NO: 743	30 aa
SEQ ID NO: 745	HepC1a segment 170	90 nts
SEQ ID NO: 746	Polypeptide encoded by SEQ ID NO: 745	30 aa
SEQ ID NO: 747	HepC1a segment 171	90 nts
SEQ ID NO: 748	Polypeptide encoded by SEQ ID NO: 747	30 aa
SEQ ID NO: 749	HepC1a segment 172	90 nts
SEQ ID NO: 750	Polypeptide encoded by SEQ ID NO: 749	30 aa
SEQ ID NO: 751	HepC1a segment 173	90 nts
SEQ ID NO: 752	Polypeptide encoded by SEQ ID NO: 751	30 aa
SEQ ID NO: 753	HepC1a segment 174	90 nts
SEQ ID NO: 754	Polypeptide encoded by SEQ ID NO: 753	30 aa
SEQ ID NO: 755	HepC1a segment 175	90 nts
SEQ ID NO: 756	Polypeptide encoded by SEQ ID NO: 755	30 aa
SEQ ID NO: 757	HepC1a segment 176	90 nts
SEQ ID NO: 758	Polypeptide encoded by SEQ ID NO: 757	30 aa
SEQ ID NO: 759	HepC1a segment 177	90 nts
SEQ ID NO: 760	Polypeptide encoded by SEQ ID NO: 759	30 aa
SEQ ID NO: 761	HepC1a segment 178	90 nts
SEQ ID NO: 762	Polypeptide encoded by SEQ ID NO: 761	30 aa
SEQ ID NO: 763	HepC1a segment 179	90 nts
SEQ ID NO: 764	Polypeptide encoded by SEQ ID NO: 763	30 aa
SEQ ID NO: 765	HepC1a segment 180	90 nts
SEQ ID NO: 766	Polypeptide encoded by SEQ ID NO: 765	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 767	HepC1a segment 181	90 nts
SEQ ID NO: 768	Polypeptide encoded by SEQ ID NO: 767	30 aa
SEQ ID NO: 769	HepC1a segment 182	90 nts
SEQ ID NO: 770	Polypeptide encoded by SEQ ID NO: 769	30 aa
SEQ ID NO: 771	HepC1a segment 183	90 nts
SEQ ID NO: 772	Polypeptide encoded by SEQ ID NO: 771	30 aa
SEQ ID NO: 773	HepC1a segment 184	90 nts
SEQ ID NO: 774	Polypeptide encoded by SEQ ID NO: 773	30 aa
SEQ ID NO: 775	HepC1a segment 185	90 nts
SEQ ID NO: 776	Polypeptide encoded by SEQ ID NO: 775	30 aa
SEQ ID NO: 777	HepC1a segment 186	90 nts
SEQ ID NO: 778	Polypeptide encoded by SEQ ID NO: 777	30 aa
SEQ ID NO: 779	HepC1a segment 187	90 nts
SEQ ID NO: 780	Polypeptide encoded by SEQ ID NO: 779	30 aa
SEQ ID NO: 781	HepC1a segment 188	90 nts
SEQ ID NO: 782	Polypeptide encoded by SEQ ID NO: 781	30 aa
SEQ ID NO: 783	HepC1a segment 189	90 nts
SEQ ID NO: 784	Polypeptide encoded by SEQ ID NO: 783	30 aa
SEQ ID NO: 785	HepC1a segment 190	90 nts
SEQ ID NO: 786	Polypeptide encoded by SEQ ID NO: 785	30 aa
SEQ ID NO: 787	HepC1a segment 191	90 nts
SEQ ID NO: 788	Polypeptide encoded by SEQ ID NO: 787	30 aa
SEQ ID NO: 789	HepC1a segment 192	90 nts
SEQ ID NO: 790	Polypeptide encoded by SEQ ID NO: 789	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 791	HepC1a segment 193	90 nts
SEQ ID NO: 792	Polypeptide encoded by SEQ ID NO: 791	30 aa
SEQ ID NO: 793	HepC1a segment 194	90 nts
SEQ ID NO: 794	Polypeptide encoded by SEQ ID NO: 793	30 aa
SEQ ID NO: 795	HepC1a segment 195	90 nts
SEQ ID NO: 796	Polypeptide encoded by SEQ ID NO: 795	30 aa
SEQ ID NO: 797	HepC1a segment 196	90 nts
SEQ ID NO: 798	Polypeptide encoded by SEQ ID NO: 797	30 aa
SEQ ID NO: 799	HepC1a segment 197	90 nts
SEQ ID NO: 800	Polypeptide encoded by SEQ ID NO: 799	30 aa
SEQ ID NO: 801	HepC1a segment 198	90 nts
SEQ ID NO: 802	Polypeptide encoded by SEQ ID NO: 801	30 aa
SEQ ID NO: 803	HepC1a segment 199	90 nts
SEQ ID NO: 804	Polypeptide encoded by SEQ ID NO: 803	30 aa
SEQ ID NO: 805	HepC1a segment 200	90 nts
SEQ ID NO: 806	Polypeptide encoded by SEQ ID NO: 805	30 aa
SEQ ID NO: 807	HepC1a segment 201	45 nts
SEQ ID NO: 808	Polypeptide encoded by SEQ ID NO: 807	15 aa
SEQ ID NO: 809	HepC1a scrambled	17955 nts
SEQ ID NO: 810	Polypeptide encoded by SEQ ID NO: 809	5985 aa
SEQ ID NO: 811	HepC Cassette A	6065 nts
SEQ ID NO: 812	Polypeptide encoded by SEQ ID NO: 811	2011 aa
SEQ ID NO: 813	HepC Cassette B	6069 nts
SEQ ID NO: 814	Polypeptide encoded by SEQ ID NO: 813	2010 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 815	HepC Cassette C	6030 nts
SEQ ID NO: 816	Polypeptide encoded by SEQ ID NO: 815	1997 aa
SEQ ID NO: 817	gp100 consensus polypeptide	661 aa
SEQ ID NO: 818	MART consensus polypeptide	118 aa
SEQ ID NO: 819	TRP-1 consensus polypeptide	248 aa
SEQ ID NO: 820	Tyros consensus polypeptide	529 aa
SEQ ID NO: 821	TRP2 consensus polypeptide	519 aa
SEQ ID NO: 822	MC1R consensus polypeptide	317 aa
SEQ ID NO: 823	MUC1F consensus polypeptide	125 aa
SEQ ID NO: 824	MUC1R consensus polypeptide	312 aa
SEQ ID NO: 825	BAGE consensus polypeptide	43 aa
SEQ ID NO: 826	GAGE-1 consensus polypeptide	138 aa
SEQ ID NO: 827	gp100ln4 consensus polypeptide	51 aa
SEQ ID NO: 828	MAGE-1 consensus polypeptide	309 aa
SEQ ID NO: 829	MAGE-3 consensus polypeptide	314 aa
SEQ ID NO: 830	PRAME consensus polypeptide	509 aa
SEQ ID NO: 831	TRP2IN2 consensus polypeptide	54 aa
SEQ ID NO: 832	NYNSO1a consensus polypeptide	180 aa
SEQ ID NO: 833	NYNSO1b consensus polypeptide	58 aa
SEQ ID NO: 834	LAGE1 consensus polypeptide	180 aa
SEQ ID NO: 835	gp100 segment 1	90 nts
SEQ ID NO: 836	Polypeptide encoded by SEQ ID NO: 835	30 aa
SEQ ID NO: 837	gp100 segment 2	90 nts
SEQ ID NO: 838	Polypeptide encoded by SEQ ID NO: 837	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 839	gp100 segment 3	90 nts
SEQ ID NO: 840	Polypeptide encoded by SEQ ID NO: 839	30 aa
SEQ ID NO: 841	gp100 segment 4	90 nts
SEQ ID NO: 842	Polypeptide encoded by SEQ ID NO: 841	30 aa
SEQ ID NO: 843	gp100 segment 5	90 nts
SEQ ID NO: 844	Polypeptide encoded by SEQ ID NO: 843	30 aa
SEQ ID NO: 845	gp100 segment 6	90 nts
SEQ ID NO: 846	Polypeptide encoded by SEQ ID NO: 845	30 aa
SEQ ID NO: 847	gp100 segment 7	90 nts
SEQ ID NO: 848	Polypeptide encoded by SEQ ID NO: 847	30 aa
SEQ ID NO: 849	gp100 segment 8	90 nts
SEQ ID NO: 850	Polypeptide encoded by SEQ ID NO: 849	30 aa
SEQ ID NO: 851	gp100 segment 9	90 nts
SEQ ID NO: 852	Polypeptide encoded by SEQ ID NO: 851	30 aa
SEQ ID NO: 853	gp100 segment 10	90 nts
SEQ ID NO: 854	Polypeptide encoded by SEQ ID NO: 853	30 aa
SEQ ID NO: 855	gp100 segment 11	90 nts
SEQ ID NO: 856	Polypeptide encoded by SEQ ID NO: 855	30 aa
SEQ ID NO: 857	gp100 segment 12	90 nts
SEQ ID NO: 858	Polypeptide encoded by SEQ ID NO: 857	30 aa
SEQ ID NO: 859	gp100 segment 13	90 nts
SEQ ID NO: 860	Polypeptide encoded by SEQ ID NO: 859	30 aa
SEQ ID NO: 861	gp100 segment 14	90 nts
SEQ ID NO: 862	Polypeptide encoded by SEQ ID NO: 861	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 863	gp100 segment 15	90 nts
SEQ ID NO: 864	Polypeptide encoded by SEQ ID NO: 863	30 aa
SEQ ID NO: 865	gp100 segment 16	90 nts
SEQ ID NO: 866	Polypeptide encoded by SEQ ID NO: 865	30 aa
SEQ ID NO: 867	gp100 segment 17	90 nts
SEQ ID NO: 868	Polypeptide encoded by SEQ ID NO: 867	30 aa
SEQ ID NO: 869	gp100 segment 18	90 nts
SEQ ID NO: 870	Polypeptide encoded by SEQ ID NO: 869	30 aa
SEQ ID NO: 871	gp100 segment 19	90 nts
SEQ ID NO: 872	Polypeptide encoded by SEQ ID NO: 871	30 aa
SEQ ID NO: 873	gp100 segment 20	90 nts
SEQ ID NO: 874	Polypeptide encoded by SEQ ID NO: 873	30 aa
SEQ ID NO: 875	gp100 segment 21	90 nts
SEQ ID NO: 876	Polypeptide encoded by SEQ ID NO: 875	30 aa
SEQ ID NO: 877	gp100 segment 22	90 nts
SEQ ID NO: 878	Polypeptide encoded by SEQ ID NO: 877	30 aa
SEQ ID NO: 879	gp100 segment 23	90 nts
SEQ ID NO: 880	Polypeptide encoded by SEQ ID NO: 879	30 aa
SEQ ID NO: 881	gp100 segment 24	90 nts
SEQ ID NO: 882	Polypeptide encoded by SEQ ID NO: 881	30 aa
SEQ ID NO: 883	gp100 segment 25	90 nts
SEQ ID NO: 884	Polypeptide encoded by SEQ ID NO: 883	30 aa
SEQ ID NO: 885	gp100 segment 26	90 nts
SEQ ID NO: 886	Polypeptide encoded by SEQ ID NO: 885	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 887	gp100 segment 27	90 nts
SEQ ID NO: 888	Polypeptide encoded by SEQ ID NO: 887	30 aa
SEQ ID NO: 889	gp100 segment 28	90 nts
SEQ ID NO: 890	Polypeptide encoded by SEQ ID NO: 889	30 aa
SEQ ID NO: 891	gp100 segment 29	90 nts
SEQ ID NO: 892	Polypeptide encoded by SEQ ID NO: 891	30 aa
SEQ ID NO: 893	gp100 segment 30	90 nts
SEQ ID NO: 894	Polypeptide encoded by SEQ ID NO: 893	30 aa
SEQ ID NO: 895	gp100 segment 31	90 nts
SEQ ID NO: 896	Polypeptide encoded by SEQ ID NO: 895	30 aa
SEQ ID NO: 897	gp100 segment 32	90 nts
SEQ ID NO: 898	Polypeptide encoded by SEQ ID NO: 897	30 aa
SEQ ID NO: 899	gp100 segment 33	90 nts
SEQ ID NO: 900	Polypeptide encoded by SEQ ID NO: 899	30 aa
SEQ ID NO: 901	gp100 segment 34	90 nts
SEQ ID NO: 902	Polypeptide encoded by SEQ ID NO: 901	30 aa
SEQ ID NO: 903	gp100 segment 35	90 nts
SEQ ID NO: 904	Polypeptide encoded by SEQ ID NO: 903	30 aa
SEQ ID NO: 905	gp100 segment 36	90 nts
SEQ ID NO: 906	Polypeptide encoded by SEQ ID NO: 905	30 aa
SEQ ID NO: 907	gp100 segment 37	90 nts
SEQ ID NO: 908	Polypeptide encoded by SEQ ID NO: 907	30 aa
SEQ ID NO: 909	gp100 segment 38	90 nts
SEQ ID NO: 910	Polypeptide encoded by SEQ ID NO: 909	30 aa

- 55 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 911	gp100 segment 39	90 nts
SEQ ID NO: 912	Polypeptide encoded by SEQ ID NO: 911	30 aa
SEQ ID NO: 913	gp100 segment 40	90 nts
SEQ ID NO: 914	Polypeptide encoded by SEQ ID NO: 913	30 aa
SEQ ID NO: 915	gp100 segment 41	90 nts
SEQ ID NO: 916	Polypeptide encoded by SEQ ID NO: 915	30 aa
SEQ ID NO: 917	gp100 segment 42	90 nts
SEQ ID NO: 918	Polypeptide encoded by SEQ ID NO: 917	30 aa
SEQ ID NO: 919	gp100 segment 43	90 nts
SEQ ID NO: 920	Polypeptide encoded by SEQ ID NO: 919	30 aa
SEQ ID NO: 921	gp100 segment 44	60nts
SEQ ID NO: 922	Polypeptide encoded by SEQ ID NO: 921	20 aa
SEQ ID NO: 923	MART segment 1	90 nts
SEQ ID NO: 924	Polypeptide encoded by SEQ ID NO: 923	30 aa
SEQ ID NO: 925	MART segment 2	90 nts
SEQ ID NO: 926	Polypeptide encoded by SEQ ID NO: 925	30 aa
SEQ ID NO: 927	MART segment 3	90 nts
SEQ ID NO: 928	Polypeptide encoded by SEQ ID NO: 927	30 aa
SEQ ID NO: 929	MART segment 4	90 nts
SEQ ID NO: 930	Polypeptide encoded by SEQ ID NO: 929	30 aa
SEQ ID NO: 931	MART segment 5	90 nts
SEQ ID NO: 932	Polypeptide encoded by SEQ ID NO: 931	30 aa
SEQ ID NO: 933	MART segment 6	90 nts
SEQ ID NO: 934	Polypeptide encoded by SEQ ID NO: 933	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 935	MART segment 7	90 nts
SEQ ID NO: 936	Polypeptide encoded by SEQ ID NO: 935	30 aa
SEQ ID NO: 937	MART segment 8	51 nts
SEQ ID NO: 938	Polypeptide encoded by SEQ ID NO: 937	17 aa
SEQ ID NO: 939	trp-1 segment 1	90 nts
SEQ ID NO: 940	Polypeptide encoded by SEQ ID NO: 939	30 aa
SEQ ID NO: 941	trp-1 segment 2	90 nts
SEQ ID NO: 942	Polypeptide encoded by SEQ ID NO: 941	30 aa
SEQ ID NO: 943	trp-1 segment 3	90 nts
SEQ ID NO: 944	Polypeptide encoded by SEQ ID NO: 943	30 aa
SEQ ID NO: 945	trp-1 segment 4	90 nts
SEQ ID NO: 946	Polypeptide encoded by SEQ ID NO: 945	30 aa
SEQ ID NO: 947	trp-1 segment 5	90 nts
SEQ ID NO: 948	Polypeptide encoded by SEQ ID NO: 947	30 aa
SEQ ID NO: 949	trp-1 segment 6	90 nts
SEQ ID NO: 950	Polypeptide encoded by SEQ ID NO: 949	30 aa
SEQ ID NO: 951	trp-1 segment 7	90 nts
SEQ ID NO: 952	Polypeptide encoded by SEQ ID NO: 951	30 aa
SEQ ID NO: 953	trp-1 segment 8	90 nts
SEQ ID NO: 954	Polypeptide encoded by SEQ ID NO: 953	30 aa
SEQ ID NO: 955	trp-1 segment 9	90 nts
SEQ ID NO: 956	Polypeptide encoded by SEQ ID NO: 955	30 aa
SEQ ID NO: 957	trp-1 segment 10	90 nts
SEQ ID NO: 958	Polypeptide encoded by SEQ ID NO: 957	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 959	trp-1 segment 11	90 nts
SEQ ID NO: 960	Polypeptide encoded by SEQ ID NO: 959	30 aa
SEQ ID NO: 961	trp-1 segment 12	90 nts
SEQ ID NO: 962	Polypeptide encoded by SEQ ID NO: 961	30 aa
SEQ ID NO: 963	trp-1 segment 13	90 nts
SEQ ID NO: 964	Polypeptide encoded by SEQ ID NO: 963	30 aa
SEQ ID NO: 965	trp-1 segment 14	90 nts
SEQ ID NO: 966	Polypeptide encoded by SEQ ID NO: 965	30 aa
SEQ ID NO: 967	trp-1 segment 15	90 nts
SEQ ID NO: 968	Polypeptide encoded by SEQ ID NO: 967	30 aa
SEQ ID NO: 969	trp-1 segment 16	81 nts
SEQ ID NO: 970	Polypeptide encoded by SEQ ID NO: 969	27 aa
SEQ ID NO: 971	tyros segment 1	90 nts
SEQ ID NO: 972	Polypeptide encoded by SEQ ID NO: 971	30 aa
SEQ ID NO: 973	tyros segment 2	90 nts
SEQ ID NO: 974	Polypeptide encoded by SEQ ID NO: 973	30 aa
SEQ ID NO: 975	tyros segment 3	90 nts
SEQ ID NO: 976	Polypeptide encoded by SEQ ID NO: 975	30 aa
SEQ ID NO: 977	tyros segment 4	90 nts
SEQ ID NO: 978	Polypeptide encoded by SEQ ID NO: 977	30 aa
SEQ ID NO: 979	tyros segment 5	90 nts
SEQ ID NO: 980	Polypeptide encoded by SEQ ID NO: 979	30 aa
SEQ ID NO: 981	tyros segment 6	90 nts
SEQ ID NO: 982	Polypeptide encoded by SEQ ID NO: 981	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 983	tyros segment 7	90 nts
SEQ ID NO: 984	Polypeptide encoded by SEQ ID NO: 983	30 aa
SEQ ID NO: 985	tyros segment 8	90 nts
SEQ ID NO: 986	Polypeptide encoded by SEQ ID NO: 985	30 aa
SEQ ID NO: 987	tyros segment 9	90 nts
SEQ ID NO: 988	Polypeptide encoded by SEQ ID NO: 987	30 aa
SEQ ID NO: 989	tyros segment 10	90 nts
SEQ ID NO: 990	Polypeptide encoded by SEQ ID NO: 989	30 aa
SEQ ID NO: 991	tyros segment 11	90 nts
SEQ ID NO: 992	Polypeptide encoded by SEQ ID NO: 991	30 aa
SEQ ID NO: 993	tyros segment 12	90 nts
SEQ ID NO: 994	Polypeptide encoded by SEQ ID NO: 993	30 aa
SEQ ID NO: 995	tyros segment 13	90 nts
SEQ ID NO: 996	Polypeptide encoded by SEQ ID NO: 995	30 aa
SEQ ID NO: 997	tyros segment 14	90 nts
SEQ ID NO: 998	Polypeptide encoded by SEQ ID NO: 997	30 aa
SEQ ID NO: 999	tyros segment 15	90 nts
SEQ ID NO: 1000	Polypeptide encoded by SEQ ID NO: 999	30 aa
SEQ ID NO: 1001	tyros segment 16	90 nts
SEQ ID NO: 1002	Polypeptide encoded by SEQ ID NO: 1001	30 aa
SEQ ID NO: 1003	tyros segment 17	90 nts
SEQ ID NO: 1004	Polypeptide encoded by SEQ ID NO: 1003	30 aa
SEQ ID NO: 1005	tyros segment 18	90 nts
SEQ ID NO: 1006	Polypeptide encoded by SEQ ID NO: 1005	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1007	tyros segment 19	90 nts
SEQ ID NO: 1008	Polypeptide encoded by SEQ ID NO: 1007	30 aa
SEQ ID NO: 1009	tyros segment 20	90 nts
SEQ ID NO: 1010	Polypeptide encoded by SEQ ID NO: 1009	30 aa
SEQ ID NO: 1011	tyros segment 21	90 nts
SEQ ID NO: 1012	Polypeptide encoded by SEQ ID NO: 1011	30 aa
SEQ ID NO: 1013	tyros segment 22	90 nts
SEQ ID NO: 1014	Polypeptide encoded by SEQ ID NO: 1013	30 aa
SEQ ID NO: 1015	tyros segment 23	90 nts
SEQ ID NO: 1016	Polypeptide encoded by SEQ ID NO: 1015	30 aa
SEQ ID NO: 1017	tyros segment 24	90 nts
SEQ ID NO: 1018	Polypeptide encoded by SEQ ID NO: 1017	30 aa
SEQ ID NO: 1019	tyros segment 25	90 nts
SEQ ID NO: 1020	Polypeptide encoded by SEQ ID NO: 1019	30 aa
SEQ ID NO: 1021	tyros segment 26	90 nts
SEQ ID NO: 1022	Polypeptide encoded by SEQ ID NO: 1021	30 aa
SEQ ID NO: 1023	tyros segment 27	90 nts
SEQ ID NO: 1024	Polypeptide encoded by SEQ ID NO: 1023	30 aa
SEQ ID NO: 1025	tyros segment 28	90 nts
SEQ ID NO: 1026	Polypeptide encoded by SEQ ID NO: 1025	30 aa
SEQ ID NO: 1027	tyros segment 29	90 nts
SEQ ID NO: 1028	Polypeptide encoded by SEQ ID NO: 1027	30 aa
SEQ ID NO: 1029	tyros segment 30	90 nts
SEQ ID NO: 1030	Polypeptide encoded by SEQ ID NO: 1029	30 aa

- 60 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1031	tyros segment 31	90 nts
SEQ ID NO: 1032	Polypeptide encoded by SEQ ID NO: 1031	30 aa
SEQ ID NO: 1033	tyros segment 32	90 nts
SEQ ID NO: 1034	Polypeptide encoded by SEQ ID NO: 1033	30 aa
SEQ ID NO: 1035	tyros segment 33	90 nts
SEQ ID NO: 1036	Polypeptide encoded by SEQ ID NO: 1035	30 aa
SEQ ID NO: 1037	tyros segment 34	90 nts
SEQ ID NO: 1038	Polypeptide encoded by SEQ ID NO: 1037	30 aa
SEQ ID NO: 1039	tyros segment 35	69 nts
SEQ ID NO: 1040	Polypeptide encoded by SEQ ID NO: 1039	23 aa
SEQ ID NO: 1041	trp2 segment 1	90 nts
SEQ ID NO: 1042	Polypeptide encoded by SEQ ID NO: 1041	30 aa
SEQ ID NO: 1043	trp2 segment 2	90 nts
SEQ ID NO: 1044	Polypeptide encoded by SEQ ID NO: 1043	30 aa
SEQ ID NO: 1045	trp2 segment 3	90 nts
SEQ ID NO: 1046	Polypeptide encoded by SEQ ID NO: 1045	30 aa
SEQ ID NO: 1047	trp2 segment 4	90 nts
SEQ ID NO: 1048	Polypeptide encoded by SEQ ID NO: 1047	30 aa
SEQ ID NO: 1049	trp2 segment 5	90 nts
SEQ ID NO: 1050	Polypeptide encoded by SEQ ID NO: 1049	30 aa
SEQ ID NO: 1051	trp2 segment 6	90 nts
SEQ ID NO: 1052	Polypeptide encoded by SEQ ID NO: 1051	30 aa
SEQ ID NO: 1053	trp2 segment 7	90 nts
SEQ ID NO: 1054	Polypeptide encoded by SEQ ID NO: 1053	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1055	trp2 segment 8	90 nts
SEQ ID NO: 1056	Polypeptide encoded by SEQ ID NO: 1055	30 aa
SEQ ID NO: 1057	trp2 segment 9	90 nts
SEQ ID NO: 1058	Polypeptide encoded by SEQ ID NO: 1057	30 aa
SEQ ID NO: 1059	trp2 segment 10	90 nts
SEQ ID NO: 1060	Polypeptide encoded by SEQ ID NO: 1059	30 aa
SEQ ID NO: 1061	trp2 segment 11	90 nts
SEQ ID NO: 1062	Polypeptide encoded by SEQ ID NO: 1061	30 aa
SEQ ID NO: 1063	trp2 segment 12	90 nts
SEQ ID NO: 1064	Polypeptide encoded by SEQ ID NO: 1063	30 aa
SEQ ID NO: 1065	trp2 segment 13	90 nts
SEQ ID NO: 1066	Polypeptide encoded by SEQ ID NO: 1065	30 aa
SEQ ID NO: 1067	trp2 segment 14	90 nts
SEQ ID NO: 1068	Polypeptide encoded by SEQ ID NO: 1067	30 aa
SEQ ID NO: 1069	trp2 segment 15	90 nts
SEQ ID NO: 1070	Polypeptide encoded by SEQ ID NO: 1069	30 aa
SEQ ID NO: 1071	trp2 segment 16	90 nts
SEQ ID NO: 1072	Polypeptide encoded by SEQ ID NO: 1071	30 aa
SEQ ID NO: 1073	trp2 segment 17	90 nts
SEQ ID NO: 1074	Polypeptide encoded by SEQ ID NO: 1073	30 aa
SEQ ID NO: 1075	trp2 segment 18	90 nts
SEQ ID NO: 1076	Polypeptide encoded by SEQ ID NO: 1075	30 aa
SEQ ID NO: 1077	trp2 segment 19	90 nts
SEQ ID NO: 1078	Polypeptide encoded by SEQ ID NO: 1077	30 aa

- 62 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1079	trp2 segment 20	90 nts
SEQ ID NO: 1080	Polypeptide encoded by SEQ ID NO: 1079	30 aa
SEQ ID NO: 1081	trp2 segment 21	90 nts
SEQ ID NO: 1082	Polypeptide encoded by SEQ ID NO: 1081	30 aa
SEQ ID NO: 1083	trp2 segment 22	90 nts
SEQ ID NO: 1084	Polypeptide encoded by SEQ ID NO: 1083	30 aa
SEQ ID NO: 1085	trp2 segment 23	90 nts
SEQ ID NO: 1086	Polypeptide encoded by SEQ ID NO: 1085	30 aa
SEQ ID NO: 1087	trp2 segment 24	90 nts
SEQ ID NO: 1088	Polypeptide encoded by SEQ ID NO: 1087	30 aa
SEQ ID NO: 1089	trp2 segment 25	90 nts
SEQ ID NO: 1090	Polypeptide encoded by SEQ ID NO: 1089	30 aa
SEQ ID NO: 1091	trp2 segment 26	90 nts
SEQ ID NO: 1092	Polypeptide encoded by SEQ ID NO: 1091	30 aa
SEQ ID NO: 1093	trp2 segment 27	90 nts
SEQ ID NO: 1094	Polypeptide encoded by SEQ ID NO: 1093	30 aa
SEQ ID NO: 1095	trp2 segment 28	90 nts
SEQ ID NO: 1096	Polypeptide encoded by SEQ ID NO: 1095	30 aa
SEQ ID NO: 1097	trp2 segment 29	90 nts
SEQ ID NO: 1098	Polypeptide encoded by SEQ ID NO: 1097	30 aa
SEQ ID NO: 1099	trp2 segment 30	90 nts
SEQ ID NO: 1100	Polypeptide encoded by SEQ ID NO: 1099	30 aa
SEQ ID NO: 1101	trp2 segment 31	90 nts
SEQ ID NO: 1102	Polypeptide encoded by SEQ ID NO: 1101	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1103	trp2 segment 32	90 nts
SEQ ID NO: 1104	Polypeptide encoded by SEQ ID NO: 1103	30 aa
SEQ ID NO: 1105	trp2 segment 33	90 nts
SEQ ID NO: 1106	Polypeptide encoded by SEQ ID NO: 1105	30 aa
SEQ ID NO: 1107	trp2 segment 34	84 nts
SEQ ID NO: 1108	Polypeptide encoded by SEQ ID NO: 1107	28 aa
SEQ ID NO: 1109	MC1R segment 1	90 nts
SEQ ID NO: 1110	Polypeptide encoded by SEQ ID NO: 1109	30 aa
SEQ ID NO: 1111	MC1R segment 2	90 nts
SEQ ID NO: 1112	Polypeptide encoded by SEQ ID NO: 1111	30 aa
SEQ ID NO: 1113	MC1R segment 3	90 nts
SEQ ID NO: 1114	Polypeptide encoded by SEQ ID NO: 1113	30 aa
SEQ ID NO: 1115	MC1R segment 4	90 nts
SEQ ID NO: 1116	Polypeptide encoded by SEQ ID NO: 1115	30 aa
SEQ ID NO: 1117	MC1R segment 5	90 nts
SEQ ID NO: 1118	Polypeptide encoded by SEQ ID NO: 1117	30 aa
SEQ ID NO: 1119	MC1R segment 6	90 nts
SEQ ID NO: 1120	Polypeptide encoded by SEQ ID NO: 1119	30 aa
SEQ ID NO: 1121	MC1R segment 7	90 nts
SEQ ID NO: 1122	Polypeptide encoded by SEQ ID NO: 1121	30 aa
SEQ ID NO: 1123	MC1R segment 8	90 nts
SEQ ID NO: 1124	Polypeptide encoded by SEQ ID NO: 1123	30 aa
SEQ ID NO: 1125	MC1R segment 9	90 nts
SEQ ID NO: 1126	Polypeptide encoded by SEQ ID NO: 1125	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1127	MC1R segment 10	90 nts
SEQ ID NO: 1128	Polypeptide encoded by SEQ ID NO: 1127	30 aa
SEQ ID NO: 1129	MC1R segment 11	90 nts
SEQ ID NO: 1130	Polypeptide encoded by SEQ ID NO: 1129	30 aa
SEQ ID NO: 1131	MC1R segment 12	90 nts
SEQ ID NO: 1132	Polypeptide encoded by SEQ ID NO: 1131	30 aa
SEQ ID NO: 1133	MC1R segment 13	90 nts
SEQ ID NO: 1134	Polypeptide encoded by SEQ ID NO: 1133	30 aa
SEQ ID NO: 1135	MC1R segment 14	90 nts
SEQ ID NO: 1136	Polypeptide encoded by SEQ ID NO: 1135	30 aa
SEQ ID NO: 1137	MC1R segment 15	90 nts
SEQ ID NO: 1138	Polypeptide encoded by SEQ ID NO: 1137	30 aa
SEQ ID NO: 1139	MC1R segment 16	90 nts
SEQ ID NO: 1140	Polypeptide encoded by SEQ ID NO: 1139	30 aa
SEQ ID NO: 1141	MC1R segment 17	90 nts
SEQ ID NO: 1142	Polypeptide encoded by SEQ ID NO: 1141	30 aa
SEQ ID NO: 1143	MC1R segment 18	90 nts
SEQ ID NO: 1144	Polypeptide encoded by SEQ ID NO: 1143	30 aa
SEQ ID NO: 1145	MC1R segment 19	90 nts
SEQ ID NO: 1146	Polypeptide encoded by SEQ ID NO: 1145	30 aa
SEQ ID NO: 1147	MC1R segment 20	90 nts
SEQ ID NO: 1148	Polypeptide encoded by SEQ ID NO: 1147	30 aa
SEQ ID NO: 1149	MC1R segment 21	63 nts
SEQ ID NO: 1150	Polypeptide encoded by SEQ ID NO: 1149	21 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1151	MUC1F segment 1	90 nts
SEQ ID NO: 1152	Polypeptide encoded by SEQ ID NO: 1151	30 aa
SEQ ID NO: 1153	MUC1F segment 2	90 nts
SEQ ID NO: 1154	Polypeptide encoded by SEQ ID NO: 1153	30 aa
SEQ ID NO: 1155	MUC1F segment 3	90 nts
SEQ ID NO: 1156	Polypeptide encoded by SEQ ID NO: 1155	30 aa
SEQ ID NO: 1157	MUC1F segment 4	90 nts
SEQ ID NO: 1158	Polypeptide encoded by SEQ ID NO: 1157	30 aa
SEQ ID NO: 1159	MUC1F segment 5	90 nts
SEQ ID NO: 1160	Polypeptide encoded by SEQ ID NO: 1159	30 aa
SEQ ID NO: 1161	MUC1F segment 6	90 nts
SEQ ID NO: 1162	Polypeptide encoded by SEQ ID NO: 1161	30 aa
SEQ ID NO: 1163	MUC1F segment 7	90 nts
SEQ ID NO: 1164	Polypeptide encoded by SEQ ID NO: 1163	30 aa
SEQ ID NO: 1165	MUC1F segment 8	72 nts
SEQ ID NO: 1166	Polypeptide encoded by SEQ ID NO: 1165	24 aa
SEQ ID NO: 1167	MUC1R segment 1	90 nts
SEQ ID NO: 1168	Polypeptide encoded by SEQ ID NO: 1167	30 aa
SEQ ID NO: 1169	MUC1R segment 2	90 nts
SEQ ID NO: 1170	Polypeptide encoded by SEQ ID NO: 1169	30 aa
SEQ ID NO: 1171	MUC1R segment 3	90 nts
SEQ ID NO: 1172	Polypeptide encoded by SEQ ID NO: 1171	30 aa
SEQ ID NO: 1173	MUC1R segment 4	90 nts
SEQ ID NO: 1174	Polypeptide encoded by SEQ ID NO: 1173	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1175	MUC1R segment 5	90 nts
SEQ ID NO: 1176	Polypeptide encoded by SEQ ID NO: 1175	30 aa
SEQ ID NO: 1177	MUC1R segment 6	90 nts
SEQ ID NO: 1178	Polypeptide encoded by SEQ ID NO: 1177	30 aa
SEQ ID NO: 1179	MUC1R segment 7	90 nts
SEQ ID NO: 1180	Polypeptide encoded by SEQ ID NO: 1179	30 aa
SEQ ID NO: 1181	MUC1R segment 8	90 nts
SEQ ID NO: 1182	Polypeptide encoded by SEQ ID NO: 1181	30 aa
SEQ ID NO: 1183	MUC1R segment 9	90 nts
SEQ ID NO: 1184	Polypeptide encoded by SEQ ID NO: 1183	30 aa
SEQ ID NO: 1185	MUC1R segment 10	90 nts
SEQ ID NO: 1186	Polypeptide encoded by SEQ ID NO: 1185	30 aa
SEQ ID NO: 1187	MUC1R segment 11	90 nts
SEQ ID NO: 1188	Polypeptide encoded by SEQ ID NO: 1187	30 aa
SEQ ID NO: 1189	MUC1R segment 12	90 nts
SEQ ID NO: 1190	Polypeptide encoded by SEQ ID NO: 1189	30 aa
SEQ ID NO: 1191	MUC1R segment 13	90 nts
SEQ ID NO: 1192	Polypeptide encoded by SEQ ID NO: 1191	30 aa
SEQ ID NO: 1193	MUC1R segment 14	90 nts
SEQ ID NO: 1194	Polypeptide encoded by SEQ ID NO: 1193	30 aa
SEQ ID NO: 1195	MUC1R segment 15	90 nts
SEQ ID NO: 1196	Polypeptide encoded by SEQ ID NO: 1195	30 aa
SEQ ID NO: 1197	MUC1R segment 16	90 nts
SEQ ID NO: 1198	Polypeptide encoded by SEQ ID NO: 1197	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1199	MUC1R segment 17	90 nts
SEQ ID NO: 1200	Polypeptide encoded by SEQ ID NO: 1199	30 aa
SEQ ID NO: 1201	MUC1R segment 18	90 nts
SEQ ID NO: 1202	Polypeptide encoded by SEQ ID NO: 1201	30 aa
SEQ ID NO: 1203	MUC1R segment 19	90 nts
SEQ ID NO: 1204	Polypeptide encoded by SEQ ID NO: 1203	30 aa
SEQ ID NO: 1205	MUC1R segment 20	90 nts
SEQ ID NO: 1206	Polypeptide encoded by SEQ ID NO: 1205	30 aa
SEQ ID NO: 1207	MUC1R segment 21	48 nts
SEQ ID NO: 1208	Polypeptide encoded by SEQ ID NO: 1207	16 aa
SEQ ID NO: 1209	Differentiation Savine	16638 nts
SEQ ID NO: 1210	Polypeptide encoded by SEQ ID NO: 1209	5546 aa
SEQ ID NO: 1211	BAGE segment 1	90 nts
SEQ ID NO: 1212	Polypeptide encoded by SEQ ID NO: 1211	30 aa
SEQ ID NO: 1213	BAGE segment 2	90 nts
SEQ ID NO: 1214	Polypeptide encoded by SEQ ID NO: 1213	30 aa
SEQ ID NO: 1215	BAGE segment 3	51 nts
SEQ ID NO: 1216	Polypeptide encoded by SEQ ID NO: 1215	17 aa
SEQ ID NO: 1217	GAGE-1 segment 1	90 nts
SEQ ID NO: 1218	Polypeptide encoded by SEQ ID NO: 1217	30 aa
SEQ ID NO: 1219	GAGE-1 segment 2	90 nts
SEQ ID NO: 1220	Polypeptide encoded by SEQ ID NO: 1219	30 aa
SEQ ID NO: 1221	GAGE-1 segment 3	90 nts
SEQ ID NO: 1222	Polypeptide encoded by SEQ ID NO: 1221	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1223	GAGE-1 segment 4	90 nts
SEQ ID NO: 1224	Polypeptide encoded by SEQ ID NO: 1223	30 aa
SEQ ID NO: 1225	GAGE-1 segment 5	90 nts
SEQ ID NO: 1226	Polypeptide encoded by SEQ ID NO: 1225	30 aa
SEQ ID NO: 1227	GAGE-1 segment 6	90 nts
SEQ ID NO: 1228	Polypeptide encoded by SEQ ID NO: 1227	30 aa
SEQ ID NO: 1229	GAGE-1 segment 7	90 nts
SEQ ID NO: 1230	Polypeptide encoded by SEQ ID NO: 1229	30 aa
SEQ ID NO: 1231	GAGE-1 segment 8	90 nts
SEQ ID NO: 1232	Polypeptide encoded by SEQ ID NO: 1231	30 aa
SEQ ID NO: 1233	GAGE-1 segment 9	66 nts
SEQ ID NO: 1234	Polypeptide encoded by SEQ ID NO: 1233	22 aa
SEQ ID NO: 1235	gp100ln4 segment 1	90 nts
SEQ ID NO: 1236	Polypeptide encoded by SEQ ID NO: 1235	30 aa
SEQ ID NO: 1237	gp100ln4 segment 2	90 nts
SEQ ID NO: 1238	Polypeptide encoded by SEQ ID NO: 1237	30 aa
SEQ ID NO: 1239	gp100ln4 segment 3	75 nts
SEQ ID NO: 1240	Polypeptide encoded by SEQ ID NO: 1239	25 aa
SEQ ID NO: 1241	MAGE-1 segment 1	90 nts
SEQ ID NO: 1242	Polypeptide encoded by SEQ ID NO: 1241	30 aa
SEQ ID NO: 1243	MAGE-1 segment 2	90 nts
SEQ ID NO: 1244	Polypeptide encoded by SEQ ID NO: 1243	30 aa
SEQ ID NO: 1245	MAGE-1 segment 3	90 nts
SEQ ID NO: 1246	Polypeptide encoded by SEQ ID NO: 1245	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1247	MAGE-1 segment 4	90 nts
SEQ ID NO: 1248	Polypeptide encoded by SEQ ID NO: 1247	30 aa
SEQ ID NO: 1249	MAGE-1 segment 5	90 nts
SEQ ID NO: 1250	Polypeptide encoded by SEQ ID NO: 1249	30 aa
SEQ ID NO: 1251	MAGE-1 segment 6	90 nts
SEQ ID NO: 1252	Polypeptide encoded by SEQ ID NO: 1251	30 aa
SEQ ID NO: 1253	MAGE-1 segment 7	90 nts
SEQ ID NO: 1254	Polypeptide encoded by SEQ ID NO: 1253	30 aa
SEQ ID NO: 1255	MAGE-1 segment 8	90 nts
SEQ ID NO: 1256	Polypeptide encoded by SEQ ID NO: 1255	30 aa
SEQ ID NO: 1257	MAGE-1 segment 9	90 nts
SEQ ID NO: 1258	Polypeptide encoded by SEQ ID NO: 1257	30 aa
SEQ ID NO: 1259	MAGE-1 segment 10	90 nts
SEQ ID NO: 1260	Polypeptide encoded by SEQ ID NO: 1259	30 aa
SEQ ID NO: 1261	MAGE-1 segment 11	90 nts
SEQ ID NO: 1262	Polypeptide encoded by SEQ ID NO: 1261	30 aa
SEQ ID NO: 1263	MAGE-1 segment 12	90 nts
SEQ ID NO: 1264	Polypeptide encoded by SEQ ID NO: 1263	30 aa
SEQ ID NO: 1265	MAGE-1 segment 13	90 nts
SEQ ID NO: 1266	Polypeptide encoded by SEQ ID NO: 1265	30 aa
SEQ ID NO: 1267	MAGE-1 segment 14.	90 nts
SEQ ID NO: 1268	Polypeptide encoded by SEQ ID NO: 1267	30 aa
SEQ ID NO: 1269	MAGE-1 segment 15	90 nts
SEQ ID NO: 1270	Polypeptide encoded by SEQ ID NO: 1269	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1271	MAGE-1 segment 16	90 nts
SEQ ID NO: 1272	Polypeptide encoded by SEQ ID NO: 1271	30 aa
SEQ ID NO: 1273	MAGE-1 segment 17	90 nts
SEQ ID NO: 1274	Polypeptide encoded by SEQ ID NO: 1273	30 aa
SEQ ID NO: 1275	MAGE-1 segment 18	90 nts
SEQ ID NO: 1276	Polypeptide encoded by SEQ ID NO: 1275	30 aa
SEQ ID NO: 1277	MAGE-1 segment 19	90 nts
SEQ ID NO: 1278	Polypeptide encoded by SEQ ID NO: 1277	30 aa
SEQ ID NO: 1279	MAGE-1 segment 20	84 nts
SEQ ID NO: 1280	Polypeptide encoded by SEQ ID NO: 1279	28 aa
SEQ ID NO: 1281	MAGE-3 segment 1	90 nts
SEQ ID NO: 1282	Polypeptide encoded by SEQ ID NO: 1281	30 aa
SEQ ID NO: 1283	MAGE-3 segment 2	90 nts
SEQ ID NO: 1284	Polypeptide encoded by SEQ ID NO: 1283	30 aa
SEQ ID NO: 1285	MAGE-3 segment 3	90 nts
SEQ ID NO: 1286	Polypeptide encoded by SEQ ID NO: 1285	30 aa
SEQ ID NO: 1287	MAGE-3 segment 4	90 nts
SEQ ID NO: 1288	Polypeptide encoded by SEQ ID NO: 1287	30 aa
SEQ ID NO: 1289	MAGE-3 segment 5	90 nts
SEQ ID NO: 1290	Polypeptide encoded by SEQ ID NO: 1289	30 aa
SEQ ID NO: 1291	MAGE-3 segment 6	90 nts
SEQ ID NO: 1292	Polypeptide encoded by SEQ ID NO: 1291	30 aa
SEQ ID NO: 1293	MAGE-3 segment 7	90 nts
SEQ ID NO: 1294	Polypeptide encoded by SEQ ID NO: 1293	30 aa

<i>SEQUENCE ID NUMBER</i>	<i>SEQUENCE</i>	<i>LENGTH</i>
SEQ ID NO: 1295	MAGE-3 segment 8	90 nts
SEQ ID NO: 1296	Polypeptide encoded by SEQ ID NO: 1295	30 aa
SEQ ID NO: 1297	MAGE-3 segment 9	90 nts
SEQ ID NO: 1298	Polypeptide encoded by SEQ ID NO: 1297	30 aa
SEQ ID NO: 1299	MAGE-3 segment 10	90 nts
SEQ ID NO: 1300	Polypeptide encoded by SEQ ID NO: 1299	30 aa
SEQ ID NO: 1301	MAGE-3 segment 11	90 nts
SEQ ID NO: 1302	Polypeptide encoded by SEQ ID NO: 1301	30 aa
SEQ ID NO: 1303	MAGE-3 segment 12	90 nts
SEQ ID NO: 1304	Polypeptide encoded by SEQ ID NO: 1303	30 aa
SEQ ID NO: 1305	MAGE-3 segment 13	90 nts
SEQ ID NO: 1306	Polypeptide encoded by SEQ ID NO: 1305	30 aa
SEQ ID NO: 1307	MAGE-3 segment 14	90 nts
SEQ ID NO: 1308	Polypeptide encoded by SEQ ID NO: 1307	30 aa
SEQ ID NO: 1309	MAGE-3 segment 15	90 nts
SEQ ID NO: 1310	Polypeptide encoded by SEQ ID NO: 1309	30 aa
SEQ ID NO: 1311	MAGE-3 segment 16	90 nts
SEQ ID NO: 1312	Polypeptide encoded by SEQ ID NO: 1311	30 aa
SEQ ID NO: 1313	MAGE-3 segment 17	90 nts
SEQ ID NO: 1314	Polypeptide encoded by SEQ ID NO: 1313	30 aa
SEQ ID NO: 1315	MAGE-3 segment 18	90 nts
SEQ ID NO: 1316	Polypeptide encoded by SEQ ID NO: 1315	30 aa
SEQ ID NO: 1317	MAGE-3 segment 19	90 nts
SEQ ID NO: 1318	Polypeptide encoded by SEQ ID NO: 1317	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1319	MAGE-3 segment 20	90 nts
SEQ ID NO: 1320	Polypeptide encoded by SEQ ID NO: 1319	30 aa
SEQ ID NO: 1321	MAGE-3 segment 21	54 nts
SEQ ID NO: 1322	Polypeptide encoded by SEQ ID NO: 1321	18 aa
SEQ ID NO: 1323	PRAME segment 1	90 nts
SEQ ID NO: 1324	Polypeptide encoded by SEQ ID NO: 1323	30 aa
SEQ ID NO: 1325	PRAME segment 2	90 nts
SEQ ID NO: 1326	Polypeptide encoded by SEQ ID NO: 1325	30 aa
SEQ ID NO: 1327	PRAME segment 3	90 nts
SEQ ID NO: 1328	Polypeptide encoded by SEQ ID NO: 1327	30 aa
SEQ ID NO: 1329	PRAME segment 4	90 nts
SEQ ID NO: 1330	Polypeptide encoded by SEQ ID NO: 1329	30 aa
SEQ ID NO: 1331	PRAME segment 5	90 nts
SEQ ID NO: 1332	Polypeptide encoded by SEQ ID NO: 1331	30 aa
SEQ ID NO: 1333	PRAME segment 6	90 nts
SEQ ID NO: 1334	Polypeptide encoded by SEQ ID NO: 1333	30 aa
SEQ ID NO: 1335	PRAME segment 7	90 nts
SEQ ID NO: 1336	Polypeptide encoded by SEQ ID NO: 1335	30 aa
SEQ ID NO: 1337	PRAME segment 8	90 nts
SEQ ID NO: 1338	Polypeptide encoded by SEQ ID NO: 1337	30 aa
SEQ ID NO: 1339	PRAME segment 9	90 nts
SEQ ID NO: 1340	Polypeptide encoded by SEQ ID NO: 1339	30 aa
SEQ ID NO: 1341	PRAME segment 10	90 nts
SEQ ID NO: 1342	Polypeptide encoded by SEQ ID NO: 1341	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1343	PRAME segment 11	90 nts
SEQ ID NO: 1344	Polypeptide encoded by SEQ ID NO: 1343	30 aa
SEQ ID NO: 1345	PRAME segment 12	90 nts
SEQ ID NO: 1346	Polypeptide encoded by SEQ ID NO: 1345	30 aa
SEQ ID NO: 1347	PRAME segment 13	90 nts
SEQ ID NO: 1348	Polypeptide encoded by SEQ ID NO: 1347	30 aa
SEQ ID NO: 1349	PRAME segment 14	90 nts
SEQ ID NO: 1350	Polypeptide encoded by SEQ ID NO: 1349	30 aa
SEQ ID NO: 1351	PRAME segment 15	90 nts
SEQ ID NO: 1352	Polypeptide encoded by SEQ ID NO: 1351	30 aa
SEQ ID NO: 1353	PRAME segment 16	90 nts
SEQ ID NO: 1354	Polypeptide encoded by SEQ ID NO: 1353	30 aa
SEQ ID NO: 1355	PRAME segment 17	90 nts
SEQ ID NO: 1356	Polypeptide encoded by SEQ ID NO: 1355	30 aa
SEQ ID NO: 1357	PRAME segment 18	90 nts
SEQ ID NO: 1358	Polypeptide encoded by SEQ ID NO: 1357	30 aa
SEQ ID NO: 1359	PRAME segment 19	90 nts
SEQ ID NO: 1360	Polypeptide encoded by SEQ ID NO: 1359	30 aa
SEQ ID NO: 1361	PRAME segment 20	90 nts
SEQ ID NO: 1362	Polypeptide encoded by SEQ ID NO: 1361	30 aa
SEQ ID NO: 1363	PRAME segment 21	90 nts
SEQ ID NO: 1364	Polypeptide encoded by SEQ ID NO: 1363	30 aa
SEQ ID NO: 1365	PRAME segment 22	90 nts
SEQ ID NO: 1366	Polypeptide encoded by SEQ ID NO: 1365	30 aa

- 74 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1367	PRAME segment 23	90 nts
SEQ ID NO: 1368	Polypeptide encoded by SEQ ID NO: 1367	30 aa
SEQ ID NO: 1369	PRAME segment 24	90 nts
SEQ ID NO: 1370	Polypeptide encoded by SEQ ID NO: 1369	30 aa
SEQ ID NO: 1371	PRAME segment 25	90 nts
SEQ ID NO: 1372	Polypeptide encoded by SEQ ID NO: 1371	30 aa
SEQ ID NO: 1373	PRAME segment 26	90 nts
SEQ ID NO: 1374	Polypeptide encoded by SEQ ID NO: 1373	30 aa
SEQ ID NO: 1375	PRAME segment 27	90 nts
SEQ ID NO: 1376	Polypeptide encoded by SEQ ID NO: 1375	30 aa
SEQ ID NO: 1377	PRAME segment 28	90 nts
SEQ ID NO: 1378	Polypeptide encoded by SEQ ID NO: 1377	30 aa
SEQ ID NO: 1379	PRAME segment 29	90 nts
SEQ ID NO: 1380	Polypeptide encoded by SEQ ID NO: 1379	30 aa
SEQ ID NO: 1381	PRAME segment 30	90 nts
SEQ ID NO: 1382	Polypeptide encoded by SEQ ID NO: 1381	30 aa
SEQ ID NO: 1383	PRAME segment 31	90 nts
SEQ ID NO: 1384	Polypeptide encoded by SEQ ID NO: 1383	30 aa
SEQ ID NO: 1385	PRAME segment 32	90 nts
SEQ ID NO: 1386	Polypeptide encoded by SEQ ID NO: 1385	30 aa
SEQ ID NO: 1387	PRAME segment 33	90 nts
SEQ ID NO: 1388	Polypeptide encoded by SEQ ID NO: 1387	30 aa
SEQ ID NO: 1389	PRAME segment 34	54 nts
SEQ ID NO: 1390	Polypeptide encoded by SEQ ID NO: 1389	18 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1391	TRP2IN2 segment 1	90 nts
SEQ ID NO: 1392	Polypeptide encoded by SEQ ID NO: 1391	30 aa
SEQ ID NO: 1393	TRP2IN2 segment 2	90 nts
SEQ ID NO: 1394	Polypeptide encoded by SEQ ID NO: 1393	30 aa
SEQ ID NO: 1395	TRP2IN2 segment 3	84 nts
SEQ ID NO: 1396	Polypeptide encoded by SEQ ID NO: 1395	28 aa
SEQ ID NO: 1397	NYNSO1a segment 1	90 nts
SEQ ID NO: 1398	Polypeptide encoded by SEQ ID NO: 1397	30 aa
SEQ ID NO: 1399	NYNSO1a segment 2	90 nts
SEQ ID NO: 1400	Polypeptide encoded by SEQ ID NO: 1399	30 aa
SEQ ID NO: 1401	NYNSO1a segment 3	90 nts
SEQ ID NO: 1402	Polypeptide encoded by SEQ ID NO: 1401	30 aa
SEQ ID NO: 1403	NYNSO1a segment 4	90 nts
SEQ ID NO: 1404	Polypeptide encoded by SEQ ID NO: 1403	30 aa
SEQ ID NO: 1405	NYNSO1a segment 5	90 nts
SEQ ID NO: 1406	Polypeptide encoded by SEQ ID NO: 1405	30 aa
SEQ ID NO: 1407	NYNSO1a segment 6	90 nts
SEQ ID NO: 1408	Polypeptide encoded by SEQ ID NO: 1407	30 aa
SEQ ID NO: 1409	NYNSO1a segment 7	90 nts
SEQ ID NO: 1410	Polypeptide encoded by SEQ ID NO: 1409	30 aa
SEQ ID NO: 1411	NYNSO1a segment 8	90 nts
SEQ ID NO: 1412	Polypeptide encoded by SEQ ID NO: 1411	30 aa
SEQ ID NO: 1413	NYNSO1a segment 9	90 nts
SEQ ID NO: 1414	Polypeptide encoded by SEQ ID NO: 1413	30 aa

- 76 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1415	NYNSO1a segment 10	90 nts
SEQ ID NO: 1416	Polypeptide encoded by SEQ ID NO: 1415	30 aa
SEQ ID NO: 1417	NYNSO1a segment 11	90 nts
SEQ ID NO: 1418	Polypeptide encoded by SEQ ID NO: 1417	30 aa
SEQ ID NO: 1419	NYNSO1a segment 12	57 nts
SEQ ID NO: 1420	Polypeptide encoded by SEQ ID NO: 1419	19 aa
SEQ ID NO: 1421	NYNSO1b segment 1	90 nts
SEQ ID NO: 1422	Polypeptide encoded by SEQ ID NO: 1421	30 aa
SEQ ID NO: 1423	NYNSO1b segment 2	90 nts
SEQ ID NO: 1424	Polypeptide encoded by SEQ ID NO: 1423	30 aa
SEQ ID NO: 1425	NYNSO1b segment 3	90 nts
SEQ ID NO: 1426	Polypeptide encoded by SEQ ID NO: 1425	30 aa
SEQ ID NO: 1427	NYNSO1b segment 4	51 nts
SEQ ID NO: 1428	Polypeptide encoded by SEQ ID NO: 1427	
SEQ ID NO: 1429	LAGE1 segment 1	90 nts
SEQ ID NO: 1430	Polypeptide encoded by SEQ ID NO: 1429	30 aa
SEQ ID NO: 1431	LAGE1 segment 2	90 nts
SEQ ID NO: 1432	Polypeptide encoded by SEQ ID NO: 1431	30 aa
SEQ ID NO: 1433	LAGE1 segment 3	90 nts
SEQ ID NO: 1434	Polypeptide encoded by SEQ ID NO: 1433	30 aa
SEQ ID NO: 1435	LAGE1 segment 4	90 nts
SEQ ID NO: 1436	Polypeptide encoded by SEQ ID NO: 1435	30 aa
SEQ ID NO: 1437	LAGE1 segment 5	90 nts
SEQ ID NO: 1438	Polypeptide encoded by SEQ ID NO: 1437	30 aa

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1439	LAGE1 segment 6	90 nts
SEQ ID NO: 1440	Polypeptide encoded by SEQ ID NO: 1439	30 aa
SEQ ID NO: 1441	LAGE1 segment 7	90 nts
SEQ ID NO: 1442	Polypeptide encoded by SEQ ID NO: 1441	30 aa
SEQ ID NO: 1443	LAGE1 segment 8	90 nts
SEQ ID NO: 1444	Polypeptide encoded by SEQ ID NO: 1443	30 aa
SEQ ID NO: 1445	LAGE1 segment 9	90 nts
SEQ ID NO: 1446	Polypeptide encoded by SEQ ID NO: 1445	30 aa
SEQ ID NO: 1447	LAGE1 segment 10	90 nts
SEQ ID NO: 1448	Polypeptide encoded by SEQ ID NO: 1447	30 aa
SEQ ID NO: 1449	LAGE1 segment 11	90 nts
SEQ ID NO: 1450	Polypeptide encoded by SEQ ID NO: 1449	30 aa
SEQ ID NO: 1451	LAGE1 segment 12	57 nts
SEQ ID NO: 1452	Polypeptide encoded by SEQ ID NO: 1451	19 aa
SEQ ID NO: 1453	Melanoma cancer specific Savine	10623 nts
SEQ ID NO: 1454	Polypeptide encoded by SEQ ID NO: 1453	3541 aa
SEQ ID NO: 1455	Figure 16 A1S1 99mer	99 nts
SEQ ID NO: 1456	Figure 16 A1S2 100mer	100 nts
SEQ ID NO: 1457	Figure 16 A1S3 100mer	100 nts
SEQ ID NO: 1458	Figure 16 A1S4 100mer	100 nts
SEQ ID NO: 1459	Figure 16 A1S5 100mer	100 nts
SEQ ID NO: 1460	Figure 16 A1S6 99mer	99 nts
SEQ ID NO: 1461	Figure 16 A1S7 97mer	99 nts
SEQ ID NO: 1462	Figure 16 A1S8 100mer	100 nts

- 78 -

SEQUENCE ID NUMBER	SEQUENCE	LENGTH
SEQ ID NO: 1463	Figure 16 A1S9 100mer	100 nts
SEQ ID NO: 1464	Figure 16 A1S10 75mer	76 nts
SEQ ID NO: 1465	Figure 16 A1F 20mer	20 nts
SEQ ID NO: 1466	Figure 16 A1R 20mer	20 nts
SEQ ID NO: 1467	Amino acid sequence of immunostimulatory domain of an invasin protein from <i>Yersinia</i> spp.	16 aa

DETAILED DESCRIPTION OF THE INVENTION

1. Definitions

The articles "*a*" and "*an*" are used herein to refer to one or to more than one (*i.e.*, to at least one) of the grammatical object of the article. By way of example, "an element"
5 means one element or more than one element.

As used herein, the term "*about*" refers to a quantity, level, value, dimension, size, or amount that varies by as much as 30%, preferably by as much as 20%, and more preferably by as much as 10% to a reference quantity, level, value, dimension, size, or amount.

10 By "*antigen-binding molecule*" is meant a molecule that has binding affinity for a target antigen. It will be understood that this term extends to immunoglobulins, immunoglobulin fragments and non-immunoglobulin derived protein frameworks that exhibit antigen-binding activity.

The term "*clade*" as used herein refers to a hypothetical species of an organism
15 and its descendants or a monophyletic group of organisms. Clades carry a definition, based on ancestry, and a diagnosis, based on synapomorphies. It should be noted that diagnoses of clades could change while definitions do not.

Throughout this specification, unless the context requires otherwise, the words "*comprise*", "*comprises*" and "*comprising*" will be understood to imply the inclusion of a
20 stated step or element or group of steps or elements but not the exclusion of any other step or element or group of steps or elements.

By "*expression vector*" is meant any autonomous genetic element capable of directing the synthesis of a protein encoded by the vector. Such expression vectors are known by practitioners in the art.

25 As used herein, the term "*function*" refers to a biological, enzymatic, or therapeutic function.

"Homology" refers to the percentage number of amino acids that are identical or constitute conservative substitutions as defined in Table B *infra*. Homology may be determined using sequence comparison programs such as GAP (Deveraux *et al.* 1984, *Nucleic Acids Research* 12, 387-395). In this way, sequences of a similar or substantially different length to those cited herein might be compared by insertion of gaps into the alignment, such gaps being determined, for example, by the comparison algorithm used by GAP.

To enhance an immune response ("immunoenhancement"), as is well-known in the art, means to increase an animal's capacity to respond to foreign or disease-specific antigens (e.g., cancer antigens) *i.e.*, those cells primed to attack such antigens are increased in number, activity, and ability to detect and destroy the those antigens. Strength of immune response is measured by standard tests including: direct measurement of peripheral blood lymphocytes by means known to the art; natural killer cell cytotoxicity assays (see, e.g., Provinciali M. *et al* (1992, *J. Immunol. Meth.* 155: 19-24), cell proliferation assays (see, e.g., Vollenweider, I. and Groseurth, P. J. (1992, *J. Immunol. Meth.* 149: 133-135), immunoassays of immune cells and subsets (see, e.g., Loeffler, D. A., *et al.* (1992, *Cytom.* 13: 169-174); Rivoltini, L., *et al.* (1992, *Can. Immunol. Immunother.* 34: 241-251); or skin tests for cell-mediated immunity (see, e.g., Chang, A. E. *et al* (1993, *Cancer Res.* 53: 1043-1050). Any statistically significant increase in strength of immune response as measured by the foregoing tests is considered "enhanced immune response" "immunoenhancement" or "immunopotentialiation" as used herein. Enhanced immune response is also indicated by physical manifestations such as fever and inflammation, as well as healing of systemic and local infections, and reduction of symptoms in disease, *i.e.*, decrease in tumour size, alleviation of symptoms of a disease or condition including, but not restricted to, leprosy, tuberculosis, malaria, naphthous ulcers, herpetic and papillomatous warts, gingivitis, arteriosclerosis, the concomitants of AIDS such as Kaposi's sarcoma, bronchial infections, and the like. Such physical manifestations also define "enhanced immune response" "immunoenhancement" or "immunopotentialiation" as used herein.

Reference herein to "immuno-interactive" includes reference to any interaction, reaction, or other form of association between molecules and in particular where one of the molecules is, or mimics, a component of the immune system.

- 81 -

By "*isolated*" is meant material that is substantially or essentially free from components that normally accompany it in its native state.

By "*modulating*" is meant increasing or decreasing, either directly or indirectly, an immune response against a target antigen of a member selected from the group
5 consisting of a cancer and an organism, preferably a pathogenic organism.

By "*natural gene*" is meant a gene that naturally encodes a protein.

The term "*natural polypeptide*" as used herein refers to a polypeptide that exists in nature.

By "*obtained from*" is meant that a sample such as, for example, a polynucleotide
10 extract or polypeptide extract is isolated from, or derived from, a particular source of the host. For example, the extract can be obtained from a tissue or a biological fluid isolated directly from the host.

The term "*oligonucleotide*" as used herein refers to a polymer composed of a multiplicity of nucleotide residues (deoxyribonucleotides or ribonucleotides, or related
15 structural variants or synthetic analogues thereof) linked via phosphodiester bonds (or related structural variants or synthetic analogues thereof). Thus, while the term "*oligonucleotide*" typically refers to a nucleotide polymer in which the nucleotide residues and linkages between them are naturally occurring, it will be understood that the term also includes within its scope various analogues including, but not restricted to, peptide nucleic
20 acids (PNAs), phosphoramidates, phosphorothioates, methyl phosphonates, 2-O-methyl ribonucleic acids, and the like. The exact size of the molecule can vary depending on the particular application. An oligonucleotide is typically rather short in length, generally from about 10 to 30 nucleotide residues, but the term can refer to molecules of any length, although the term "*polynucleotide*" or "*nucleic acid*" is typically used for large
25 oligonucleotides.

By "*operably linked*" is meant that transcriptional and translational regulatory polynucleotides are positioned relative to a polypeptide-encoding polynucleotide in such a manner that the polynucleotide is transcribed and the polypeptide is translated.

- 82 -

The term "*parent polypeptide*" as used herein typically refers to a polypeptide encoded by a natural gene. However, it is possible that the parent polypeptide corresponds to a protein that is not naturally-occurring but has been engineered using recombinant techniques. In this instance, a polynucleotide encoding the parent polypeptide may
5 comprise different but synonymous codons relative to a natural gene encoding the same polypeptide. Alternatively, the parent polypeptide may not correspond to a natural polypeptide sequence. For example, the parent polypeptide may comprise one or more consensus sequences common to a plurality of polypeptides.

The term "*patient*" refers to patients of human or other mammal and includes any
10 individual it is desired to examine or treat using the methods of the invention. However, it will be understood that "*patient*" does not imply that symptoms are present. Suitable mammals that fall within the scope of the invention include, but are not restricted to, primates, livestock animals (*e.g.*, sheep, cows, horses, donkeys, pigs), laboratory test animals (*e.g.*, rabbits, mice, rats, guinea pigs, hamsters), companion animals (*e.g.*, cats,
15 dogs) and captive wild animals (*e.g.*, foxes, deer, dingoes).

By "*pharmaceutically-acceptable carrier*" is meant a solid or liquid filler, diluent or encapsulating substance that can be safely used in topical or systemic administration to a mammal.

"*Polypeptide*", "*peptide*" and "*protein*" are used interchangeably herein to refer to
20 a polymer of amino acid residues and to variants and synthetic analogues of the same. Thus, these terms apply to amino acid polymers in which one or more amino acid residues is a synthetic non-naturally occurring amino acid, such as a chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally-occurring amino acid polymers.

25 The term "*polynucleotide*" or "*nucleic acid*" as used herein designates mRNA, RNA, cRNA, cDNA or DNA. The term typically refers to oligonucleotides greater than 30 nucleotide residues in length.

By "*primer*" is meant an oligonucleotide which, when paired with a strand of DNA, is capable of initiating the synthesis of a primer extension product in the presence of
30 a suitable polymerising agent. The primer is preferably single-stranded for maximum

efficiency in amplification but can alternatively be double-stranded. A primer must be sufficiently long to prime the synthesis of extension products in the presence of the polymerisation agent. The length of the primer depends on many factors, including application, temperature to be employed, template reaction conditions, other reagents, and source of primers. For example, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 15 to 35 or more nucleotide residues, although it can contain fewer nucleotide residues. Primers can be large polynucleotides, such as from about 35 nucleotides to several kilobases or more. Primers can be selected to be "substantially complementary" to the sequence on the template to which it is designed to hybridise and serve as a site for the initiation of synthesis. By "substantially complementary", it is meant that the primer is sufficiently complementary to hybridise with a target polynucleotide. Preferably, the primer contains no mismatches with the template to which it is designed to hybridise but this is not essential. For example, non-complementary nucleotide residues can be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the template. Alternatively, non-complementary nucleotide residues or a stretch of non-complementary nucleotide residues can be interspersed into a primer, provided that the primer sequence has sufficient complementarity with the sequence of the template to hybridise therewith and thereby form a template for synthesis of the extension product of the primer.

"Probe" refers to a molecule that binds to a specific sequence or sub-sequence or other moiety of another molecule. Unless otherwise indicated, the term "probe" typically refers to a polynucleotide probe that binds to another polynucleotide, often called the "target polynucleotide", through complementary base pairing. Probes can bind target polynucleotides lacking complete sequence complementarity with the probe, depending on the stringency of the hybridisation conditions. Probes can be labelled directly or indirectly.

By "*recombinant polypeptide*" is meant a polypeptide made using recombinant techniques, *i.e.*, through the expression of a recombinant or synthetic polynucleotide.

Terms used to describe sequence relationships between two or more polynucleotides or polypeptides include "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity" and "substantial identity". A "reference sequence" is at least 12 but frequently 15 to 18 and often at least 25 monomer

- 84 -

units, inclusive of nucleotides and amino acid residues, in length. Because two polynucleotides may each comprise (1) a sequence (*i.e.*, only a portion of the complete polynucleotide sequence) that is similar between the two polynucleotides, and (2) a sequence that is divergent between the two polynucleotides, sequence comparisons between two (or more) polynucleotides are typically performed by comparing sequences of the two polynucleotides over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window" refers to a conceptual segment of at least 50 contiguous positions, usually about 50 to about 100, more usually about 100 to about 150 in which a sequence is compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. The comparison window may comprise additions or deletions (*i.e.*, gaps) of about 20% or less as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. Optimal alignment of sequences for aligning a comparison window may be conducted by computerised implementations of algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Drive Madison, WI, USA) or by inspection and the best alignment (*i.e.*, resulting in the highest percentage homology over the comparison window) generated by any of the various methods selected. Reference also may be made to the BLAST family of programs as for example disclosed by Altschul *et al.*, 1997, *Nucl. Acids Res.* 25:3389. A detailed discussion of sequence analysis can be found in Unit 19.3 of Ausubel *et al.*, "Current Protocols in Molecular Biology", John Wiley & Sons Inc, 1994-1998, Chapter 15.

The term "*sequence identity*" as used herein refers to the extent that sequences are identical on a nucleotide-by-nucleotide basis or an amino acid-by-amino acid basis over a window of comparison. Thus, a "*percentage of sequence identity*" is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, I) or the identical amino acid residue (*e.g.*, Ala, Pro, Ser, Thr, Gly, Val, Leu, Ile, Phe, Tyr, Trp, Lys, Arg, His, Asp, Glu, Asn, Gln, Cys and Met) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. For the purposes of the present

- 85 -

invention, "*sequence identity*" will be understood to mean the "match percentage" calculated by the DNASIS computer program (Version 2.5 for windows; available from Hitachi Software engineering Co., Ltd., South San Francisco, California, USA) using standard defaults as used in the reference manual accompanying the software.

5 The term "*synthetic polynucleotide*" as used herein refers to a polynucleotide formed *in vitro* by the manipulation of a polynucleotide into a form not normally found in nature. For example, the synthetic polynucleotide can be in the form of an expression vector. Generally, such expression vectors include transcriptional and translational regulatory polynucleotide operably linked to the polynucleotide.

10 The term "*synonymous codon*" as used herein refers to a codon having a different nucleotide sequence than another codon but encoding the same amino acid as that other codon.

By "*translational efficiency*" is meant the efficiency of a cell's protein synthesis machinery to incorporate the amino acid encoded by a codon into a nascent polypeptide chain. This efficiency can be evidenced, for example, by the rate at which the cell is able to synthesise the polypeptide from an RNA template comprising the codon, or by the amount of the polypeptide synthesised from such a template.

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By "*vector*" is meant a polynucleotide molecule, preferably a DNA molecule derived, for example, from a plasmid, bacteriophage, yeast or virus, into which a polynucleotide can be inserted or cloned. A vector preferably contains one or more unique restriction sites and can be capable of autonomous replication in a defined host cell including a target cell or tissue or a progenitor cell or tissue thereof, or be integrable with the genome of the defined host such that the cloned sequence is reproducible. Accordingly, the vector can be an autonomously replicating vector, *i.e.*, a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, *e.g.*, a linear or closed circular plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector can contain any means for assuring self-replication. Alternatively, the vector can be one which, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. A vector system can comprise a single vector or plasmid, two or more vectors or plasmids, which together contain the total DNA to be introduced

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- 86 -

into the genome of the host cell, or a transposon. The choice of the vector will typically depend on the compatibility of the vector with the host cell into which the vector is to be introduced. In the present case, the vector is preferably a viral or viral-derived vector, which is operably functional in animal and preferably mammalian cells. Such vector may
5 be derived from a poxvirus, an adenovirus or yeast. The vector can also include a selection marker such as an antibiotic resistance gene that can be used for selection of suitable transformants. Examples of such resistance genes are known to those of skill in the art and include the *nptII* gene that confers resistance to the antibiotics kanamycin and G418 (Geneticin®) and the *hph* gene which confers resistance to the antibiotic hygromycin B.

2. *Synthetic polypeptides*

The inventors have surprisingly discovered that the structure of a parent polypeptide can be disrupted sufficiently to impede, abrogate or otherwise alter at least one function of the parent polypeptide, while simultaneously minimising the destruction of potentially useful epitopes that are present in the parent polypeptide, by fusing, coupling or otherwise linking together different segments of the parent polypeptide in a different relationship relative to their linkage in the parent polypeptide. As a result of this change in relationship, the sequence of the linked segments in the resulting synthetic polypeptide is different to a sequence contained within the parent polypeptide. The synthetic polypeptides of the invention are useful as immunopotentiating agents, and are referred to elsewhere in the specification as scrambled antigen vaccines, super attenuated vaccines or "*Savines*".

Thus, the invention broadly resides in a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein said segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide.

It is preferable but not essential that the segments in said synthetic polypeptide are linked sequentially in a different order or arrangement relative to that of corresponding segments in said at least one parent polypeptide. For example, in the case of a parent polypeptide that comprises three contiguous or overlapping segments A-B-C-D, these segments may be linked in 23 other possible orders to form a synthetic polypeptide. These orders may be selected from the group consisting of: A-B-D-C, A-C-B-D, A-C-D-B, A-D-B-C, A-D-C-B, B-A-C-D, B-A-D-C, B-C-A-D, B-C-D-A, B-D-A-C, B-D-C-A, C-A-B-D, C-A-D-B, C-B-A-D, C-B-D-A, C-D-A-B, C-D-B-A, D-A-B-C, D-A-C-B, D-B-A-C, D-B-C-A, D-C-A-B, and D-C-B-A. Although the rearrangement of the segments is preferably random, it is especially preferable to exclude or otherwise minimise rearrangements that result in complete or partial reassembly of the parent sequence (*e.g.*, ADBC, BACD, DABC). It will be appreciated, however, that the probability of such complete or partial reassembly diminishes as the number of segments for rearrangement increases.

The order of the segments is suitably shuffled, reordered or otherwise rearranged relative to the order in which they exist in the parent polypeptide so that the structure of the polypeptide is disrupted sufficiently to impede, abrogate or otherwise alter at least one

- 88 -

function associated with the parent polypeptide. Preferably, the segments of the parent polypeptide are randomly rearranged in the synthetic polypeptide.

The parent polypeptide is suitably a polypeptide that is associated with a disease or condition. For example, the parent polypeptide may be a polypeptide expressed by a pathogenic organism or a cancer. Alternatively, the parent polypeptide can be a self peptide related to an autoimmune disease including, but are not limited to, diseases such as diabetes (*e.g.*, juvenile diabetes), multiple sclerosis, rheumatoid arthritis, myasthenia gravis, atopic dermatitis, and psoriasis and ankylosing spondylitis. Accordingly, the synthetic molecules of the present invention may also have utility for the induction of tolerance in a subject afflicted with an autoimmune disease or condition or with an allergy or other condition to which tolerance is desired. For example tolerance may be induced by contacting an immature dendritic cell of the individual to be treated with a synthetic polypeptide of the invention or by expressing in an immature dendritic cell a synthetic polynucleotide of the invention. Tolerance may also be induced against antigens causing allergic responses (*e.g.*, asthma, hay fever). In this case, the parent polypeptide is suitably an allergenic protein including, but not restricted to, house-dust-mite allergenic proteins as for example described by Thomas and Smith (1998, *Allergy*, 53(9): 821-832).

The pathogenic organism includes, but is not restricted to, yeast, a virus, a bacterium, and a parasite. Any natural host of the pathogenic organism is contemplated by the present invention and includes, but is not limited to, mammals, avians and fish. In a preferred embodiment, the pathogenic organism is a virus, which may be an RNA virus or a DNA virus. Preferably, the RNA virus is Human Immunodeficiency Virus (HIV), Poliovirus, and Influenza virus, Rous sarcoma virus, or a Flavivirus such as Japanese encephalitis virus. In a preferred embodiment, the RNA virus is a Hepatitis virus including, but not limited to, Hepatitis strains A, B and C. Suitably, the DNA virus is a Herpesvirus including, but not limited to, Herpes simplex virus, Epstein-Barr virus, Cytomegalovirus and Parvovirus. In a preferred embodiment, the virus is HIV and the parent polypeptide is suitably selected from env, gag, pol, vif, vpr, tat, rev, vpu and nef, or combination thereof. In an alternate preferred embodiment, the virus is Hepatitis C1a virus and the parent polypeptide is the Hepatitis C1a virus polyprotein.

In another embodiment, the pathogenic organism is a bacterium, which includes, but is not restricted to, *Neisseria* species, *Meningococcal* species, *Haemophilus* species, *Salmonella* species, *Streptococcal* species, *Legionella* species and *Mycobacterium* species.

In yet another embodiment, the pathogenic organism is a parasite, which includes,
5 but is not restricted to, *Plasmodium* species, *Schistosoma* species, *Leishmania* species, *Trypanosoma* species, *Toxoplasma* species and *Giardia* species.

Any cancer or tumour is contemplated by the present invention. For example, the cancer or tumour includes, but is not restricted to, melanoma, lung cancer, breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic cancer, stomach cancer, bladder
10 cancer, kidney cancer, post transplant lymphoproliferative disease (PTLD), Hodgkin's Lymphoma and the like. Preferably, the cancer or tumour relates to melanoma. In a preferred embodiment of this type, the parent polypeptide is a melanocyte differentiation antigen which is suitably selected from gp100, MART, TRP-1, Tyros, TRP2, MC1R, MUC1F, MUC1R or a combination thereof. In an alternate preferred embodiment of this
15 type, the parent polypeptide is a melanoma-specific antigen which is suitably selected from BAGE, GAGE-1, gp100In4, MAGE-1, MAGE-3, PRAME, TRP2IN2, NYNSO1a, NYNSO1b, LAGE1 or a combination thereof.

In a preferred embodiment, the segments are selected on the basis of size. A segment according to the invention may be of any suitable size that can be utilised to elicit
20 an immune response against an antigen encoded by the parent polypeptide. A number of factors can influence the choice of segment size. For example, the size of a segment should be preferably chosen such that it includes, or corresponds to the size of, T cell epitopes and their processing requirement. Practitioners in the art will recognise that class I-restricted T cell epitopes can be between 8 and 10 amino acids in length and if placed next to unnatural
25 flanking residues, such epitopes can generally require 2 to 3 natural flanking amino acids to ensure that they are efficiently processed and presented. Class II-restricted T cell epitopes can range between 12 and 25 amino acids in length and may not require natural flanking residues for efficient proteolytic processing although it is believed that natural flanking residues may play a role. Another important feature of class II-restricted epitopes
30 is that they generally contain a core of 9-10 amino acids in the middle which bind specifically to class II MHC molecules with flanking sequences either side of this core

- 90 -

stabilising binding by associating with conserved structures on either side of class II MHC antigens in a sequence independent manner (Brown *et al.*, 1993). Thus the functional region of class II-restricted epitopes is typically less than 15 amino acids long. The size of linear B cell epitopes and the factors effecting their processing, like class II-restricted epitopes, are quite variable although such epitopes are frequently smaller in size than 15 amino acids. From the foregoing, it is preferable, but not essential, that the size of the segment is at least 4 amino acids, preferably at least 7 amino acids, more preferably at least 12 amino acids, more preferably at least 20 amino acids and more preferably at least 30 amino acids. Suitably, the size of the segment is less than 2000 amino acids, more preferably less than 1000 amino acids, more preferably less than 500 amino acids, more preferably less than 200 amino acids, more preferably less than 100 amino acids, more preferably less than 80 amino acids and even more preferably less than 60 amino acids and still even more preferably less than 40 amino acids. In this regard, it is preferable that the size of the segments is as small as possible so that the synthetic polypeptide adopts a functionally different structure relative to the structure of the parent polypeptide. It is also preferable that the size of the segments is large enough to minimise loss of T cell epitopes. In an especially preferred embodiment, the size of the segment is about 30 amino acids.

An optional spacer may be utilised to space adjacent segments relative to each other. Accordingly, an optional spacer may be interposed between some or all of the segments. The spacer suitably alters proteolytic processing and/or presentation of adjacent segment(s). In a preferred embodiment of this type, the spacer promotes or otherwise enhances proteolytic processing and/or presentation of adjacent segment(s). Preferably, the spacer comprises at least one amino acid. The at least one amino acid is suitably a neutral amino acid. The neutral amino acid is preferably alanine. Alternatively, the at least one amino acid is cysteine.

In a preferred embodiment, segments are selected such that they have partial sequence identity or homology with one or more other segments. Suitably, at one or both ends of a respective segment there is comprised at least 4 contiguous amino acids, preferably at least 7 contiguous amino acids, more preferably at least 10 contiguous amino acids, more preferably at least 15 contiguous amino acids and even more preferably at least 20 contiguous amino acids that are identical to, or homologous with, an amino acid sequence contained within one or more other of said segments. Preferably, at the or each

- 91 -

end of a respective segment there is comprised less than 500 contiguous amino acids, more preferably less than 200 contiguous amino acids, more preferably less than 100 contiguous amino acids, more preferably less than 50 contiguous amino acids, more preferably less than 40 contiguous amino acids, and even more preferably less than 30 contiguous amino acids that are identical to, or homologous with, an amino acid sequence contained within one or more other of said segments. Such sequence overlap (also referred to elsewhere in the specification as "*overlapping fragments*" or "*overlapping segments*") is preferable to ensure potential epitopes at segment boundaries are not lost and to ensure that epitopes at or near segment boundaries are processed efficiently if placed beside or near amino acids that inhibit processing. Preferably, the segment size is about twice the size of the overlap.

In a preferred embodiment, when segments have partial sequence homology therebetween, the homologous sequences suitably comprise conserved and/or non-conserved amino acid differences. Exemplary conservative substitutions are listed in the following table.

15 **TABLE B**

<i>Original Residue</i>	<i>Exemplary Substitutions</i>
Ala	Ser
Arg	Lys
Asn	Gln, His
Asp	Glu
Cys	Ser
Gln	Asn
Glu	Asp
Gly	Pro
His	Asn, Gln
Ile	Leu, Val
Leu	Ile, Val

- 92 -

<i>Original Residue</i>	<i>Exemplary Substitutions</i>
Lys	Arg, Gln, Glu
Met	Leu, Ile,
Phe	Met, Leu, Tyr
Ser	Thr
Thr	Ser
Trp	Tyr
Tyr	Trp, Phe
Val	Ile, Leu

Conserved or non-conserved differences may correspond to polymorphisms in corresponding parent polypeptides. Polymorphic polypeptides are expressed by various pathogenic organisms and cancers. For example, the polymorphic polypeptides may be expressed by different viral strains or clades or by cancers in different individuals.

Sequence overlap between respective segments is preferable to minimise destruction of any epitope sequences that may result from any shuffling or rearrangement of the segments relative to their existing order in the parent polypeptide. If overlapping segments as described above are employed to form a synthetic polypeptide, it may not be necessary to change the order in which those segments are linked together relative to the order in which corresponding segments are normally present in the parent polypeptide. In this regard, such overlapping segments when linked together in the synthetic polypeptide can adopt a different structure relative to the structure of the parent polypeptide, wherein the different structure does not provide for one or more functions associated with the parent polypeptide. For example, in the case of four segments A-B-C-D each spanning 30 contiguous amino acids of the parent polypeptide and having a 10-amino acid overlapping sequence with one or more adjacent segments, the synthetic polypeptide will have duplicated 10-amino acid sequences bridging segments A-B, B-C and C-D. The presence of these duplicated sequences may be sufficient to render a different structure and to abrogate or alter function relative to the parent polypeptide.

- 93 -

In a preferred embodiment, segment size is about 30 amino acids and sequence overlap at one or both ends of a respective segment is about 15 amino acids. However, it will be understood that other suitable segment sizes and sequence overlap sizes are contemplated by the present invention, which can be readily ascertained by persons of skill
5 in the art.

It is preferable but not necessary to utilise all the segments of the parent polypeptide in the construction of the synthetic polypeptide. Suitably, at least 30%, preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, even more preferably at least 70%, even more preferably at least 80% and still even more
10 preferably at least 90% of the parent polypeptide sequence is used in the construction of the synthetic polypeptide. However, it will be understood that the more sequence information from a parent polypeptide that is utilised to construct the synthetic polypeptide, the greater the population coverage will be of the synthetic polypeptide as an immunogen. Preferably, no sequence information from the parent polypeptide is excluded
15 (e.g., because of an apparent lack of immunological epitopes).

Persons of skill in the art will appreciate that when preparing a synthetic polypeptide against a pathogenic organism (e.g., a virus) or a cancer, it may be preferable to use sequence information from a plurality of different polypeptides expressed by the organism or the cancer. Accordingly, in a preferred embodiment, segments from a plurality
20 of different polypeptides are linked together to form a synthetic polypeptide according to the invention. It is preferable in this respect to utilise as many parent polypeptides as possible from, or in relation to, a particular source in the construction of the synthetic polypeptide. The source of parent polypeptides includes, but is not limited to, a pathogenic organism and a cancer. Suitably, at least about 30%, preferably at least 40%, more
25 preferably at least 50%, even more preferably at least 60%, even more preferably at least 70%, even more preferably at least 80% and still even more preferably at least 90% of the parent polypeptides expressed by the source is used in the construction of the synthetic polypeptide. Preferably, parent polypeptides from a virus include, but are not restricted to, latent polypeptides, regulatory polypeptides or polypeptides expressed early during their
30 replication cycle. Suitably, parent polypeptides from a parasite or bacterium include, but are not restricted to, secretory polypeptides and polypeptides expressed on the surface of

the parasite or bacteria. It is preferred that parent polypeptides from a cancer or tumour are cancer specific polypeptides.

Suitably, hypervariable sequences within the parent polypeptide are excluded from the construction of the synthetic polypeptide.

5 The synthetic polypeptides of the inventions may be prepared by any suitable procedure known to those of skill in the art. For example, the polypeptide may be synthesised using solution synthesis or solid phase synthesis as described, for example, in Chapter 9 of Atherton and Shephard (1989, *Solid Phase Peptide Synthesis: A Practical Approach*. IRL Press, Oxford) and in Roberge *et al* (1995, *Science* 269: 202). Syntheses
10 may employ, for example, either *t*-butyloxycarbonyl (*t*-Boc) or 9-fluorenylmethyloxycarbonyl (Fmoc) chemistries (see Chapter 9.1, of Coligan *et al.*, *CURRENT PROTOCOLS IN PROTEIN SCIENCE*, John Wiley & Sons, Inc. 1995-1997; Stewart and Young, 1984, *Solid Phase Peptide Synthesis*, 2nd ed. Pierce Chemical Co., Rockford, Ill; and Atherton and Shephard, *supra*).

15 Alternatively, the polypeptides may be prepared by a procedure including the steps of:

(a) preparing a synthetic construct including a synthetic polynucleotide encoding a synthetic polypeptide wherein said synthetic polynucleotide is operably linked to a regulatory polynucleotide, wherein said synthetic polypeptide comprises a plurality of
20 different segments of a parent polypeptide, wherein said segments are linked together in a different relationship relative to their linkage in the parent polypeptide;

(b) introducing the synthetic construct into a suitable host cell;

(c) culturing the host cell to express the synthetic polypeptide from said synthetic construct; and

25 (d) isolating the synthetic polypeptide.

The synthetic construct is preferably in the form of an expression vector. For example, the expression vector can be a self-replicating extra-chromosomal vector such as a plasmid, or a vector that integrates into a host genome. Typically, the regulatory polynucleotide may include, but is not limited to, promoter sequences, leader or signal

- 95 -

sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and termination sequences, and enhancer or activator sequences. Constitutive or inducible promoters as known in the art are contemplated by the invention. The promoters may be either naturally occurring promoters, or hybrid promoters that combine elements of
5 more than one promoter. The regulatory polynucleotide will generally be appropriate for the host cell used for expression. Numerous types of appropriate expression vectors and suitable regulatory polynucleotides are known in the art for a variety of host cells.

In a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the
10 art and will vary with the host cell used.

The expression vector may also include a fusion partner (typically provided by the expression vector) so that the synthetic polypeptide of the invention is expressed as a fusion polypeptide with said fusion partner. The main advantage of fusion partners is that they assist identification and/or purification of said fusion polypeptide. In order to express
15 said fusion polypeptide, it is necessary to ligate a polynucleotide according to the invention into the expression vector so that the translational reading frames of the fusion partner and the polynucleotide coincide.

Well known examples of fusion partners include, but are not limited to, glutathione-S-transferase (GST), Fc portion of human IgG, maltose binding protein (MBP)
20 and hexahistidine (HIS₆), which are particularly useful for isolation of the fusion polypeptide by affinity chromatography. For the purposes of fusion polypeptide purification by affinity chromatography, relevant matrices for affinity chromatography are glutathione-, amylose-, and nickel- or cobalt-conjugated resins respectively. Many such matrices are available in "kit" form, such as the QIAexpress™ system (Qiagen) useful with
25 (HIS₆) fusion partners and the Pharmacia GST purification system. In a preferred embodiment, the recombinant polynucleotide is expressed in the commercial vector pFLAG™.

Another fusion partner well known in the art is green fluorescent protein (GFP). This fusion partner serves as a fluorescent "tag" which allows the fusion polypeptide of the
30 invention to be identified by fluorescence microscopy or by flow cytometry. The GFP tag is useful when assessing subcellular localisation of a fusion polypeptide of the invention,

- 96 -

or for isolating cells which express a fusion polypeptide of the invention. Flow cytometric methods such as fluorescence activated cell sorting (FACS) are particularly useful in this latter application. Preferably, the fusion partners also have protease cleavage sites, such as for Factor X_a, Thrombin and inteins (protein introns), which allow the relevant protease to partially digest the fusion polypeptide of the invention and thereby liberate the recombinant polypeptide of the invention therefrom. The liberated polypeptide can then be isolated from the fusion partner by subsequent chromatographic separation. Fusion partners according to the invention also include within their scope "epitope tags", which are usually short peptide sequences for which a specific antibody is available. Well known examples of epitope tags for which specific monoclonal antibodies are readily available include c-Myc, influenza virus, haemagglutinin and FLAG tags. Alternatively, a fusion partner may be provided to promote other forms of immunity. For example, the fusion partner may be an antigen-binding molecule that is immuno-interactive with a conformational epitope on a target antigen or to a post-translational modification of a target antigen (e.g., an antigen-binding molecule that is immuno-interactive with a glycosylated target antigen).

The step of introducing the synthetic construct into the host cell may be effected by any suitable method including transfection, and transformation, the choice of which will be dependent on the host cell employed. Such methods are well known to those of skill in the art.

Synthetic polypeptides of the invention may be produced by culturing a host cell transformed with the synthetic construct. The conditions appropriate for protein expression will vary with the choice of expression vector and the host cell. This is easily ascertained by one skilled in the art through routine experimentation.

Suitable host cells for expression may be prokaryotic or eukaryotic. One preferred host cell for expression of a polypeptide according to the invention is a bacterium. The bacterium used may be *Escherichia coli*. Alternatively, the host cell may be an insect cell such as, for example, *SF9* cells that may be utilised with a baculovirus expression system.

The synthetic polypeptide may be conveniently prepared by a person skilled in the art using standard protocols as for example described in Sambrook, *et al.*, MOLECULAR CLONING. A LABORATORY MANUAL (Cold Spring Harbor Press, 1989), in particular

Sections 16 and 17; Ausubel *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (John Wiley & Sons, Inc. 1994-1998), in particular Chapters 10 and 16; and Coligan *et al.*, CURRENT PROTOCOLS IN PROTEIN SCIENCE (John Wiley & Sons, Inc. 1995-1997), in particular Chapters 1, 5 and 6.

- 5 The amino acids of the synthetic polypeptide can be any non-naturally occurring or any naturally occurring amino acid. Examples of unnatural amino acids and derivatives during peptide synthesis include but are not limited to, use of 4-amino butyric acid, 6-aminoheptanoic acid, 4-amino-3-hydroxy-5-phenylpentanoic acid, 4-amino-3-hydroxy-6-methylheptanoic acid, t-butylglycine, norleucine, norvaline, phenylglycine, ornithine, 10 sarcosine, 2-thienyl alanine and/or D-isomers of amino acids. A list of unnatural amino acids contemplated by the present invention is shown in TABLE C.

TABLE C

<i>Non-conventional amino acid</i>	<i>Non-conventional amino acid</i>
α -aminobutyric acid	L-N-methylalanine
α -amino- α -methylbutyrate	L-N-methylarginine
aminocyclopropane-carboxylate	L-N-methylasparagine
aminoisobutyric acid	L-N-methylaspartic acid
aminonorbornyl-carboxylate	L-N-methylcysteine
cyclohexylalanine	L-N-methylglutamine
cyclopentylalanine	L-N-methylglutamic acid
L-N-methylisoleucine	L-N-methylhistidine
D-alanine	L-N-methylleucine
D-arginine	L-N-methyllysine
D-aspartic acid	L-N-methylmethionine
D-cysteine	L-N-methylnorleucine
D-glutamate	L-N-methylnorvaline
D-glutamic acid	L-N-methylornithine

<i>Non-conventional amino acid</i>	<i>Non-conventional amino acid</i>
D-histidine	L-N-methylphenylalanine
D-isoleucine	L-N-methylproline
D-leucine	L-N-methylserine
D-lysine	L-N-methylthreonine
D-methionine	L-N-methyltryptophan
D-ornithine	L-N-methyltyrosine
D-phenylalanine	L-N-methylvaline
D-proline	L-N-methylethylglycine
D-serine	L-N-methyl-t-butylglycine
D-threonine	L-norleucine
D-tryptophan	L-norvaline
D-tyrosine	α -methyl-aminoisobutyrate
D-valine	α -methyl- γ -aminobutyrate
D- α -methylalanine	α -methylcyclohexylalanine
D- α -methylarginine	α -methylcyclopentylalanine
D- α -methylasparagine	α -methyl- α -naphthylalanine
D- α -methylaspartate	α -methylpenicillamine
D- α -methylcysteine	N-(4-aminobutyl)glycine
D- α -methylglutamine	N-(2-aminoethyl)glycine
D- α -methylhistidine	N-(3-aminopropyl)glycine
D- α -methylisoleucine	N-amino- α -methylbutyrate
D- α -methylleucine	α -naphthylalanine
D- α -methyllysine	N-benzylglycine
D- α -methylmethionine	N-(2-carbamylethyl)glycine
D- α -methylornithine	N-(carbamylmethyl)glycine

- 99 -

<i>Non-conventional amino acid</i>	<i>Non-conventional amino acid</i>
D- α -methylphenylalanine	N-(2-carboxyethyl)glycine
D- α -methylproline	N-(carboxymethyl)glycine
D- α -methylserine	N-cyclobutylglycine
D- α -methylthreonine	N-cycloheptylglycine
D- α -methyltryptophan	N-cyclohexylglycine
D- α -methyltyrosine	N-cyclodecylglycine
L- α -methylleucine	L- α -methyllysine
L- α -methylmethionine	L- α -methylnorleucine
L- α -methylnorvaline	L- α -methylornithine
L- α -methylphenylalanine	L- α -methylproline
L- α -methylserine	L- α -methylthreonine
L- α -methyltryptophan	L- α -methyltyrosine
L- α -methylvaline	L-N-methylhomophenylalanine
N-(N-(2,2-diphenylethyl carbonylmethyl)glycine	N-(N-(3,3-diphenylpropyl carbonylmethyl)glycine
1-carboxy-1-(2,2-diphenyl-ethyl amino)cyclopropane	

The invention also contemplates modifying the synthetic polypeptides of the invention using ordinary molecular biological techniques so as to alter their resistance to proteolytic degradation or to optimise solubility properties or to render them more suitable as an immunogenic agent.

3. Preparation of synthetic polynucleotides of the invention

The invention contemplates synthetic polynucleotides encoding the synthetic polypeptides as for example described in Section 2 *supra*. Polynucleotides encoding segments of a parent polypeptide can be produced by any suitable technique. For example, such polynucleotides can be synthesised *de novo* using readily available machinery.

- 100 -

Sequential synthesis of DNA is described, for example, in U.S. Patent No 4,293,652. Instead of *de novo* synthesis, recombinant techniques may be employed including use of restriction endonucleases to cleave a polynucleotide encoding at least a segment of the parent polypeptide and use of ligases to ligate together in frame a plurality of cleaved
5 polynucleotides encoding different segments of the parent polypeptide. Suitable recombinant techniques are described for example in the relevant sections of Ausubel, *et al.* (*supra*) and of Sambrook, *et al.*, (*supra*) which are incorporated herein by reference. Preferably, the synthetic polynucleotide is constructed using splicing by overlapping extension (SOEing) as for example described by Horton *et al.* (1990, *Biotechniques* 8(5):
10 528-535; 1995, *Mol Biotechnol.* 3(2): 93-99; and 1997, *Methods Mol Biol.* 67: 141-149). However, it should be noted that the present invention is not dependent on, and not directed to, any one particular technique for constructing the synthetic construct.

Various modifications to the synthetic polynucleotides may be introduced as a means of increasing intracellular stability and half-life. Possible modifications include but
15 are not limited to the addition of flanking sequences of ribo- or deoxy- nucleotides to the 5' and/or 3' ends of the molecule or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the oligodeoxyribonucleotide backbone.

The invention therefore contemplates a method of producing a synthetic polynucleotide as broadly described above, comprising linking together in the same
20 reading frame at least two nucleic acid sequences encoding different segments of a parent polypeptide to form a synthetic polynucleotide, which encodes a synthetic polypeptide according to the invention. Suitably, nucleic acid sequences encoding at least 10 segments, preferably at least 20 segments, more preferably at least 40 segments and more preferably at least 100 segments of a parent polypeptide are employed to produce the synthetic
25 polynucleotide.

Preferably, the method further comprises selecting segments of the parent polypeptide, reverse translating the selected segments and preparing nucleic acid sequences encoding the selected segments. It is preferred that the method further comprises randomly linking the nucleic acid sequences together to form the synthetic polynucleotide.
30 The nucleic acid sequences may be oligonucleotides or polynucleotides.

- 101 -

Suitably, segments are selected on the basis of size. Additionally, or in the alternative, segments are selected such that they have partial sequence identity or homology (*i.e.*, sequence overlap) with one or more other segments. A number of factors can influence segment size and sequence overlap as mentioned above. In the case of
5 sequence overlap, large amounts of duplicated nucleic acid sequences can sometimes result in sections of nucleic acid being lost during nucleic acid amplification (*e.g.*, polymerase chain reaction, PCR) of such sequences, recombinant plasmid propagation in a bacterial host or during amplification of recombinant viruses containing such sequences. Accordingly, in a preferred embodiment, nucleic acid sequences encoding segments having
10 sequence identity or homology with one or more other encoded segments are not linked together in an arrangement in which the identical or homologous sequences are contiguous. Also, it is preferable that different codons are used to encode a specific amino acid in a duplicated region. In this context, an amino acid of a parent polypeptide sequence is preferably reverse translated to provide a codon which, in the context of adjacent or local
15 sequence elements, has a lower propensity of forming an undesirable sequence (*e.g.*, a duplicated sequence or a palindromic sequence) that is refractory to the execution of a task (*e.g.*, cloning or sequencing). Alternatively, segments may be selected such that they contain a carboxyl terminal leucine residue or such that reverse translated sequences encoding the segments contain restriction enzyme sites for convenient splicing of the
20 reverse translated sequences.

The method optionally further comprises linking a spacer oligonucleotide encoding at least one spacer residue between segment-encoding nucleic acids. Such spacer residue(s) may be advantageous in ensuring that epitopes within the segments are processed and presented efficiently. Preferably, the spacer oligonucleotide encodes 2 to 3
25 spacer residues. The spacer residue is suitably a neutral amino acid, which is preferably alanine.

Optionally, the method further comprises linking in the same reading frame as other segment-containing nucleic acid sequences at least one variant nucleic acid sequence which encodes a variant segment having a homologous but not identical amino acid
30 sequence relative to other encoded segments. Suitably, the variant segment comprises conserved and/or non-conserved amino acid differences relative to one or more other encoded segments. Such differences may correspond to polymorphisms as discussed

above. In a preferred embodiment, degenerate bases are designed or built in to the at least one variant nucleic acid sequence to give rise to all desired homologous sequences.

When a large number of polymorphisms is intended to be covered, it is preferred that multiple synthetic polynucleotides are constructed rather than a single synthetic polynucleotide, which encodes all variant segments. For example, if there is less than 85%
5 homology between polymorphic polypeptides, then it is preferred that more than one synthetic polynucleotide is constructed.

Preferably, the method further comprises optimising the codon composition of the synthetic polynucleotide such that it is translated efficiently by a host cell. In this regard, it
10 is well known that the translational efficiency of different codons varies between organisms and that such differences in codon usage can be utilised to enhance the level of protein expression in a particular organism. In this regard, reference may be made to Seed *et al.* (International Application Publication No WO 96/09378) who disclose the replacement of existing codons in a parent polynucleotide with synonymous codons to
15 enhance expression of viral polypeptides in mammalian host cells. Preferably, the first or second most frequently used codons are employed for codon optimisation.

Preferably, gene splicing by overlap extension or "gene SOEing" (*supra*) is employed for the construction of the synthetic polynucleotide which is a PCR-based method of recombining DNA sequences without reliance on restriction sites and of directly
20 generating mutated DNA fragments *in vitro*. By modifying the sequences incorporated into the 5'-ends of the primers, any pair of PCR products can be made to share a common sequence at one end. Under PCR conditions, the common sequence allows strands from two different fragments to hybridise to one another, forming an overlap. Extension of this overlap by DNA polymerase yields a recombinant molecule. However, a problem with
25 long synthetic constructs is that mutations generally incorporate into amplified products during synthesis. In this instance, it is preferred that resolvase treatment is employed at various steps of the synthesis. Resolvases are bacteriophage-encoded endonucleases which recognise disruptions or mispairing of double stranded DNA and are primarily used by bacteriophages to resolve Holliday junctions (Mizuuchi, 1982; Youil *et al.*, 1995). For
30 example, T7 endonuclease I can be employed in synthetic DNA constructions to recognise mutations and cleave corrupted dsDNA. The mutated DNA strands are then hybridised to

- 103 -

non-mutant or correct DNA sequences, which results in a mispairing of DNA bases. The mispaired bases are recognised by the resolvase, which then cleaves the DNA nearby leaving only correctly hybridised sequences intact. Preferably a thermostable resolvase enzyme is employed during splicing or amplification so that errors are not incorporated in
5 downstream synthesis products.

Synthetic polynucleotides according to the invention can be operably linked to a regulatory polynucleotide in the form a synthetic construct as for example described in Section 2 *supra*. Synthetic constructs of the invention have utility *inter alia* as nucleic acid vaccines. The choice of regulatory polynucleotide and synthetic construct will depend on
10 the intended host.

Exemplary expression vectors for expression of a synthetic polypeptide according to the invention include, but are not restricted to, modified Ankara Vaccinia virus as for example described by Allen *et al.* (2000, *J. Immunol.* 164(9): 4968-4978), fowlpox virus as for example described by Boyle and Coupar (1988, *Virus Res.* 10: 343-356) and the herpes
15 simplex amplicons described for example by Fong *et al.* in U.S. Patent No. 6,051,428. Alternatively, Adenovirus and Epstein-Barr virus vectors, which are preferably capable of accepting large amounts of DNA or RNA sequence information, can be used.

Preferred promoter sequences that can be utilised for expression of synthetic polypeptides include the P7.5 or PE/L promoters as for example disclosed by Kumar and
20 Boyle. (1990, *Virology* 179: 151-158), CMV and RSV promoters.

The synthetic construct optionally further includes a nucleic acid sequence encoding an immunostimulatory molecule. The immunostimulatory molecule may be fusion partner of the synthetic polypeptide. Alternatively, the immunostimulatory molecule may be translated separately from the synthetic polypeptide. Preferably, the
25 immunostimulatory molecule comprises a general immunostimulatory peptide sequence. For example, the immunostimulatory peptide sequence may comprise a domain of an invasin protein (Inv) from the bacteria *Yersinia* spp as for example disclosed by Brett *et al.* (1993, *Eur. J. Immunol.* 23: 1608-1614). This immune stimulatory property results from the capability of this invasin domain to interact with the $\beta 1$ integrin molecules present on T
30 cells, particularly activated immune or memory T cells. A preferred embodiment of the invasin domain (Inv) for linkage to a synthetic polypeptide has been previously described

- 104 -

in U.S. Pat. No. 5,759,551. The said Inv domain has the sequence: Thr-Ala-Lys-Ser-Lys-Lys-Phe-Pro-Ser-Tyr-Thr-Ala-Thr-Tyr-Gln-Phe [SEQ ID NO; 1467] or is an immune stimulatory homologue thereof from the corresponding region in another *Yersinia* species invasin protein. Such homologues thus may contain substitutions, deletions or insertions of
5 amino acid residues to accommodate strain to strain variation, provided that the homologues retain immune stimulatory properties. The general immunostimulatory sequence may optionally be linked to the synthetic polypeptide by a spacer sequence.

In an alternate embodiment, the immunostimulatory molecule may comprise an immunostimulatory membrane or soluble molecule, which is suitably a T cell co-
10 stimulatory molecule. Preferably, the T cell co-stimulatory molecule is a B7 molecule or a biologically active fragment thereof, or a variant or derivative of these. The B7 molecule includes, but is not restricted to, B7-1 and B7-2. Preferably, the B7 molecule is B7-1. Alternatively, the T cell co-stimulatory molecule may be an ICAM molecule such as ICAM-1 and ICAM-2.

15 In another embodiment, the immunostimulatory molecule can be a cytokine, which includes, but is not restricted to, an interleukin, a lymphokine, tumour necrosis factor and an interferon. Alternatively, the immunostimulatory molecule may comprise an immunomodulatory oligonucleotide as for example disclosed by Krieg in U.S. Patent No. 6,008,200.

20 Suitably, the size of the synthetic polynucleotide does not exceed the ability of host cells to transcribe, translate or proteolytically process and present epitopes to the immune system. Practitioners in the art will also recognise that the size of the synthetic polynucleotide can impact on the capacity of an expression vector to express the synthetic polynucleotide in a host cell. In this connection, it is known that the efficacy of DNA
25 vaccination reduces with expression vectors greater than 20-kb. In such situations it is preferred that a larger number of smaller synthetic constructs is utilised rather than a single large synthetic construct.

4. Immunopotentiating compositions

The invention also contemplates a composition, comprising an
30 immunopotentiating agent selected from the group consisting of a synthetic polypeptide as

- 105 -

described in Section 2, and a synthetic polynucleotide or a synthetic construct as described in Section 3, together with a pharmaceutically acceptable carrier. One or more immunopotentiating agents can be used as actives in the preparation of immunopotentiating compositions. Such preparation uses routine methods known to persons skilled in the art. Typically, such compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid prior to injection may also be prepared. The preparation may also be emulsified. The active immunogenic ingredients are often mixed with excipients that are pharmaceutically acceptable and compatible with the active ingredient. Suitable excipients are, for example, water, saline, dextrose, glycerol, ethanol, or the like and combinations thereof. In addition, if desired, the vaccine may contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents, and/or adjuvants that enhance the effectiveness of the vaccine. Examples of adjuvants which may be effective include but are not limited to: aluminium hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thur-MDP), N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 1983A, referred to as MTP-PE), and RIBI, which contains three components extracted from bacteria, monophosphoryl lipid A, trehalose dimycolate and cell wall skeleton (MPL+TDM+CWS) in a 2% squalene/Tween 80 emulsion. For example, the effectiveness of an adjuvant may be determined by measuring the amount of antibodies resulting from the administration of the composition, wherein those antibodies are directed against one or more antigens presented by the treated cells of the composition.

The immunopotentiating agents may be formulated into a composition as neutral or salt forms. Pharmaceutically acceptable salts include the acid addition salts (formed with free amino groups of the peptide) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids such as acetic, oxalic, tartaric, maleic, and the like. Salts formed with the free carboxyl groups may also be derived from inorganic basis such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic basis as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine, and the like.

- 106 -

If desired, devices or compositions containing the immunopotentiating agents suitable for sustained or intermittent release could be, in effect, implanted in the body or topically applied thereto for the relatively slow release of such materials into the body.

The compositions are conventionally administered parenterally, by injection, for example, either subcutaneously or intramuscularly. Additional formulations which are suitable for other modes of administration include suppositories and, in some cases, oral formulations. For suppositories, traditional binders and carriers may include, for example, polyalkylene glycols or triglycerides; such suppositories may be formed from mixtures containing the active ingredient in the range of 0.5% to 10%, preferably 1%-2%. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium carbonate, and the like. These compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and contain 10%-95% of active ingredient, preferably 25%-70%.

Administration of the gene therapy construct to said mammal, preferably a human, may include delivery via direct oral intake, systemic injection, or delivery to selected tissue(s) or cells, or indirectly via delivery to cells isolated from the mammal or a compatible donor. An example of the latter approach would be stem cell therapy, wherein isolated stem cells having potential for growth and differentiation are transfected with the vector comprising the *Sox18* nucleic acid. The stem cells are cultured for a period and then transferred to the mammal being treated.

With regard to nucleic acid based compositions, all modes of delivery of such compositions are contemplated by the present invention. Delivery of these compositions to cells or tissues of an animal may be facilitated by microprojectile bombardment, liposome mediated transfection (e.g., lipofectin or lipofectamine), electroporation, calcium phosphate or DEAE-dextran-mediated transfection, for example. In an alternate embodiment, a synthetic construct may be used as a therapeutic or prophylactic composition in the form of a "naked DNA" composition as is known in the art. A discussion of suitable delivery methods may be found in Chapter 9 of CURRENT PROTOCOLS IN MOLECULAR BIOLOGY (Eds. Ausubel *et al.*; John Wiley & Sons Inc., 1997 Edition) or on the Internet site DNA vaccine.com. The compositions may be administered by intradermal (e.g., using panjel™ delivery) or intramuscular routes.

- 107 -

The step of introducing the synthetic polynucleotide into a target cell will differ depending on the intended use and species, and can involve one or more of non-viral and viral vectors, cationic liposomes, retroviruses, and adenoviruses such as, for example, described in Mulligan, R.C., (1993 *Science* 260 926-932) which is hereby incorporated by
5 reference. Such methods can include, for example:

- A. Local application of the synthetic polynucleotide by injection (Wolff *et al.*, 1990, *Science* 247 1465-1468, which is hereby incorporated by reference), surgical implantation, instillation or any other means. This method can also be used in combination with local application by injection, surgical implantation, instillation or
10 any other means, of cells responsive to the protein encoded by the synthetic polynucleotide so as to increase the effectiveness of that treatment. This method can also be used in combination with local application by injection, surgical implantation, instillation or any other means, of another factor or factors required for the activity of said protein.
- 15 B. General systemic delivery by injection of DNA, (Calabretta *et al.*, 1993, *Cancer Treat. Rev.* 19 169-179, which is incorporated herein by reference), or RNA, alone or in combination with liposomes (Zhu *et al.*, 1993, *Science* 261 209-212, which is incorporated herein by reference), viral capsids or nanoparticles (Bertling *et al.*, 1991, *Biotech. Appl. Biochem.* 13 390-405, which is incorporated herein by reference) or any
20 other mediator of delivery. Improved targeting might be achieved by linking the synthetic polynucleotide to a targeting molecule (the so-called "magic bullet" approach employing, for example, an antibody), or by local application by injection, surgical implantation or any other means, of another factor or factors required for the activity of the protein encoding said synthetic polynucleotide, or of cells responsive to said
25 protein.
- C. Injection or implantation or delivery by any means, of cells that have been modified *ex vivo* by transfection (for example, in the presence of calcium phosphate: Chen *et al.*, 1987, *Mole. Cell Biochem.* 7 2745-2752, or of cationic lipids and polyamines: Rose *et al.*, 1991, *BioTech.* 10 520-525, which articles are incorporated herein by reference),
30 infection, injection, electroporation (Shigekawa *et al.*, 1988, *BioTech.* 6 742-751, which is incorporated herein by reference) or any other way so as to increase the

- 108 -

expression of said synthetic polynucleotide in those cells. The modification can be mediated by plasmid, bacteriophage, cosmid, viral (such as adenoviral or retroviral; Mulligan, 1993, *Science* 260 926-932; Miller, 1992, *Nature* 357 455-460; Salmons *et al.*, 1993, *Hum. Gen. Ther.* 4 129-141, which articles are incorporated herein by reference) or other vectors, or other agents of modification such as liposomes (Zhu *et al.*, 1993, *Science* 261 209-212, which is incorporated herein by reference), viral capsids or nanoparticles (Bertling *et al.*, 1991, *Biotech. Appl. Biochem.* 13 390-405, which is incorporated herein by reference), or any other mediator of modification. The use of cells as a delivery vehicle for genes or gene products has been described by Barr *et al.*, 1991, *Science* 254 1507-1512 and by Dhawan *et al.*, 1991, *Science* 254 1509-1512, which articles are incorporated herein by reference. Treated cells can be delivered in combination with any nutrient, growth factor, matrix or other agent that will promote their survival in the treated subject.

Also encapsulated by the present invention is a method for treatment and/or prophylaxis of a disease or condition, comprising administering to a patient in need of such treatment a therapeutically effective amount of a composition as broadly described above. The disease or condition may be caused by a pathogenic organism or a cancer as for example described above.

In a preferred embodiment, the immunopotentiating composition of the invention is suitable for treatment of, or prophylaxis against, a cancer. Cancers which could be suitably treated in accordance with the practices of this invention include cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, oesophagus, brain, testicle, uterus, melanoma and the various leukemias and lymphomas.

In an alternate embodiment, the immunopotentiating composition is suitable for treatment of, or prophylaxis against, a viral, bacterial or parasitic infection. Viral infections contemplated by the present invention include, but are not restricted to, infections caused by HIV, Hepatitis, Influenza, Japanese encephalitis virus, Epstein-Barr virus and respiratory syncytial virus. Bacterial infections include, but are not restricted to, those caused by *Neisseria* species, *Meningococcal* species, *Haemophilus* species *Salmonella* species, *Streptococcal* species, *Legionella* species and *Mycobacterium* species. Parasitic

- 109 -

infections encompassed by the invention include, but are not restricted to, those caused by *Plasmodium* species, *Schistosoma* species, *Leishmania* species, *Trypanosoma* species, *Toxoplasma* species and *Giardia* species.

The above compositions or vaccines may be administered in a manner compatible
5 with the dosage formulation, and in such amount as is therapeutically effective to alleviate patients from the disease or condition or as is prophylactically effective to prevent incidence of the disease or condition in the patient. The dose administered to a patient, in the context of the present invention, should be sufficient to effect a beneficial response in a patient over time such as a reduction or cessation of blood loss. The quantity of the
10 composition or vaccine to be administered may depend on the subject to be treated inclusive of the age, sex, weight and general health condition thereof. In this regard, precise amounts of the composition or vaccine for administration will depend on the judgement of the practitioner. In determining the effective amount of the composition or vaccine to be administered in the treatment of a disease or condition, the physician may
15 evaluate the progression of the disease or condition over time. In any event, those of skill in the art may readily determine suitable dosages of the composition or vaccine of the invention.

In a preferred embodiment, DNA-based immunopotentiating agent (e.g., 100 µg) is delivered intradermally into a patient at day 1 and at week 8 to prime the patient. A
20 recombinant poxvirus (e.g., at 10^7 pfu/mL) from which substantially the same immunopotentiating agent can be expressed is then delivered intradermally as a booster at weeks 16 and 24, respectively.

The effectiveness of the immunisation may be assessed using any suitable technique. For example, CTL lysis assays may be employed using stimulated splenocytes
25 or peripheral blood mononuclear cells (PBMC) on peptide coated or recombinant virus infected cells using ^{51}Cr labelled target cells. Such assays can be performed using for example primate, mouse or human cells (Allen *et al.*, 2000, *J. Immunol.* 164(9): 4968-4978 also Woodberry *et al.*, *infra*). Alternatively, the efficacy of the immunisation may be monitored using one or more techniques including, but not limited to, HLA class I
30 Tetramer staining - of both fresh and stimulated PBMCs (see for example Allen *et al.*, *supra*), proliferation assays (Allen *et al.*, *supra*), Elispot™ Assays and intracellular INF-

gamma staining (Allen *et al.*, *supra*), ELISA Assays - for linear B cell responses; and Western blots of cell sample expressing the synthetic polynucleotides.

5. *Computer related embodiments*

The design or construction of a synthetic polypeptide sequence or a synthetic polynucleotide sequence according to the invention is suitably facilitated with the assistance of a computer programmed with software, which *inter alia* fragments a parent sequence into fragments, and which links those fragments together in a different relationship relative to their linkage in the parent sequence. The ready use of a parent sequence for the construction of a desired synthetic molecule according to the invention requires that it be stored in a computer-readable format. Thus, in accordance with the present invention, sequence data relating to a parent molecule (e.g., a parent polypeptide) is stored in a machine-readable storage medium, which is capable of processing the data to fragment the sequence of the parent molecule into fragments and to link together the fragments in a different relationship relative to their linkage in the parent molecule.

Therefore, another embodiment of the present invention provides a machine-readable data storage medium, comprising a data storage material encoded with machine readable data which, when used by a machine programmed with instructions for using said data, fragments a parent sequence into fragments, and links those fragments together in a different relationship relative to their linkage in the parent sequence. In a preferred embodiment of this type, a machine-readable data storage medium is provided that is capable of reverse translating the sequence of a respective fragment to provide a nucleic acid sequence encoding the fragment and to link together in the same reading frame each of the nucleic acid sequences to provide a polynucleotide sequence that codes for a polypeptide sequence in which said fragments are linked together in a different relationship relative to their linkage in a parent polypeptide sequence.

In another embodiment, the invention encompasses a computer for designing the sequence of a synthetic polypeptide and/or a synthetic polynucleotide of the invention, wherein the computer comprises wherein said computer comprises: (a) a machine readable data storage medium comprising a data storage material encoded with machine readable data, wherein said machine readable data comprises the sequence of a parent polypeptide; (b) a working memory for storing instructions for processing said machine-readable data;

- 111 -

(c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium, for processing said machine-readable data into said synthetic polypeptide sequence and/or said synthetic polynucleotide; and (d) an output hardware coupled to said central processing unit, for receiving said synthetic polypeptide sequence
5 and/or said synthetic polynucleotide.

In yet another embodiment, the invention contemplates a computer program product for designing the sequence of a synthetic polynucleotide of the invention, comprising code that receives as input the sequence of a parent polypeptide, code that fragments the sequence of the parent polypeptide into fragments, code that reverse
10 translates the sequence of a respective fragment to provide a nucleic acid sequence encoding the fragment, code that links together in the same reading frame each said nucleic acid sequence to provide a polynucleotide sequence that codes for a polypeptide sequence in which said fragments are linked together in a different relationship relative to their linkage in the parent polypeptide sequence, and a computer readable medium that stores
15 the codes.

A version of these embodiments is presented in Figure 23, which shows a system
10 including a computer 11 comprising a central processing unit ("CPU") 20, a working memory 22 which may be, e.g., RAM (random-access memory) or "core" memory, mass storage memory 24 (such as one or more disk drives or CD-ROM drives), one or more
20 cathode-ray tube ("CRT") display terminals 26, one or more keyboards 28, one or more input lines 30, and one or more output lines 40, all of which are interconnected by a conventional bidirectional system bus 50.

Input hardware 36, coupled to computer 11 by input lines 30, may be implemented in a variety of ways. For example, machine-readable data of this invention
25 may be inputted via the use of a modem or modems 32 connected by a telephone line or dedicated data line 34. Alternatively or additionally, the input hardware 36 may comprise CD. Alternatively, ROM drives or disk drives 24 in conjunction with display terminal 26, keyboard 28 may also be used as an input device.

Output hardware 46, coupled to computer 11 by output lines 40, may similarly be
30 implemented by conventional devices. By way of example, output hardware 46 may include CRT display terminal 26 for displaying a synthetic polynucleotide sequence or a synthetic polypeptide sequence as described herein. Output hardware might also include a

- 112 -

printer 42, so that hard copy output may be produced, or a disk drive 24, to store system output for later use.

In operation, CPU 20 coordinates the use of the various input and output devices 36,46 coordinates data accesses from mass storage 24 and accesses to and from working
5 memory 22, and determines the sequence of data processing steps. A number of programs may be used to process the machine readable data of this invention. Exemplary programs may use for example the steps outlined in the flow diagram illustrated in Figure 24. Broadly, these steps include (1) inputting at least one parent polypeptide sequence; (2) optionally adding to alanine spacers at the ends of each polypeptide sequence; (3)
10 fragmenting the polypeptide sequences into fragments (*e.g.*, 30 amino acids long), which are preferably overlapping (*e.g.*, by 15 amino acids); (4) reverse translating the fragment to provide a nucleic acid sequence for each fragment and preferably using for the reverse translation first and second most translationally efficient codons for a cell type, wherein the codons are preferably alternated out of frame with each other in the overlaps of
15 consecutive fragments; (5) randomly rearranging the fragments; (6) checking whether rearranged fragments recreate at least a portion of a parent polypeptide sequence; (7) repeating randomly rearranging the fragments when rearranged fragments recreate said at least a portion; or otherwise (8) linking the rearranged fragments together to produce a synthetic polypeptide sequence and/or a synthetic polynucleotide sequence; and (9)
20 outputting said synthetic polypeptide sequence and/or a synthetic polynucleotide sequence. An example of an algorithm which uses *inter alia* the aforementioned steps is shown in Figure 25. By way of example, this algorithm has been used for the design of synthetic polynucleotides and synthetic polypeptides according to the present invention for Hepatitis C 1a and for melanoma, as illustrated in Figures 26 and 27.

25 Figure 28 shows a cross section of a magnetic data storage medium 100 which can be encoded with machine readable data, or set of instructions, for designing a synthetic molecule of the invention, which can be carried out by a system such as system 10 of Figure 23. Medium 100 can be a conventional floppy diskette or hard disk, having a suitable substrate 101, which may be conventional, and a suitable coating 102, which may
30 be conventional, on one or both sides, containing magnetic domains (not visible) whose polarity or orientation can be altered magnetically. Medium 100 may also have an opening (not shown) for receiving the spindle of a disk drive or other data storage device 24. The

- 113 -

magnetic domains of coating 102 of medium 100 are polarised or oriented so as to encode in manner which may be conventional, machine readable data such as that described herein, for execution by a system such as system 10 of Figure 23.

Figure 29 shows a cross section of an optically readable data storage medium 110
5 which also can be encoded with such a machine-readable data, or set of instructions, for designing a synthetic molecule of the invention, which can be carried out by a system such as system 10 of Figure 23. Medium 110 can be a conventional compact disk read only memory (CD-ROM) or a rewritable medium such as a magneto-optical disk, which is optically readable and magneto-optically writable. Medium 100 preferably has a suitable
10 substrate 111, which may be conventional, and a suitable coating 112, which may be conventional, usually of one side of substrate 111.

In the case of CD-ROM, as is well known, coating 112 is reflective and is impressed with a plurality of pits 113 to encode the machine-readable data. The arrangement of pits is read by reflecting laser light off the surface of coating 112. A
15 protective coating 114, which preferably is substantially transparent, is provided on top of coating 112.

In the case of a magneto-optical disk, as is well known, coating 112 has no pits 113, but has a plurality of magnetic domains whose polarity or orientation can be changed magnetically when heated above a certain temperature, as by a laser (not shown). The
20 orientation of the domains can be read by measuring the polarisation of laser light reflected from coating 112. The arrangement of the domains encodes the data as described above.

In order that the invention may be readily understood and put into practical effect, particular preferred non-limiting embodiments will now be described as follows.

EXAMPLES

EXAMPLE 1

Preparation of an HIV Savine

Experimental Protocol

5 *Plasmids*

The plasmid pDNAVacc is ampicillin resistant and contains an expression cassette comprising a CMV promoter and enhancer, a synthetic intron, a multiple cloning site (MCS) and a SV40poly A signal sequence (Thomson *et al.*, 1998). The plasmid pTK7.5 and contains a selection cassette, a pox virus 7.5 early/late promoter and a MCS
10 flanked on either side by Vaccinia virus TK gene sequences.

Recombinant Vaccinia Viruses

Recombinant Vaccinia viruses expressing the *gag*, *env* (IIB) and *pol* (LAI) genes of HIV-1 were used as previously described and denoted VV-GAG, VV-POL, VV-ENV (Woodberry *et al.*, 1999; Kent *et al.*, 1998).

15 *Marker Rescue Recombination*

Recombinant Vaccinia viruses containing Savine constructs were generated by marker rescue recombination, using protocols described previously (Boyle *et al.*, 1985). Plaque purified viruses were tested for the TK phenotype and for the appropriate genome arrangement by Southern blot and PCR.

20 *Oligonucleotides*

Oligonucleotides 50 nmol scale and desalted were purchased from Life Technologies. Short oligonucleotides were resuspended in 100 µL of water, their concentration determined, then diluted to 20 µM for use in PCR or sequencing reactions. Long oligonucleotides for splicing reactions were denatured for 5 minutes at 94°C in
25 20 µL of formamide loading buffer then 0.5 µL gel purified on a 6% polyacrylamide gel.

- 115 -

Gel slices containing full-length oligonucleotides were visualised with ethidium bromide, excised, placed in Eppendorf™ tubes, combined with 200 µL of water before being crushed using the plunger of a 1 mL syringe. Before being used in splicing reactions the crushed gel was resuspended in an appropriate volume of buffer and 1-2 µL of the
5 resuspendate used directly in the splicing reactions.

Sequencing

Sequencing was performed using Dye terminator sequencing reactions and analyzed by the Biomedical Resource Facility at the John Curtin School of Medical Research using an ABI automated sequencer.

10 *Restimulation of Lymphocytes from HIV Infected Patients*

Two pools of recombinant Vaccinia viruses containing VV-AC1 + VV-BC1 (Pool 1) or VV-AC2 + VV-BC2 + VV-CC2 (Pool 2) were used to restimulate lymphocytes from the blood samples of HIV-infected patients. Briefly CTL lines were generated from HIV-infected donor PBMC. A fifth of the total PBMC were infected with either Pool 1 or Pool 2
15 Vaccinia viruses then added back to the original cell suspension. The infected cell suspension was then cultured with IL-7 for 1 week.

CTL Assays

Restimulated PBMCs were used as effectors in a standard ⁵¹Cr-release CTL assay. Targets were autologous EBV-transformed lymphoblastoid cell lines (LCLs) infected with
20 the following viruses : Pool 1, Pool 2, VV-GAG, VV-POL or VV-ENV. Assay controls included uninfected targets, targets infected with VV-lacZ (virus control) and K562 cells.

Results

HIV Savine Design

A main goal of the Savine strategy is to include as much protein sequence
25 information from a pathogen or cancer as possible in such a way that potential T cell epitopes remain intact and so that the vaccine or therapy is extremely safe. An HIV Savine is described herein not only to compare this strategy to other strategies but also, to produce

- 116 -

an HIV vaccine that would provide the maximum possible population coverage as well as catering for the major HIV clades.

A number of design criteria was first determined to exploit the many advantages of using a synthetic approach. One advantage is that it is possible to use consensus protein sequences to design these vaccines. Using consensus sequences for a highly variable virus like HIV should provide better vaccine coverage because individual viral isolate sequences may have lost epitopes which induce CTL against the majority of other viral isolates. Thus, using the consensus sequences of each HIV clade rather than individual isolate sequences should provide better vaccine coverage. Taking this one step further, a consensus sequence that covers all HIV clades should theoretically provide better coverage than using just the consensus sequences for individual clades. Before designing such a sequence however, it was decided that a more appropriate and focussed HIV vaccine might be constructed if the various clades were first ranked according to their relative importance. To establish such a ranking the following issues were considered, current prevalence of each clade, the rate at which each clade is increasing and the capacity of various regions of the world to cope with the HIV pandemic (Figures 1 and 2). These criteria produced the following ranking, Clade E \geq clade A > clade C > clade B > clade D > other clades. Clades E and A were considered to almost equal since they are very similar except in their envelope protein sequences, which differ considerably.

Another advantage of synthesising a designed sequence is that it is possible to incorporate degenerate sequences into their design. In the case of HIV, this means that more than one amino acid can be included at various positions to improve the ability of the vaccine to cater for the various HIV clades and isolates. Coverage is improved because mutations in different HIV clades and also in individual isolate sequences, while mostly destroying specific T cell epitopes, can result in the formation of new potentially useful epitopes nearby (Goulder *et al.*, 1997). Incorporating degenerate amino acid sequences, however, also means that more than one construct must be made and mixed together. The number of constructs required depends on the frequency with which mutations are incorporated into the design. While this approach requires the construction of additional constructs, these constructs can be prepared from the same set of degenerate long oligonucleotides, significantly reducing the cost of providing such considerable interclade coverage.

- 117 -

A set of degeneracy rules was developed for the incorporation of amino acid mutations into the design which meant that a maximum of eight constructs would be required so that theoretically all combinations were present, as follows: 1) Two amino acids at three positions (or less) within any group of nine amino acids (*i.e.*, present in a CTL epitope); 2) Three amino acids at one position and two at another (or not) within any group of nine amino acids; 3) Four amino acids at one position and two at another (or not) within any group of nine amino acids. The reason why these rules were applied to nine amino acids (the average CTL epitope size) and not to larger stretches of amino acid sequence to cater for class II restricted epitopes, is because class II-restricted epitopes generally have a core sequence of nine amino acids in the middle which bind specifically to class II MHC molecules with the extra flanking sequences stabilising binding, by associating with either side of class II MHC antigens in a largely sequence independent manner (Brown *et al.*, 1993).

Using the HIV clade ranking described above, the amino acid degeneracy rules and in some situations the similarity between amino acids, a degenerate consensus protein sequence was designed for each HIV protein using the consensus protein sequences for each HIV clade compiled by the Los Alamos HIV sequence database (Figures 3-11) (HIV Molecular Immunology Database, 1997). It is important to note that in some situations the order with which each of the above design criteria was applied was altered. Each time this was done the primary goal however was to increase the ability of the vaccine to cater for interclade differences. Two isolate sequences, GenBank accession U51189 and U46016, for clade E and clade C, respectively, were used when a consensus sequence for some HIV proteins from these two clades was unavailable (Gao *et al.*, 1996; Salminen *et al.*, 1996). The design of a consensus sequence for the hypervariable regions of the HIV envelope protein and in some cases between these regions (hypervariable regions 1-2 and 3-5) was difficult and so these regions were excluded from the vaccine design.

Once a degenerate consensus sequence was designed for each HIV protein, an approach was then determined for incorporating all the protein sequences safely into the vaccine. One convenient approach to ensure that a vaccine will be safe is to systematically fragment and randomly rearrange the protein sequences together thus abrogating or otherwise altering their structure and function. The protein sequences still have to be immunologically functional however, meaning that the process used to fragment the

- 118 -

sequences should not destroy potential epitopes. To decide on the best approach for systematically fragmenting protein sequences, the main criteria used was the size of T epitopes and their processing requirements. Class I-restricted T cell epitopes are 8-10 amino acids long and generally require 2-3 natural flanking amino acids to ensure their efficient processing and presentation if placed next to unnatural flanking residues (Del Val *et al.*, 1991; Thomson *et al.*, 1995). Class II-restricted T cell epitopes range between 12-25 amino acids long and do appear to require natural flanking residues for processing however, it is difficult to rule out a role for natural flanking residues in all cases due to the complexity of their processing pathways (Thomson *et al.*, 1998). Also class II-restricted epitopes despite being larger than CTL epitopes generally have a core sequence of 9-10 amino acids, which binds to MHC molecules in a sequence specific fashion. Thus, based on current knowledge, it was decided that an advantageous approach was to overlap the fragments by at least 15 amino acids to ensure that potential epitopes which might lie across fragment boundaries are not lost and to ensure that CTL epitopes near fragment boundaries, that are placed beside or near inhibitory amino acids in adjacent fragments, are processed efficiently. In deciding the optimal fragment size, the main criteria used were that size had to be small enough to cause the maximum disruption to the structure and function of proteins but large enough to cover the sequence information as efficiently as possible without any further unnecessary duplication. Based on these criteria the fragments would be twice the overlap size, in this case 30 amino acids long.

The designed degenerate protein sequences were then separated into fragments 30 amino acid long and overlapping by fifteen amino acids. Two alanine amino acids were also added to the start and end of the first and last fragment for each protein or envelop protein segment to ensure these fragments were not placed directly adjacent to amino acids capable of blocking epitope processing (Del Val *et al.*, 1991). The next step was to reverse translate each protein sequence back into DNA. Duplicating DNA sequences was avoided when constructing DNA sequences encoding a tandem repeat of identical or homologous amino acid sequences to maximise expression of the Savine. In this regard, the first and second most commonly used mammalian codons (shown in Figure 12) were assigned to amino acids in these repeat regions, wherein a first codon was used to encode an amino acid in one of the repeated sequences and wherein a second but synonymous codon was used for the other repeated sequence (*e.g.*, see the gag HIV protein in Figure 13). To cater

- 119 -

for the designed amino acid mutations more than one base was assigned to some positions using the IUPAC DNA codes without exceeding more than three base variations (eight possible combinations) in any group of 27 bases (Figure 12). Where a particular combination of amino acids could not be incorporated, because too many degenerate bases would be required, some or all of the amino acid degeneracy was removed according to the protein consensus design rules outlined above. Also the degenerate codons were checked to determine if they could encode a stop codon, if stop codons could not be avoided then the amino acid degeneracy was also simplified again according to the protein consensus design rules outlined above.

10 The designed DNA segments were then scrambled randomly and joined to create twenty-two subcassettes approximately 840 bp in size. Extra DNA sequences incorporating sites for one of the cohesive restriction enzymes *XbaI*, *SpeI*, *AvrII* or *NheI* and 3 additional base pairs (to cater for premature Taq polymerase termination) were then added to each end of each subcassette (Figure 14). Some of these extra DNA sequences also contained, 15 the cohesive restriction sites for *SaII* or *XhoI*, Kozak signal sequences and start or stop codons to enable the subcassettes to be joined and expressed either as three large cassettes or one full length protein (Figures 14 and 15).

In designing the HIV Savine one issue that required investigation was whether such a large DNA molecule would be fully expressed and whether epitopes encoded near 20 the end of the molecule would be efficiently presented to the immune system. The inventors also wished to show that mixing two or more degenerate Savine constructs together could induce T cell responses that recognise mutated sequences. To examine both issues DNA coding for a degenerate murine influenza nucleoprotein CTL epitope, NP365-373, which differs by two amino acids at positions 71 and 72 in influenza strain A/PR/8/34 25 compared to the A/NT/60/68strain and restricted by H2-Db, was inserted before the last stop codon at the end of the HIV Savine design (Figure 15). An important and unusual characteristic of both of these naturally occurring NP365-373 sequences, which enabled the present inventors to examine the effectiveness of incorporating mutated sequences, is that they generate CTL responses which do not cross react with the alternate sequence 30 (Townsend *et. al.*, 1986). This is an unusual characteristic because epitopes not destroyed by mutation usually induce CTL responses that cross-react.

- 120 -

Up to ten long oligonucleotides up to 100 bases long and two short amplification oligonucleotides were synthesised to enable construction of each subcassette (Life Technologies). In designing each oligonucleotide the 3' end and in most cases also the 5' end had to be either a 'c' or a 'g' to ensure efficient extension during PCR splicing. The overlap region for each long oligonucleotide was designed to be at least 16 bp with approximately 50% G/C content. Also oligonucleotide overlaps were not placed where degenerate DNA bases coded for degenerate amino acids to avoid splicing difficulties later. Where this was too difficult some degenerate bases were removed according to the protein consensus design rules outlined above and indicated in Figure 12. Figure 16 shows an example of the oligonucleotides design for each subcassette.

Construction of the HIV Savine

Five of each group of ten designed oligonucleotides were spliced together using stepwise asymmetric PCR (Sandhu *et al.*, 1992) and Splicing by Overlap Extension (SOEing) (Figure 17a). Each subcassette was then PCR amplified, cloned into pBluescript™ II KS⁻ using *Bam*HI/*Eco*RI and 16 individual clones sequenced. Mutations, deletions and insertions were present in the large majority of the clones for each subcassette, despite acrylamide gel purification of the long oligonucleotides. In order to construct a functional Savine with minimal mutations, two clones for each subcassette with no insertions or deletions and hence a complete open reading frame and with minimal numbers of non-designed mutations, were selected from the sixteen available. The subcassettes were then excised from their plasmids and joined by stepwise PCR-amplified ligation using the polymerase blend Elongase™ (Life Technology), T4 DNA ligase and the cohesive restriction enzymes *Xba*I/*Spe*I/*Avr*II/*Nhe*I, to generate two copies of cassettes A, B and C as outlined in Figure 14 and shown in Figure 17b. Predicted sequences for these cassettes are shown in Figure 30. Each cassette was then reamplified by PCR with Elongase™, cloned into pBluescript™ II KS⁻ and 3 of the resulting plasmid clones sequenced using 12 of the 36 sequencing primers designed to cover the full length construct. Clones with minimal or no further mutations were selected for transfer into plasmids for DNA vaccination or used to make recombinant poxviruses. A summary of the number of designed and non-designed mutations in each Savine construct is presented in Table 1.

TABLE I

Summary of mutations

Construct	No. aas	Number of mutations			
		Designed	Expected in 2 clones	Actual in 2 clones	Non-designed
Cassette A	1896	249	124	107	5 (AC1), 8 (AC2)
Cassette B	1184	260	130	124	11 (BC1), 4 (BC2)
Cassette C	1969	276	138	121	10 (CC1), 14 (CC2)
Full length	5742	785	392	352	26 (FL1), 26 (FL2)

Summary of the mutations present in the two full-length clones constructed as determined by sequencing. Includes the number of mutations designed, expected and actually present in the 2 clones and the number of non-designed mutations in each cassette and full-length clone.

HIV Savine DNA vaccines and Recombinant Vaccinia viruses

To test the immunological effectiveness of the HIV Savine constructs the cassette sequences were transferred into DNA vaccine and poxvirus vectors. These vectors when used either separately in immunological assays described below or together in a 'prime-boost' protocol which has been shown previously to generate strong T cell responses *in vivo* (Kent *et al.*, 1997).

DNA Vaccination plasmids were constructed by excising the cassettes from the selected plasmid clones with *XbaI/XhoI* (cassette A) or *XbaI/SaII* (cassettes B and C) and ligating them into pDNAVacc cut with *XbaI/XhoI* to create pDVAC1, pDVAC2, pDVBC1, pDVBC2, pDVCC1, pDVCC2, respectively (Figure 18a). These plasmids were then further modified by cloning into their *XbaI* site a DNA fragment excised using *XbaI/AvrII* from pTUMERA2 and encoding a synthetic endoplasmic reticulum (ER) signal sequence from the Adenovirus E1A protein (Persson *et al.*, 1980) (Figure 18a). ER signal sequences have been shown previously to enhance the presentation of both CTL and T helper epitopes *in vivo* (Ishioka, G.Y., 1999; Thomson *et al.*, 1998). The plasmids pDVERAC1, pDVERBC1, pDVERCC1 and pDVERAC2, pDVERBC2, pDVERCC2 were then mixed

- 122 -

together to create, plasmid pool 1 and pool 2 respectively. Each plasmid pool collectively encodes one copy of the designed full-length HIV Savine.

Plasmids to generate recombinant Vaccinia viruses which express HIV Savine sequences were constructed by excising the various HIV Savine cassettes from the selected plasmid clones using *Bam*HI/*Xho*I (cassette A) or *Bam*HI/*Sal*I (cassettes B and C) and cloned into the marker rescue plasmid, pTK7.5, cleaved with *Bam*HI/*Sal*I. These pTK7.5-derived plasmids were then used to generate recombinant Vaccinia viruses by marker rescue recombination using established protocols (Boyle *et al.*, 1985) to generate VV-AC1, VV-AC2, VV-BC1, VV-BC2, VV-CC1 and VV-CC2 (Figure 18b).

Two further DNA vaccine plasmids were constructed each encoding a version of the full length HIV Savine (Figure 18c). Briefly, the two versions of cassette B were excised with *Xho*I and cloned into the corresponding selected plasmid clones containing cassette A sequences that were cut with *Xho*I/*Sal*I to generate pBSAB1 and pBSAB2 respectively. The joined A/B cassettes in pBSAB1 and pBSAB2 were excised with *Xba*I/*Xho*I and cloned into pDVCC1 and pDVCC2, respectively, and cleaved with *Xba*I/*Xho*I to generate pDVFL1 and pDVFL2. These were then further modified to contain an ER signal sequence using the same cloning strategy as outlined in figure 18a.

Restimulation of HIV specific lymphocytes from HIV infected patients

The present inventors examined the capacity of the HIV Savine to restimulate HIV-specific polyclonal CTL responses from HIV-infected patients. PBMCs from three different patients were restimulated *in vitro* with two HIV Savine Vaccinia virus pools (Pool 1 included VV-AC1 and VV-BC1; Pool 2 included VV-AC2, VV-BC2 and VV-CC2) then used in CTL lysis assays against LCLs infected either with one of the Savine Vaccinia virus pools or Vaccinia viruses which express gag, env or pol. Figure 19 clearly shows, that in all three assays, both HIV Savine viral pools restimulated HIV-specific CTL responses which could recognise targets expressing whole natural HIV antigens and not targets which were uninfected or infected with the control Vaccinia virus. Furthermore, in all three cases, both pools restimulated responses that recognised all three natural HIV antigens. This result suggests that the combined Savine constructs will provide broader immunological coverage than single antigen based vaccine approaches. The level of lysis in each case of targets infected with Savine viral pools was significantly higher than the

- 123 -

lysis recorded for any other infected target. This probably reflects the combined CTL responses to gag, pol, and env plus other HIV antigens not analysed here but whose sequences are also incorporated into the Savine constructs.

CTL recognition of each HIV antigen is largely controlled by each patient's HLA background hence the pattern of CTL lysis for whole HIV antigens is different in each patient. Interestingly, this CTL lysis pattern did not change when the second Savine Vaccinia virus pool was used for CTL restimulation. In these assays, therefore, the inventors were unable to demonstrate clear differences between pools 1 and 2, despite pool 1 lacking a Vaccinia virus expressing cassette CC1 and despite the many amino acid differences between the A and B cassettes in each pool (see table 1).

From the foregoing, the present inventors have developed a novel vaccine/therapeutic strategy. In one embodiment, pathogen or cancer protein sequences are systemically fragmented, reverse translated back into DNA, rearranged randomly then joined back together. The designed synthetic DNA sequence is then constructed using long oligonucleotides and can be transferred into a range of delivery vectors. The vaccine vectors used here were DNA vaccine plasmids and recombinant poxvirus vectors which have been previously shown to elicit strong T cell responses when used together in a 'prime-boost' protocol (Kent *et al.*, 1997). An important advantage of scrambled antigen vaccines or 'Savines' is that the amount of starting sequence information for the design can be easily expanded to include the majority of the protein sequences from a pathogen or for cancer, thereby providing the maximum possible vaccine or therapy coverage for a given population.

An embodiment of the systematic fragmentation approach described herein was based on the size and processing requirements for T cell epitopes and was designed to cause maximal disruption to the structure and function of protein sequences. This fragmentation approach ensures that the maximum possible range of T cell epitopes will be present from any incorporated protein sequence without the protein being functional and able to compromise vaccine safety

Another important advantage of Savines is that consensus protein sequences can be used for their design. This feature is only applicable when the design needs to cater for pathogen or cancer antigens whose sequence varies considerably. HIV is a highly

- 124 -

mutagenic virus, hence this feature was utilised extensively to design a vaccine which has the potential to cover not only field isolates of HIV but also the major HIV clades involved in the current HIV pandemic. To construct the HIV Savine, one set of long oligonucleotides was synthesised, which included degenerate bases in such a way that 8
5 constructs are theoretically required for the vaccine to contain all combinations in any stretch of 9 amino acids. The inventors believe that this approach can be improved for the following reasons: 1) While degenerate bases should be theoretically equally represented, in practice some degenerate bases were biased towards one base or the other, leading to a lower than expected frequency of the designed mutations in the two full length HIV
10 Savines which were constructed (see Table 1). 2) Only sequence combinations actually present in the HIV clade consensus sequences are required to get full clade coverage, hence the number of full length constructs needed could be reduced. To reduce the number of constructs however, separate sets of long oligonucleotides would have to be synthesised, significantly increasing the cost, time and effort required to generate a vaccine capable of
15 such considerable vaccine coverage.

A significant problem during the construction of the HIV Savine synthetic DNA sequence was the incorporation of non-designed mutations. The most serious types of mutations were insertions, deletions or those giving rise to stop codons, all of which change the frame of the synthesised sequences and/or caused premature truncation of the
20 Savine proteins. These types of mutation were removed during construction of the HIV Savines by sequencing multiple clones after subcassette and cassette construction and selecting functional clones. The major source of these non-designed mutations was in the long oligonucleotides used for Savine synthesis, despite their gel purification. This problem could be reduced by making the initial subcassettes smaller thereby reducing the
25 possibility of corrupted oligonucleotides being incorporated into each subcassette clone. The second major cause of non-designed mutations was the large number of PCR cycles required for the PCR and ligation-mediated joining of the subcassettes. Including extra sequencing and clone selection steps during the subcassette joining process should help to reduce the frequency of non-designed mutations in future constructs. Finally, another
30 method that could help reduce the frequency of such mutations at all stages is to use resolvase treatment. Resolvases are bacteriophage-encoded endonucleases which recognise disruptions to double stranded DNA and are primarily used by bacteriophages to resolve

- 125 -

Holliday junctions (Mizuuchi, 1982; Youil *et al.*, 1995). T7 endonuclease I has already been used by the present inventors in synthetic DNA constructions to recognise mutations and cleave corrupted dsDNA to allow gel purification of correct sequences. Cleavage of corrupted sequences occurs because after a simple denaturing and hybridisation step
5 mutated DNA hybridises to correct DNA sequences and results in a mispairing of DNA bases which is able to be recognised by the resolvase. This method resulted in a 50% reduction in the frequency of errors. Further optimisation of this method and the use of a thermostable version of this type of enzyme could further reduce the frequency of errors during long Savine construction.

10 Two pools of Vaccinia viruses expressing Savine cassettes were both shown to restimulate HIV-specific responses from three different patients infected with B clade HIV viruses. These results provide a clear indication that the HIV Savine should provide broad coverage of the population because each patient had a different HLA pattern yet both pools were able to restimulate HIV-specific CTL responses in all three patients against all three
15 natural HIV proteins tested. Also, both pools were shown to restimulate virtually identical CTL patterns in all three patients. This result was unexpected because some responses should have been lost or gained due to the amino acid differences between the two pools and because Pool 1 is only capable of expressing 2/3 of the full length HIV Savine. There are two suggested reasons why the pattern of CTL lysis was not altered between the two
20 viral pools. Firstly, the sequences in the Savine constructs are nearly all duplicated because the fragment sequences overlap. Hence the loss of a third of the Savine may not have excluded sufficient T cell epitopes for differences to be detected in only three patient samples against only three HIV proteins. Secondly, while mutations often destroy T cell epitopes, if they remain functional, then the CTL they generate frequently can recognise
25 alternate epitope sequences. Taken together this finding indirectly suggests that combining only two Savine constructs may provide robust multiclade coverage. Further experiments are being carried out to directly examine the capacity of the HIV Savine to stimulate CTL generated by different strains of HIV virus. The capacity of the two HIV-1 Savine Vaccinia vector pools to stimulate CD4+ T cell HIV-1 specific responses from infected
30 patients was also tested (Figure 20). Both patients showed significant proliferation of CD4+ T cells although both pools did not show consistent patterns suggesting that the two pools may provide wider vaccine coverage than using either pool independently.

- 126 -

The present inventors have generated a novel vaccine strategy, which has been used to generate what the inventors believe to be the most effective HIV candidate vaccine to date. The inventors have used this vaccine to immunise naive mice. Figure 21 shows conclusively that the HIV-1 Savine described above can generate a Gag and Nef CTL
5 response in naïve mice. It should be noted, however, that the Nef CTL epitope appeared to exist only in Pool 1 since it was not restimulated by Pool 2. This is further proof of the utility of combining HIV-1 Savine Pool 1 and Pool 2 components together to provide broader vaccine coverage.

The HIV-1 Savine Vaccinia vectors have also been used to restimulate *in vivo*
10 HIV-1 responses in pre-immune *M. nemestrina* monkeys. These experiments (Figure 22) showed, by INF- γ ELISPOT and CD69 expression on both CD4 and CD8 T cells, that the ability of the HIV-1 SAVINE to restimulate HIV-1 specific responses in vivo is equivalent or perhaps better than another HIV-1 candidate vaccine.

This is a generic strategy able to be applied to many other human infections or
15 cancers where T-cell responses are considered to be important for protection or recovery. With this in mind the inventors have begun constructing Savines for melanoma, cervical cancer and Hepatitis C. In the case of melanoma, the majority of the currently identified melanoma antigens have been divided into two groups, one containing antigens associated with melanoma and one containing differentiation antigens from melanocytes, which are
20 often upregulated in melanomas. Two Savine constructs are presently being constructed to cater for these two groups. The reason for making the distinction is that treatment of melanoma might first proceed using the Savine that incorporates fragments of melanoma specific antigens only. If this Savine fails to control some metastases then the less specific Savine containing the melanocyte-specific antigens can then be used. It is important to
25 point out that other cancers also express many of the antigens specific to melanomas *e.g.*, testicular and breast cancers. Hence the melanoma specific Savine may have therapeutic benefits for other cancers.

A small Savine is also being constructed for cervical cancer. This Savine will contain two antigens, E6 and E7, from two strains of human papilloma virus (HPV), HPV-
30 16 and HPV-18, directly linked with causing the majority of cervical cancers worldwide. There is a large number of sequence differences in these two antigens between the two

- 127 -

strains which would normally require two Savines to be constructed. However since this Savine is small, the antigen fragments from both strains are being scrambled together. While it is normally better for the Savine approach to include all or a majority of the antigens from a virus, in this case only E6 and E7 are expressed during viral latency or in cervical carcinomas. Hence in the interests of simplicity, the rest of the HPV genome will not be included although all HPV antigens would be desirable in a Savine against genital warts.

Two Savines have also been constructed for two strains of hepatitis C, a major cause of liver disease in the world. Hepatitis C is similar to HIV in the requirements for a vaccine or therapeutic. However, the major hepatitis C strains share significantly lower homology, 69-79%, with one another than do the various HIV clades. To cater for this the inventors have decided to construct two separate constructs to cater for the two major strains present in Australia, types 1a and 3a, which together cause approximately 80-95% of hepatitis C infections in this country. Both constructs will be approximately the same size as the HIV Savine but will be blended together into a single vaccine or therapy.

Overall it is believed that the Savine vaccine strategy is a generic technology likely to be applied to a wide range of human diseases. It is also believed that because it is not necessary to characterise each antigen, this technology will be actively applied to animal vaccines as well where research into vaccines or therapies is often inhibited by the lack of specific reagents, modest research budgets and poor returns on animal vaccines.

EXAMPLE 2

Hepatitis C Savine

Synthetic immunomodulatory molecules have also been designed for treating Hepatitis C. In one example, the algorithm of Figure 25 was applied to a consensus polyprotein sequence of Hepatitis C 1a to facilitate its segmentation into overlapping segments (30 aa segments overlapping by 15 aa), the rearrangement of these segments into a scrambled order and the output of Savine nucleic acid and amino acid sequences, as shown in Figure 26. Exemplary DNA cassettes (A, B and C) are also shown in Figure 26, which contain suitable restriction enzyme sites at their ends to facilitate their joining into a single expressible open reading frame.

EXAMPLE 3***Melanoma Savine***

The algorithm of Figure 25 was also applied to melanocyte differentiation antigens (gp100, MART, TRP-1, Tyros, Trp-2, MC1R, MUC1F and MUC1R) and to
5 melanoma specific antigens (BAGE, GAGE-1, gp100In4, MAGE-1, MAGE-3, PRAME, TRP2IN2, NYNSO1a, NYNSO1b and LAGE1), as shown in Figure 27, to provide separate Savine nucleic acid and amino acid sequences for treating or preventing melanoma.

EXAMPLE 4***Resolvase Repair Experiment***

10 A resolvase can be used advantageously to repair errors in polynucleotides. The following procedure outlines resolvase repair of a synthetic 340 bp fragment in which DNA errors were common.

Method

The 340 bp fragment was PCR amplified and gel purified on a 4% agarose gel.
15 After spin purifying, 10ul of the eluate corresponding to approximately 100 ng was subjected to the resolvase repair treatment. The rest of the DNA sample was stored for later cloning as the untreated control.

2 μ L of 10xPCR buffer, 2 μ L of 20 mM $MgCl_2$ and 6 μ L of MilliQ™ water (MQW) and Taq DNA polymerase were added to the 10 μ L DNA sample. The mixture
20 was subjected to the following thermal profile; 95°C for 5min, 65°C for 30min, cooled and held at 37°C. Five μ L of 10xT7 endonuclease I buffer, 8 μ L of 1/50 μ L of T7endoI enzyme stock and 17 μ L of MQW were added, mixed and incubated for 30 min. Loading buffer was added to the sample and the sample was electrophoresed on a 4% agarose gel. A faint band corresponding to the full length fragment was excised and subjected to 15 further
25 cycles of PCR. The amplified fragment was agarose gel purified and, along with the untreated DNA sample, cloned into pBluescript. Eleven plasmid clones for each DNA sample were sequenced and the number and type of errors compared (see table)

Buffers were as follows:

10x T7endonuclease buffer

2.5ml 1M TRIS pH7.8, 0.5ml 1M $MgCl_2$, 25 μ L 1 M DTT, 50 μ L 10mg/mL BSA, 2 mL MQW made up to a total of 5 mL.

5 T7 endonuclease I stock

Concentrated sample of enzyme prepared by, and obtained from, Jeff Babon (St Vincent's Hospital) was diluted 1/50 using the following dilution buffer: 50 μ L 1 M TRIS pH7.8, 0.1 μ L 1M EDTA pH8, 5 μ L 100 mM glutathione, 50 μ L 10mg/mL BSA, 2.3 mL MQW, 2.5 mL glycerol made up to a total of 5 mL.

10 Results

The results are summarised in Tables 2 and 3.

TABLE 2

Total Errors	
Unreated	Resolvase treated
A/T to G/C = 6	A/T to G/C = 1
G/C to A/T = 12	G/C to A/T = 7
A/T to deletion = 1	A/T to deletion = 1
G/C to deletion = 6	G/C to deletion = 3

TABLE 3

Clone summary	
Unreated	Resolvase treated
6/11 contained deletions	3/11 contained deletions
9/11 contained mutations	7/11 contained mutations

- 130 -

Clone summary	
Untreated	Resolvase treated
2/11 correct	3/11 correct

Discussion/Conclusion

While overall the number of correct clones obtained was not significantly different, there was a significant difference in the level of errors. This reduction in errors becomes more significant as greater numbers of long oligonucleotides are joined into the one construct *i.e.*, increasing the difference between untreated *versus* treated samples in the chance of obtaining a correct clone. It is believed that combining another resolvase such as T4 endonuclease VII may further enhance repair or increase the bias against errors.

Importantly, this experiment was not optimised *e.g.*, by using proofreading PCR enzymes or optimised conditions. Finally if the repair reaction is carried out during normal PCR, for example, by including a thermostable resolvase, it is believed that amplification of already damaged long oligonucleotides, and the normal accumulation of PCR induced errors, even using error reading polymerases during PCR, could be reduced significantly. The repair of damaged long oligonucleotides is particularly important for synthesis of long DNA fragment such as in Savines because, while the rate of long oligonucleotide damage is typically <5%, after joining 10 oligonucleotides, the error rate approaches 50%. This is true even using the best proofreading PCR enzymes because these enzymes do not verify the sequence integrity using correct oligonucleotide templates that exist as a significant majority (95%) in a joining reaction.

The disclosure of every patent, patent application, and publication cited herein is incorporated herein by reference in its entirety.

The citation of any reference herein should not be construed as an admission that such reference is available as "Prior Art" to the instant application

Throughout the specification the aim has been to describe the preferred embodiments of the invention without limiting the invention to any one embodiment or specific collection of features. Those of skill in the art will therefore appreciate that, in

- 131 -

light of the instant disclosure, various modifications and changes can be made in the particular embodiments exemplified without departing from the scope of the present invention. All such modifications and changes are intended to be included within the scope of the appended claims.

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WHAT IS CLAIMED IS:

1. A synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide.
2. The synthetic polypeptide of claim 1, consisting essentially of different segments of a single parent polypeptide.
3. The synthetic polypeptide of claim 1, consisting essentially of different segments of a plurality of different parent polypeptides.
4. The synthetic polypeptide of claim 1, wherein the segments in said synthetic polypeptide are linked sequentially in a different order or arrangement relative to their linkage in said at least one parent polypeptide.
5. The synthetic polypeptide of claim 4, wherein the segments in said synthetic polypeptide are randomly rearranged relative to their order or arrangement in said at least one parent polypeptide.
6. The synthetic polypeptide of claim 1, wherein the size of an individual segment is at least 4 amino acids.
7. The synthetic polypeptide of claim 6, wherein the size of an individual segment is from about 20 to about 60 amino acids.
8. The synthetic polypeptide of claim 7, wherein the size of an individual segment is about 30 amino acids.
9. The synthetic polypeptide of claim 7, comprising at least 30% of the parent polypeptide sequence.
10. The synthetic polypeptide of claim 1, wherein at least one of said segments comprises partial sequence identity or homology to one or more other said segments.
11. The synthetic polypeptide of claim 10, wherein the sequence identity or homology is contained at one or both ends of an individual segment.

12. The synthetic polypeptide of claim 11, wherein one or both ends of said segment comprises at least 4 contiguous amino acids that are identical to, or homologous with, an amino acid sequence contained within one or more other of said segments.
13. The synthetic polypeptide of claim 10, wherein the size of an individual segment is about twice the size of the sequence that is identical or homologous to the or each other said segment.
14. The synthetic polypeptide of claim 13, wherein the size of an individual segment is about 30 amino acids and the size of the sequence that is identical or homologous to the or each other said segment is about 15 amino acids.
15. The synthetic polypeptide of claim 1, wherein an optional spacer is interposed between some or all of the segments.
16. The synthetic polypeptide of claim 15, wherein the spacer alters proteolytic processing and/or presentation of adjacent segment(s).
17. The synthetic polypeptide of claim 16, wherein the spacer comprises at least one neutral amino acid.
18. The synthetic polypeptide of claim 16, wherein the spacer comprises at least one alanine residue.
19. The synthetic polypeptide of claim 1, wherein the at least one parent polypeptide is associated with a disease or condition.
20. The synthetic polypeptide of claim 1, wherein the at least one parent polypeptide is selected from a polypeptide of a pathogenic organism, a cancer-associated polypeptide, an autoimmune disease-associated polypeptide, an allergy-associated polypeptide or a variant or derivative of these.
21. The synthetic polypeptide of claim 1, wherein the at least one parent polypeptide is a polypeptide of a virus.
22. The synthetic polypeptide of claim 21, wherein the virus is selected from a Human Immunodeficiency Virus (HIV) or a Hepatitis virus.
23. The synthetic polypeptide of claim 22, wherein the virus is a Human Immunodeficiency Virus (HIV) and the at least one parent polypeptide is selected from env, gag, pol, vif, vpr, tat, rev, vpu and nef, or a combination thereof.

24. The synthetic polypeptide of claim 1, wherein the at least one parent polypeptide is a cancer-associated polypeptide.
25. The synthetic polypeptide of claim 24, wherein the cancer is melanoma.
26. The synthetic polypeptide of claim 25, wherein the at least one parent polypeptide is a melanocyte differentiation antigen.
27. The synthetic polypeptide of claim 25, wherein the at least one parent polypeptide is a melanocyte differentiation antigen selected from gp100, MART, TRP-1, Tyros, TRP2, MC1R, MUC1F, MUC1R or a combination thereof.
28. The synthetic polypeptide of claim 25, wherein the at least one parent polypeptide is a melanoma-specific antigen.
29. The synthetic polypeptide of claim 25, wherein the at least one parent polypeptide is a melanoma-specific antigen selected from BAGE, GAGE-1, gp100In4, MAGE-1, MAGE-3, PRAME, TRP2IN2, NYNSO1a, NYNSO1b, LAGE1 or a combination thereof.
30. A synthetic polynucleotide encoding a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide.
31. A method for producing the synthetic polynucleotide encoding a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide, said method comprising:
- linking together in the same reading frame a plurality of nucleic acid sequences encoding different segments of the at least one parent polypeptide to form a synthetic polynucleotide whose sequence encodes said segments linked together in a different relationship relative to their linkage in the at least one parent polypeptide.
32. The method of claim 31, further comprising fragmenting the sequence of a respective parent polypeptide into fragments and linking said fragments together in a different relationship relative to their linkage in a respective parent polypeptide sequence.

33. The method of claim 32, wherein the fragments are randomly linked together.
34. The method of claim 31, further comprising reverse translating the sequence of a respective parent polypeptide or a segment thereof to provide a nucleic acid sequence encoding said parent polypeptide or said segment.
35. The method of claim 34, wherein an amino acid of a respective parent polypeptide sequence is reverse translated to provide a codon, which has higher translational efficiency than other synonymous codons in a cell of interest.
36. The method of claim 35, wherein an amino acid of said parent polypeptide sequence is reverse translated to provide a codon which, in the context of adjacent or local sequence elements, has a lower propensity of forming an undesirable sequence that is refractory to the execution of a task.
37. The method of claim 35, wherein an amino acid of said parent polypeptide sequence is reverse translated to provide a codon which, in the context of adjacent or local sequence elements, has a lower propensity of forming an undesirable sequence selected from a palindromic sequence or a duplicated sequence, which is refractory to the execution of a task selected from cloning or sequencing.
38. The method of claim 31, further comprising linking a spacer oligonucleotide encoding at least one spacer residue between segment-encoding nucleic acids.
39. The method of claim 38, wherein spacer oligonucleotide encodes 2 to 3 spacer residues.
40. The method of claim 38 or claim 39, wherein the spacer residue is a neutral amino acid.
41. The method of claim 38 or claim 39, wherein the spacer residue is alanine.
42. The method of claim 31, further comprising linking in the same reading frame as other segment-containing nucleic acid sequences at least one variant nucleic acid sequence which encodes a variant segment having a homologous but not identical amino acid sequence relative to other encoded segments.

43. The method of claim 42, wherein the variant segment comprises conserved and/or non-conserved amino acid differences relative to one or more other encoded segments.
44. The method of claim 43, wherein the differences correspond to sequence polymorphisms.
45. The method of claim 44, wherein degenerate bases are designed or built in to the at least one variant nucleic acid sequence to give rise to all desired homologous sequences.
46. The method of claim 31, further comprising optimising the codon composition of the synthetic polynucleotide such that it is translated efficiently by a host cell.
47. A synthetic construct comprising a synthetic polynucleotide encoding a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide, wherein said synthetic polynucleotide is operably linked to a regulatory polynucleotide.
48. The synthetic construct of claim 47, further including a nucleic acid sequence encoding an immunostimulatory molecule.
49. The synthetic construct of claim 48, wherein the immunostimulatory molecule comprises a domain of an invasin protein (Inv).
50. The synthetic construct of claim 48, wherein the immunostimulatory molecule comprises the sequence set forth in SEQ ID NO: 1467 or an immune stimulatory homologue thereof.
51. The synthetic construct of claim 48, wherein the immunostimulatory molecule is a T cell co-stimulatory molecule.
52. The synthetic construct of claim 48, wherein the immunostimulatory molecule is a T cell co-stimulatory molecule selected from a B7 molecule or an ICAM molecule.
53. The synthetic construct of claim 48, wherein the immunostimulatory molecule is a B7 molecule or a biologically active fragment thereof, or a variant or derivative of these.

54. The synthetic construct of claim 48, wherein the immunostimulatory molecule is a cytokine selected from an interleukin, a lymphokine, tumour necrosis factor or an interferon.

55. The synthetic construct of claim 48, wherein the immunostimulatory molecule is an immunomodulatory oligonucleotide.

56. An immunopotentiating composition, comprising an immunopotentiating agent selected from the synthetic polypeptide of claim 1, the synthetic polynucleotide of claim 30 or the synthetic construct of claim 47, together with a pharmaceutically acceptable carrier.

57. The composition of claim 56, further comprising an adjuvant.

58. A method for modulating an immune response, which response is preferably directed against a pathogen or a cancer, comprising administering to a patient in need of such treatment an effective amount of an immunopotentiating agent selected from the synthetic polypeptide of claim 1, the synthetic polynucleotide of claim 30, the synthetic construct of claim 47, or the composition of claim 56.

59. A method for treatment and/or prophylaxis of a disease or condition, comprising administering to a patient in need of such treatment an effective amount of an immunopotentiating agent selected from selected from the synthetic polypeptide of claim 1, the synthetic polynucleotide of claim 30, the synthetic construct of claim 47, or the composition of claim 56.

60. A computer program product for designing the sequence of a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide, said program product comprising:

- code that receives as input the sequence of said at least one parent polypeptide;
- code that fragments the sequence of a respective parent polypeptide into fragments;
- code that links together said fragments in a different relationship relative to their linkage in said parent polypeptide sequence; and

- a computer readable medium that stores the codes.

61. The computer program product of claim 60, further comprising code that randomly rearranges said fragments.

62. The computer program product of claim 60, further comprising code that links the sequence of a spacer residue to the sequence of said at least one parent polypeptide or to said fragments.

63. A computer program product for designing the sequence of a synthetic polynucleotide encoding a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide, comprising:

- code that receives as input the sequence of at least one parent polypeptide;
- code that fragments the sequence of a respective parent polypeptide into fragments;
- code that reverse translates the sequence of a respective fragment to provide a nucleic acid sequence encoding said fragment;
- code that links together in the same reading frame each said nucleic acid sequence to provide a polynucleotide sequence that codes for a polypeptide sequence in which said fragments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide sequence; and
- a computer readable medium that stores the codes.

64. The computer program product of claim 63, further comprising code that randomly rearranges said nucleic acid sequences.

65. The computer program product of claim 64, further comprising code that reverse translates an amino acid of a respective parent polypeptide sequence to provide a codon, which has higher translational efficiency than other synonymous codons in a cell of interest.

66. The computer program product of claim 63, further comprising code that reverse translates an amino acid of a respective parent polypeptide sequence to provide a codon

which, in the context of adjacent or local sequence elements, has a lower propensity of forming an undesirable sequence that is refractory to the execution of a task.

67. The computer program product of claim 63, further comprising code that links a spacer oligonucleotide to one or more of said nucleic acid sequences.

68. A computer for designing the sequence of a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide, wherein said computer comprises:

- (a) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said machine-readable data comprise the sequence of at least one parent polypeptide;

- (b) a working memory for storing instructions for processing said machine-readable data;

- (c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium, for processing said machine readable data to provide said synthetic polypeptide sequence; and

- (d) an output hardware coupled to said central processing unit, for receiving said synthetic polypeptide sequence.

69. The computer of claim 68, wherein the processing of said machine readable data comprises fragmenting the sequence of a respective parent polypeptide into fragments and linking together said fragments in a different relationship relative to their linkage in the sequence of said parent polypeptide.

70. The computer of claim 68, wherein the processing of said machine readable data comprises randomly rearranging said fragments.

71. The computer of claim 68, wherein the processing of said machine readable data comprises linking the sequence of a spacer residue to the sequence of said at least one parent polypeptide or to said fragments.

72. A computer for designing the sequence of a synthetic polynucleotide encoding a synthetic polypeptide comprising a plurality of different segments of at least one parent polypeptide, wherein the segments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide, wherein said computer comprises:

(a) a machine-readable data storage medium comprising a data storage material encoded with machine-readable data, wherein said machine-readable data comprise the sequence of at least one parent polypeptide;

(b) a working memory for storing instructions for processing said machine-readable data;

(c) a central-processing unit coupled to said working memory and to said machine-readable data storage medium, for processing said machine readable data to provide said synthetic polynucleotide sequence; and

(d) an output hardware coupled to said central processing unit, for receiving said synthetic polynucleotide sequence.

73. The computer of claim 72, wherein the processing of said machine readable data comprises fragmenting the sequence of a respective parent polypeptide into fragments, reverse translating the sequence of a respective fragment to provide a nucleic acid sequence encoding said fragment and linking together in the same reading frame each said nucleic acid sequence to provide a polynucleotide sequence that codes for a polypeptide sequence in which said fragments are linked together in a different relationship relative to their linkage in the at least one parent polypeptide sequence.

74. The computer of claim 72, wherein the processing of said machine readable data comprises randomly rearranging said nucleic acid sequences.

75. The computer of claim 72, wherein the processing of said machine readable data comprises reverse translating an amino acid of a respective parent polypeptide sequence to provide a codon, which has higher translational efficiency than other synonymous codons in a cell of interest.

76. The computer of claim 72, wherein the processing of said machine readable data comprises reverse translating an amino acid of a respective parent polypeptide sequence to provide a codon which, in the context of adjacent or local sequence elements, has a lower propensity of forming an undesirable sequence that is refractory to the execution of a task.

77. The computer of claim 72, wherein the processing of said machine readable data comprises linking a spacer oligonucleotide to one or more of said nucleic acid sequences.

1/216

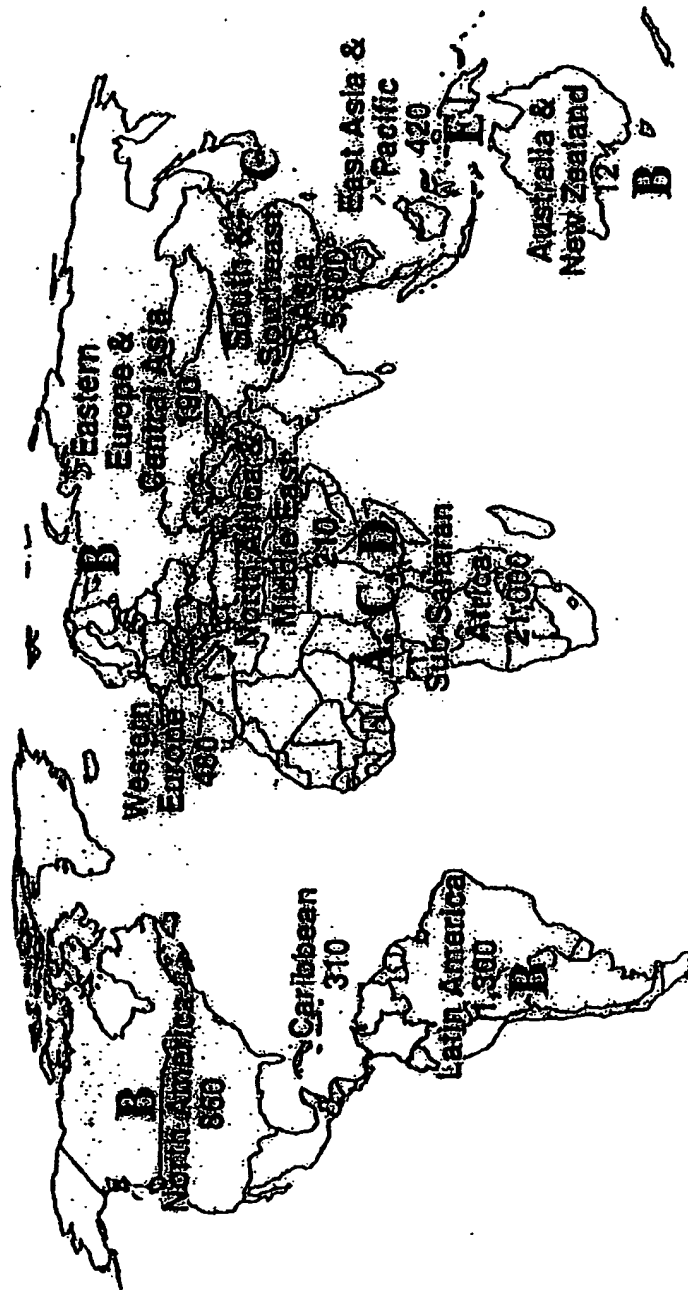


FIGURE 1

2/216

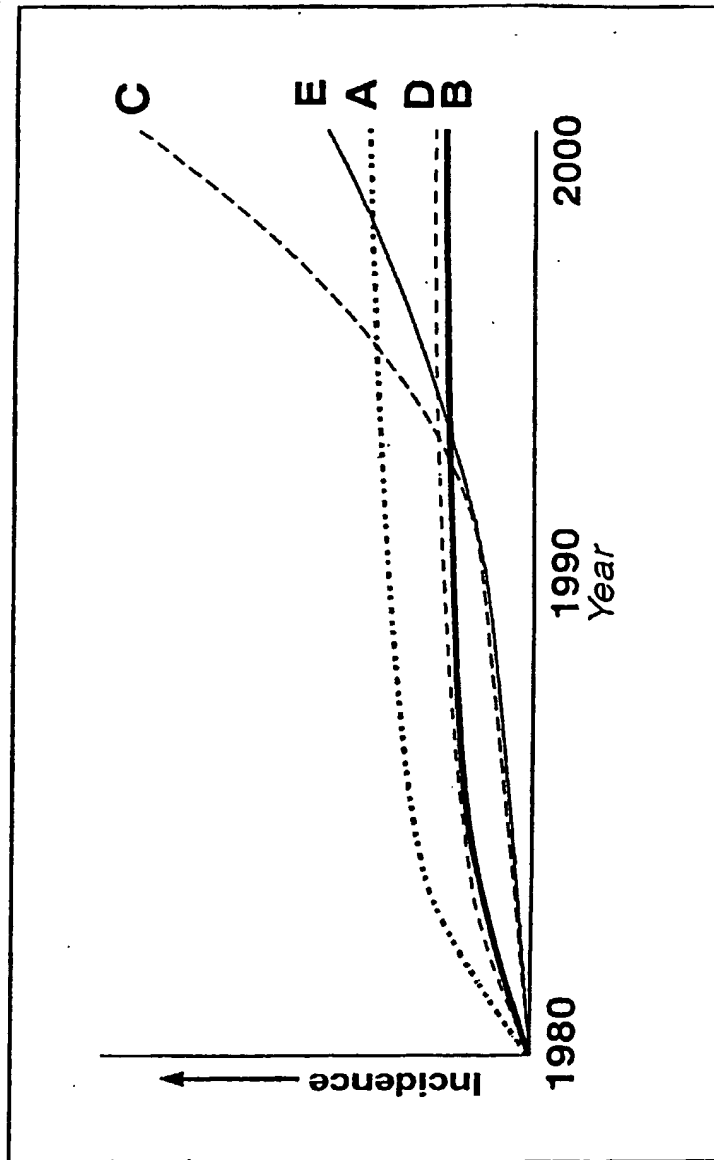


FIGURE 2

3/216

p17 ->	/<-	nls	->/
/<-	membrane binding	->/	
DESIGNED SEQ	MGARASVLSGGKLDawEKIRLRPGGKKKYKMKHLVWASRELERFALNPGILLETAEGCQQLIEQLQSALKT	70	
MUTATED AAs	R E RL I S S K G P Q		
E-ISOLATE	MGARASVLSGGKLDawEKIRLRPGGKKKYKMKHLVWASRELERFALNPGILLETAEGCQQLIEQLQSTLKT	70	
CONSENSUS-A	mGARASvLsggkLDawekIrLRPgGkKkYrIkhIvwAsreLerFaLnPsIlLeTaegcqqimeQlqsalkt	70	
CONSENSUS-B	-----e-r-----k-i-----v-g---s---R--lg---ps-q-	70	
CONSENSUS-C	-----i-r-----?-?-?-h-Mi-----g---s---k--ik---P-Q-	69	
CONSENSUS-D	-----?-?-?-?-?-i-----G---s---k--ig---P-ig-	68	
CONSENSUS-F	-----?-?-?-?-?-i-g---s---rk--lg---ps-Q-	70	
CONSENSUS-G	-----?-?-?-?-?-?-?-G---T-----??-P?-Q-	63	
CONSENSUS-H	-----?-?-?-?-?-?-?-L-?I---P---	64	
CONSENSUS-O	-----?-?-?-?-?-?-S-?-?-?-C-?-?-?-E?LLQ--EP---	62	
CONSENSUS-CPZ	-----?-?-?-?-?-?-M?-?-?-?-?-?-?-K???-P?P???	42	
	/<- nls ->/		
DESIGNED SEQ	GSEELKSLYNTIATLWCVHQRIEVKDTKEALDKIEEQKKSQOK.....TQAAAA..DT.GS...SSKV		
MUTATED AAs	T R F V D R V N K N Q		
E-ISOLATE	GSEELKSLYNTIATLWCVHQRIEVKDTKEALDKIEEVQKKSQOKK.....QAAAA..DT.GS...SSKV		
CONSENSUS-A	g?eElkSLfntvatLycvHqrIdvkdTKeAlDkiEeignKskgk?????tqgaaA..?T.gs?...sskv	126	
CONSENSUS-B	-s---r---y-----e-----E---k-----a-----??d--n??-q-	128	
CONSENSUS-C	-T---r---?-?-?-e-r-----E---?Q-----k..ad?-k.....	120	
CONSENSUS-D	-s-----?-?-?-e-e-----e-m-E-----k-----a---t..D..rn....-Q-	125	
CONSENSUS-F	-S---r---y---v---f---vE-----L-E---q-----?---dK.....	123	
CONSENSUS-G	-T---?-?-?-?-?-?-e-----eEV-Ka-kn-Q-----?---??..e?..n....-q-	110	
CONSENSUS-H	-T---Q---LL-?-?-?-?-?-?-?-?-?-?-?-?-T?..DK.??..??-?	106	
CONSENSUS-O	-S??-?-?-AI?V-W---N-??I?-?-Q-Q-IQ-LK-V.M?-RKS...A-AAKE.....?RQ?	106	
CONSENSUS-CPZ	?S????-??V-W-?-?????-?-?-K?????Q??T-S---??G????-????-???????	61	
	p17 \ / p24		
DESIGNED SEQSQNYPIVQNAQGMVHQPLSPRTLNAWVKVIEEKGFNPEVIPMFSALESEGATPDQLNMMLNIVGGH		
MUTATED AAs	L AI V A S T T T		
E-ISOLATESQNYPIVQNAQGMVHQPLSPRTLNAWVKVIEEKGFNPEVIPMFSALESEGATPDQLNMMLNIVGGH		
CONSENSUS-A	????SqNYPIVQNAqgOm?hQ?lSPRTLNAwVKviEekaFspEVIPmFsaLSEGATpQdLnmMLNiVgGH	190	
CONSENSUS-B	-----l---v---ai-----v-----T---T---	194	
CONSENSUS-C	-----L---v---ai-----?-T-----T---T---	185	
CONSENSUS-D	-----L---v---ai-----t-----T---	191	
CONSENSUS-F	-----l---v---i-----T-----T---	188	
CONSENSUS-G	-----i-----v-----t-----T---	174	
CONSENSUS-H	-----?V---AI-----V-----A-----?	170	
CONSENSUS-O	-----?-?-?-V---AI-----AV-----N---I---M-----??Y-I-T-?-AI---	168	
CONSENSUS-CPZ	-----??-?-?-?-?-?-?-V-----?-?-?-T---A-?-?	107	
DESIGNED SEQ	QAAMQMLKETINEEAAEWDRVHPVHAGPIPPGQMREPRGSDIAGTTSTLQEQIGWMTN...NPPiPVGDI		
MUTATED AAs	D I VA I A S V E		
E-ISOLATE	QAAMQMLKETINEEAAEWDRVHPVHAGPIPPGQMREPRGSDIAGTTSTLQEQIGWMTN...NPPiPVGDI		
CONSENSUS-A	QAAMQMLKdtInEeAAewDr?HPVhAgPippgQmREPrGSDIAGtTStlqEqigwmTs...NPPiPVGdI	256	
CONSENSUS-B	-----e-----l---a-----n-----e-	261	
CONSENSUS-C	-----l-----vA-----a-----?	251	
CONSENSUS-D	-----E-----l---A-----?-e-----e-	257	
CONSENSUS-F	-----L---q-----i-----q-----v---e-	255	
CONSENSUS-G	-----I---Q-----I---?-R-----e-	239	
CONSENSUS-H	-----?-?-?-A-----?-?-?-?	233	
CONSENSUS-O	-G-L-V--EV-----?-T-P??-L---I---T-----Q---?-T-R.??-??-	229	
CONSENSUS-CPZ	-G---V--EV-----L-T-----L-----?-?-?-????-??-??-	160	
	/<- MHR ->/		

FIGURE 3

SUBSTITUTE SHEET (RULE 26)

4/216

		p24 \/ \/ 'p2' \/ p7	Zn-motif /<-
DESIGNED SEQ	SILKALGTGATLEEMMTACQGVGGPSHKARVLAEAMSQA...TH.AN...IMMQRGNF.KGQKRIIKCFN		
MUTATED AAs	T R P S G V NN R P V		
ISOLATE-E	SILKALGTGATLEEMMTACQGVGGPSHKARVLAEAMSQA...QH.AN...IMMQRGNF.KGQTR.IKCFN		
CONSENSUS-A	sILraLg?gAtLeEMMTacQgVggPgHKArvLAEAmSqv...q???n??iMmQrGnf.rgqkr?iKCFN		38
CONSENSUS-B	T--K--Pa-----tn-s.at?-----n-rKtv----		39
CONSENSUS-C	T-----P--s-----s-----a...nn-----s--K-p--iv----		38
CONSENSUS-D	t--K--P?-----s-----a...tn.s-ta-----K-prki----		39
CONSENSUS-F	T--K--P-----a...TN--?a-----ks--K--R-iv----		38
CONSENSUS-G	T--?--P-----?-----A...SG--A-A--?--K??--K-P??-----?		36
CONSENSUS-H	?--?-----SI-----?-----?-----TN--?A--?--K--K--R-I?-----		35
CONSENSUS-O	Q--K?--P?-----V-----T-----A?AQQDLKGGYTA.VF-----QN.P?R-G-----		35
CONSENSUS-CPZ	?--K-----?-----?-----?-----?-----?-----VF?--?--G??--?-----		26
		pol cds -> p7 \/ 'p1' \/ p6	
DESIGNED SEQ	CGKEGHLARNCRAPRKKGCNKCGKEGHQMKDCT..E.RQANFLGKIWPSNKG.RPGNFPQSKP.....		
MUTATED AAs	I K R H L R		
ISOLATE-E	CGKEGHLARNCRAPRKKGCNKCGKEGHQMKDCT..E.RQANFLGKIWPSNKG.RPGNFPQSKP.....		
CONSENSUS-A	CGKEGHLARNCRAPRKKGCNKCGKEGHQMKDCT..e.rQANFlgkiwpsSsKG.RPgNFPQSRp.....		443
CONSENSUS-B	-----i-k-----h-----l-----???????		453
CONSENSUS-C	-----i-----?-----?-----L-----???????		439
CONSENSUS-D	-----i-k-----h-----l-----		449
CONSENSUS-F	-----i-k-----r-----n-----L-----		445
CONSENSUS-G	-----?-----?-----?-----H-----L--?--?		414
CONSENSUS-H	-----?-----?-----?-----?-----L-----		406
CONSENSUS-O	-----I--?-----Q-----?..NG?-----Y--PGGT-----YV--???		411
CONSENSUS-CPZ	-----?-----K--R--R--Q-----?--?--?--?--V-----?--?--?--?--V--?--?--?		306
		vpr binding p6 terminus / (80%)	
DESIGNED SEQEPTAPPAE.....NF.GPGEETT.PS....PKQEQKD....KEHYPPSASLKSFLGNDPLSQ		
MUTATED AAs	S R Q P L L S		
ISOLATE-EEPTAPPAE.....NW.GMGEE.....QKD....KEHPPPSVSLKSFLGNDPLSQ		
CONSENSUS-AEPTAPPAE.....?f?gmgeeit.s?...pkqeqkd...?ke??ppl?slKSFLGNDplSQ		485
CONSENSUS-B	??..???-----e.....s.rf--t-tps???q--pi-----ly?--a--r-----s--\$		500
CONSENSUS-C	???????-----S..rF--t..pa.....p--??--?--t-----x		479
CONSENSUS-D	-----S..F-----PS....q-----?--ly--a-----		495
CONSENSUS-F	-----?-----?-----PS....egly--a-----		482
CONSENSUS-G	-----?-----S..?--?--?--PS....P??-----LY?-----		440
CONSENSUS-H	-----S..F--M..P-----?--?--?--?-----		436
CONSENSUS-O	-----?--S--M-----?VK.?Q....EN--?--G....?--LY--FA-----T-Q\$		444
CONSENSUS-CPZ	-----I-----Y..?Q--?K?-----?--?--?--?--?L--?-----?--?--		333

CONSENSUS A-CPZ FROM LOS ALAMOS HIV SEQUENCE DATABASE
ISOLATE-E SEQ FROM ISOLATE 93TH253 THAILAND

Underlined AA are not present in all overlapping segments

FIGURE 3 (Cont)

SUBSTITUTE SHEET (RULE 26)

5/216

DESIGNED SEQ	FFRE.NLAFQOGKAREF.....SSE..QTGANSSASRKLGDGGG.....AER..Q	
MUTATED AAS	P E P R PT D	
ISOLATE-E	FFRE.NLAFQOGKAREF.....SSE..QTGANSSASRKLGDGGG.....AER..Q	
CONSENSUS-A	FFRE.NLAFQOGKAREF.....SSE..QT??NS?TSR?LWDGG?D??..L?....??G?E?..Q	35
CONSENSUS-B	----d---p--k--e-????????????---Ra--p--r--E-qVw--r--nnS-S???-EA-adr...-	49
ISOLATE-C	----T---K--E-----P-----RA--P-T---QV.RGSN....T.FSEAGAER..Q	
CONSENSUS-D	----d---P--K--GEI.....RA--P---E-RVW--r--NP-S....eT-A-R...-	48
CONSENSUS-O	---?..?--SGGH---QL.....CA--TS-PI-P-?.....GSE.....GT-ES?---G??	35
CONSENSUS-U	----P--K--E-----P-----RA--P---E-RVW--G--K.T-S....ET-A-R...-	48
CONSENSUS-CPZ	----??????????-L.....CA-????--?--?--????-?--?--?--?--?--?--?--?	13
protease		
V / <- gag cds end		
DESIGNED SEQ	GT..SSSFSPQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEDINLPGKWKPKMIGGIGGPIKVRQYD	
MUTATED AAS	LN V I EM R	
ISOLATE-E	GT..SSSFSPQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEDINLPGKWKPKMIGGIGGPIKVRQYD	
CONSENSUS-A	G?..??SF?FPQITLWQRPLVTI?IGQIEALLDTGADDTVLEDINLPGKWKPK?IGGIGGPIKVRQYD	96
CONSENSUS-B	---tV--s-----ik-g---K-----eM---r---M-----	116
ISOLATE-C	---LN-G---K-----E-----M-----	
CONSENSUS-D	---TV--n-----IK-G---K-----Em-----M-----	115
CONSENSUS-O	R...A-??CL---P--D--I--A-VG-H-C-?-----NN-Q-E-?-?-M-----KE-?	94
CONSENSUS-U	---IV--S-----V--RVG---K-----E-----M-----	115
CONSENSUS-CPZ	?-?	55
protease V / p66, p51		
DESIGNED SEQ	QILIEICGKKAIGTVLVGPTPVNIIGRNMLTQIGCTLNFPISPIDTVPVKLPGMDGPKVKQWPLTEEKI	
MUTATED AAS	I H L L R E	
ISOLATE-E	QILIEICGKKAIGTVLVGPTPVNIIGRNMLTQIGCTLNFPISPIDTVPVKLPGMDGPKVKQWPLTEEKI	
CONSENSUS-A	QILIEICGKK?IGTVLVGPTPVNIIGRNMLTQIGCTLNFPISPIDTVPVKLKP?MDGPKVKQWPLTEEKI	164
CONSENSUS-B	-----H-A-----L-----G-----	186
ISOLATE-C	---I-----A-----M---L-R-----G-----	
CONSENSUS-D	---?--A-----L-----G-----	184
CONSENSUS-O	NVTV-??-?EVQ-----?--I--GL-----AP-----G-----S?---	159
CONSENSUS-U	-----A--I-----C-----R-----	185
CONSENSUS-CPZ	?V?-?-??R?V?--?	106
M41L D67N K70R		
DESIGNED SEQ	KALTEICKEMEKEGKISKIGPENPYNTVPVFAIKKDKSTKWRKLVDPRELNKRTQDFWEVQLGIPHPAGLK	
MUTATED AAS	A T K R I	
ISOLATE-E	KALTEICKEMEKEGKISKIGPENPYNTVPVFAIKKDKSTKWRKLVDPRELNKRTQDFWEVQLGIPHPAGLK	
CONSENSUS-A	KALT?IC?EMEKEGKISKIGPENPYNTVPVFAIKKDKSTKWRKLVDPRELNKRTQDFWEVQLGIPH?AGLK	231
CONSENSUS-B	---vE--T-----P-----	256
ISOLATE-C	---A--E--Q---R-----P-----	
CONSENSUS-D	---E--T-----R-----I-----P-----	254
CONSENSUS-O	E---A--Q---Q---R-----I-----?-----?-----PG---	227
CONSENSUS-U	---E--KD-----L-----N-----P-----	255
CONSENSUS-CPZ	?--?E--??-?	164
polymerase motif		
DESIGNED SEQ	KKKSVTVLVDVGDAYFSVPLDESFRKYTAFTIPSINNTPGIRYQYNVLPQGNKGSIPAIFQSSMTKILEPF	
MUTATED AAS	KD T P PQ	
ISOLATE-E	KKKSVTVLVDVGDAYFSVPLDESFRKYTAFTIPSINNTPGIRYQYNVLPQGNKGSIPAIFQSSMTKILEPF	
CONSENSUS-A	KKKSVTVLVDVGDAYFSVPLD??FRKYTAFTIPS?NNETPG?RYQYNVLPQGNKGS?P?IFQ?SMTKILEPF	295
CONSENSUS-B	---kd-----i-----A--s-----	326
ISOLATE-C	---EG-----T-----I-----P--S--PQ---	
CONSENSUS-D	---eD-----I-----I-----A--S-----	324
CONSENSUS-O	Q?Q-----C--PD-----V-----A--S-----D---	295
CONSENSUS-U	---ED-----I-----I-----A--S-----	325
CONSENSUS-CPZ	?-----D-----?-----?-----?	225

FIGURE 4

SUBSTITUTE SHEET (RULE 26)

6/216

DESIGNED SEQ	QPIELPEKDSWTVNDIQKLVGKLNWASQIYAGIKVKQLCKLLRGTKALTDIVPLTEEAELEENREI..	
MUTATED AAS	V E P R A E T A	
ISOLATE-E	QPIELPEKDSWTVNDIQKLVGKLNWASQIYAGIKVKQLCKLLRGTKALTDIVPLTEEAELEENREI..	
CONSENSUS-A	QP??LPEKDSWTVNDIQKLVGKLNWASQIYAGIK?KQLC?LLRGAKALTDIV?LTEEALELAENREI..	421
CONSENSUS-B	--Iv-----V--k--t--Evip-----	464
ISOLATE-C	--IQ-----P--VR--K-----T-----	
CONSENSUS-D	--sIk---E-----p--Vr--K--T---EViP-----	462
CONSENSUS-O	--?IQ--?-?V-----?-Q--RV?E--K-I--T-S--EV-P-S?---E---?..	419
CONSENSUS-U	--IQ--D-E-----P--V--K-----P--A-----	463
CONSENSUS-CPZ	--?I-----???-----P-----I--?-?-?-?-?-?-?-?-?-?-??-??	329
DESIGNED SEQ	.LREPVGHVYDPSKDLVAEVQKQGDQWYQIYQEPFKNLKTGKYSRKRSASHTNDVRQLTEVVQKIATE	
MUTATED AAS	K I I G F F(error) A M G K AA V	
ISOLATE-E	.LRIPVGHVYDPSKDLVAEVQKQGDQWYQIYQEPFKNLKTGKYSRKRSASHTNDVRQLTEVVQKIATE	
CONSENSUS-A	.LK?PVHGVYDPP?KDLVAE?QKQGDQWYQIYQEPFKNLKTGKYA?KRSASHTNDVRQLTEVVQKRV??E	484
CONSENSUS-B	--e-----s--i--i--g-----rm-G-----A---iat-	533
ISOLATE-C	--E---F--S--I--I--N--P--F-----F--T-----A---IAL-	
CONSENSUS-D	--E-----S--I--i--hG-----Rm-G-----a-a---IsT-	531
CONSENSUS-O	-----Q-D--WV?I--?-??-----?EH-----?RQKAS---IR--A--?-SO-	479
CONSENSUS-U	--E-----S--I--I--G-----QY-----RIK-----A---IAQ-	532
CONSENSUS-CPZ	???-???-R??-A??-I--	367
DESIGNED SEQ	SIVINGKTPKFRLP IQRETWETWMEYNQATWIPWEFVNTPLVLKLNQLEKDPVGAETFFYVDGAASR	
MUTATED AAS	K K A TD E A V N	
ISOLATE-E	SIVINGKTPKFRLP IQRETWETWMEYNQATWIPWEFVNTPLVLKLNQLEKDPVGAETFFYVDGAASR	
CONSENSUS-A	SIVINGK?PKFRLP IQ?ETWE?WMEYNQATWIPWEFVNTPLVLKLNQLEKDP I?GAETFFYVDGAANR	550
CONSENSUS-B	-----t--k--K--t-----e--v-----	602
ISOLATE-C	-----T-----K--A--TD-----E--A--V-----	
CONSENSUS-D	-----T-----K--T--?-----E--I-----	600
CONSENSUS-O	?-?-L--?-?-VTR--T--A?-----S--I--?-?-E--?-?-PI-	541
CONSENSUS-U	-----T-----K--A--T-----TE--V-----	602
CONSENSUS-CPZ	-----?-?-?-?-?-?-A--??-----?-----??-?-?-?-P??-?-?-L-	416
DESIGNED SEQ	ETKLGKAGYVTDGRQKVISLTETTNQKTELHAIHLALQDSGSEVNIVTDSQYALGIIQAQPDRESEVV	
MUTATED AAS	IV D Q Q L L K L	
ISOLATE-E	ETKLGKAGYVTDGRQKVISLTETTNQKTELHAIHLALQDSGSEVNIVTDSQYALGIIQAQPDRESEVV	
CONSENSUS-A	ETK?GKAGYVTDGRQKVSLTETTNQKTELHAIHLALQDSGSEVNIVTDSQYALGIIQAQPDRESEV?V	618
CONSENSUS-B	---l-----d-----q-----l--k---l--	672
ISOLATE-C	---I-----I-----Q--Q-----L--K--I--	
CONSENSUS-D	---L-----Pf-D-----Q--N-----L-----K--L--	670
CONSENSUS-O	?-L-----EQ-K-?IIK-?-A-M?L?--KB?-----?-?-SS--TQ--?-PI-	602
CONSENSUS-U	---K-----Q-----Q-----K-----I--	672
CONSENSUS-CPZ	???-?-?-?-?-?-QA--?-?L?--?-???-----?-?-?-?-?-?-L-	459
DESIGNED SEQ	SQIIIEELIKKEKVYLSWVPAHKGIGGNEQVDKLVISGIRKVLFLDGINKAQEEHERYHSNNRTMASDFNL	
MUTATED AAS	N K R A SA D K NE	
ISOLATE-E	SQIIIEELIKKEKVYLSWVPAHKGIGGNEQVDKLVISGIRKVLFLDGINKAQEEHERYHSNNRTMASDFNL	
CONSENSUS-A	NQIIIEKLI?K?KVYLSWVPAHKGIGGNEQVDKLV?GIRKVLFLDGIDKAQE?HE?YH?NW?AMASDFNL	681
CONSENSUS-B	s---q--K-E--a-----a-----e--K--s--r-----	742
ISOLATE-C	---Q--S-ER-----S-----E--K--S--R--NE--I--	
CONSENSUS-D	s---Q--K-E--A-----Q-----E--K--N--R-----	740
CONSENSUS-O	Q---E-TK-E?--T-----KI--KD--R--E--Q--D--K--S--L--?-G-	669
CONSENSUS-U	---Q--Q-D-----S-----E--K--S--R-----	742
CONSENSUS-CPZ	??-?-?-K?E?I-----?-----?-----S--?-?-?-?-?-L-	510
DESIGNED SEQ	PPIVAKEIVANCDKQLKGEAMHGOVDCSPGIWQDCTHLEGKVLVAVHVASGYIEAEVIPAETGQETA	
MUTATED AAS	P S I N I	

FIGURE 4 (Cont)

SUBSTITUTE SHEET (RULE 26)

7/216

ISOLATE-C	--L-----R-----N---A---GIQ-----E-	
CONSENSUS-D	--l-----V-----A---GIK-----D-	880
CONSENSUS-O	--L---A-----P---??M-A---??IOH-----A---S---Q---D-	798
CONSENSUS-U	-----V-----A---IK-----E-	882
CONSENSUS-CPZ	--L---?---T---?---A---?I-----?---?---?---D-	631

DESIGNED SEQ	AEHLKTAVQMAVFIHNFKRKGGIGGYSAGERIIDIIATDIQTKELQKQITKIQNFRVYYRDSRDPINWGP
MUTATED AAS	<u>R</u> V S N L L

ISOLATE-E	AEHLKTAVQMAVFIHNFKRKGGIGGYSAGERIIDIIATDIQTKELQKQITKIQNFRVYYRDSRDPINWGP	
CONSENSUS-A	AEHLKTAVQMAVFIHNFKRKGGIGGYSAGERIIDIIA?DIQTKELQKQI?KIQNFRVYYRDSRDPINWGP	880
CONSENSUS-B	-----v-----t-----T-----l-----	952
ISOLATE-C	-----R-----S-----N---L-----	
CONSENSUS-D	-----T-----i-----	950
CONSENSUS-O	---?---V---T---?---L-SQ---T---L-?N-----	865
CONSENSUS-U	-----M---T-----T-----N-----	952
CONSENSUS-CPZ	--?---?---?---T?---?---?---T---??---?---L-?---?---?---?	687

	vif cds ->
DESIGNED SEQ	AKLLWKGE GAVVIQD NSDIKVVPRRKAKIIRDY GKMAGDDCVAGRQDED
MUTATED AAS	A S

ISOLATE-E	AKLLWKGE GAVVIQD NSDIKVVPRRKAKIIRDY GKMAGDDCVAGRQDED	
CONSENSUS-A	AKLLWKGE GAVVIQD NSDIKVVPRRKAKIIRDY GKMAGDDC?AGRQDED	929
CONSENSUS-B	-----v-s-----	1002
ISOLATE-C	-----A---V-----	
CONSENSUS-D	-----v-----v-s-----	1000
CONSENSUS-O	-Q-----KG-----T-SM-N--T-SESMSQPGIIP	925
CONSENSUS-U	-----v-g-----KHGTAW	1008
CONSENSUS-CPZ	-?-----QGEL-----v-s--N--KHGTAW	742

CONSENSUS A-CPZ FROM LOS ALAMOS HIV SEQUENCE DATABASE
 ISOLATE-C FROM GENBANK U46016 HIV-1 SUBTYPE C (ETHIOPIA)
 ISOLATE-E FROM GENBANK U51189 HIV-1 SUBTYPE E ISOLATE 93TH253 (THAILAND)

FIGURE 4 (Cont)

8/216

← pol cds

DESIGNED SEQ	MENRW.Q.VMIVWQVDRMRIRTWNSLVKHHMYISKAKGWFYRHHYESSQHPKVSSEVHIPLGE..ARLVI	
MUTATED AAs	L K K H N FD R D I	
ISOLATE-E	MENRW.Q.VMIVWQVDRMRIRTWNSLVKHHMYISKAKGWFYRHHYESSQHPKVSSEVHIPLGE..ARLVI	
CONSENSUS-A	MENRW.Q.VMIVWQVDRMrIRTWNSLVKHHMYSVSKAKGWFYRHHEsRhpkvsSEVHI PLGd..ARLVV	66
CONSENSUS-B	-----?-----k-----i-g-----Y--t--ri-----i	66
ISOLATE-C	MENRW Q VLIVWQVDRMKIRITWNSLVKHHMHLSRRANGWVRYRHYDYDSRHSPKVSSEVHIPLGE ARLLI	
CONSENSUS-D	-----?-----K-----Yd-p-----I-----E-----	65
CONSENSUS-O	-----L-----?---QKVKA-----Y-K-?-?-??N-?-?-Y--N-?-?-?Y-V??..-??-	54
CONSENSUS-CPZ	-????.-?-?-?-???-??-?-?-X???-????-?-?-Y????-???-?-?-??????K-?-?	34
DESIGNED SEQ	RTYWGLQTGEKDQWLGHGVSIENWRQKRYSQVDPLADQLIHLOYFDCTPSDSTIRRRAILGOIVRRRCCEYP	
MUTATED AAs	K H R H Q L S G H H A A HR S Q K <u>Y</u>	
ISOLATE-E	RTYWGLQTGEKDQWLGHGVSIENWRQKRYSQIDPDLADQLIHLOYFDCTPSDSTIRRRAILGOVVRRCCEYP	
CONSENSUS-A	RTYWGLHTGErDMHLghGVSIENrqKRYSQvDPDLAdQLIHLhyfACFSdsAIRkaILGeiVRPRCEYO	136
CONSENSUS-B	t-----q-----k-----y-----e-----n-----h-s-----	136
ISOLATE-C	RTYWGLQTGERDMHLGHGVSIENwRLRSYNTQVDPLADHLIHMHyfDCFAESAIRKaILGYRVSPRCdyQ	
CONSENSUS-D	k-----?-----Q-----KR-----G-----MY-----E7-----h-S7-----	132
CONSENSUS-O	T-----MP-----?E-----?Y-?K-I-E-T-RM-----T-T-?-?-?QR-LTK-----?	118
CONSENSUS-CPZ	T??-?-?-?-?-?-?-?-?-?-G?-?-?-T-??-??-?-?-?-?-?-?-?-?-?-?-?-K	76

vpr cds ->

DESIGNED SEQ	SGHNKVGSLQYLAL.KAL...ITPKIRPPLPSVKKLTEDRNKPQKIKGHRNHTMNGH	
MUTATED AAs	A T K K K E T R G	
ISOLATE-E	SGHNKVGSLQYLAL.KAL...TTPKRIRPPLPSVKKLTEDRNKPQKIKGHRNPTMNGH\$	
CONSENSUS-A	AGHNKVGSLQYLAL.KAL...VaPthakPPLPSvkKLTEDRWnePQKTRGHRGSr?nNgH\$	191
CONSENSUS-B	-----a-----it-k-i-----K-----K-----ht-----	191
ISOLATE-C	AGHNKVGSLQYLAL.TAL IKPKKAKPPLPSVSKLVEDKNNKPQKTRGRRGNHTMNGH	
CONSENSUS-D	---?---t---i---K-I---R-----K-----k---?---HT---	186
CONSENSUS-O	?--SQ--T--?--?--V---K????---Q?---K???I--DOL?--S---	161
CONSENSUS-CPZ	?--?Q--?--?--?--?--?--?--?--?--?--?--?--?--?--?--K??R???--EN?TR---	107

FIGURE 5

9/216

		-<- vif cds oligomerization ->/		LR domain /<-	
DESIGNED SEQ	MEQ AP EDQGPQREPYNEWALELLEELKQEA VRHFPRLHNLGQYIYETYGDTWSGVEALIRTLQQL				
MUTATED AAs	SS T H G H E I				
	N S				
ISOLATE-E	MEQ AP EDQGPQREPYNEWALELLEELKQEA VRHFPRLHNLGQYIYETYGDTWSGVEALIRTLQQL				
CONSENSUS-A	ME?..AP.EDQGPQREP??E??LELLEELKHE?VRHFPRLHNLGQYIYETYGDTWEGV?AIIRILQQL				58
CONSENSUS-B	--q??--?-----yN-Wt-----?-A-----i---?-E-----a--E-----				65
ISOLATE-C	MEQ AP EDQSSQREPYNEWTLLELLEELKQEA VRHFPRLHNLGQYIYNYGDTWEGVEAIIRILQQL				
CONSENSUS-D	--Q...-n--a--fN-Wt-----?-A-----I---S---?-E-----?-E-?------				64
CONSENSUS-O	--Q...-n--a--fN-Wt-----?-A-----p--a--y--E-----m-----				66
CONSENSUS-U	--Q...-A-----HN-WT-----Q-A-----I---S-----E-----S-----				67
CONSENSUS-CPZ	--Q...-?-?-?-?-W--T--?-N-A-----P?-????-???-?-??????-??????-??				33
LR domain ->/ tat cds ->					
DESIGNED SEQ	MPIH FRIGCQHSRIGIL RQRR RRGASRS				
MUTATED AAs	L V R I G S				
	T				
ISOLATE-E	MPIH FRIGCQHSRIGIL RQRR RRGASRS				
CONSENSUS-A	LF?H.FRIGCQHSRIGII...?GRRG.RNGA?RS\$				84
CONSENSUS-B	--i-?------r-----t...-q--a?-S--				93
ISOLATE-C	LFVH FRIGCQHSRIGIF AREKRQESW				
CONSENSUS-D	--I...-RQ--A--SS--				93
CONSENSUS-O	--t-.y-----????-rg--r--SS--				94
CONSENSUS-U	--I...-RQ--A--SS--				96
CONSENSUS-CPZ	??I-????-??-L...PQ--R.S--SN--				54

FIGURE 6

10/216

```

intramolecular      3'sj      3'sj
disulfide bonding   \//      \//
|                   | rev cds. ->/<- nls ->/

```

DESIGNED SEQ	MDPVDPNLEPWNHPGSQPTTASCCKYCKKCCFHCQLCFLKKGLGISHGRKKR	KORRGAPQSRKDQYYP	
MUTATED AAS	K K K T Y V T Y	R R SE	
	N	Q	
ISOLATE-E	MELVDPNLEPWNHPGSQPTTASCCKYCKKCCWHCQLCFLKKGLGISHGRKKR	KHRRGTPQSRKDQYYP	
CONSENSUS-A	M?PVDPnLEPwnHPGSqPtTaCskCYCK?CCwHCqlCFLnKGLGISYGrKKR..	r?RRgtPQs?kDhQnp	64
CONSENSUS-B	-e---x---k-----k---tn---k-f---v---tt-----	-Q--ra--dSqt--vs	68
CONSENSUS-C	-----?-----K-----p-----k-sY--lv---qt-----	-g--sa?-?SE-----	65
CONSENSUS-D	-d-----D-----?--p-N--h--K-Y--v---it-----	-Q--rp--9gQa--?--	66
CONSENSUS-F	-EL---D-----P-T---R-F--w---TT-----	KQ-HR-----SQI---DL	68
CONSENSUS-O	-D---E?P--H---?--Q?P--NN---R-Y--YV---??-----	---???AAA--P?KD--	55
CONSENSUS-U	-D---K-----K-T---K-Y--PV-----	-P--RS--NSE-----	68
CONSENSUS-CP2	-D-?-????-?-???-?-?--NN---Y---?--TK-----	-?--??-T??S?NN-D?	45

exon \ exon

DESIGNED SEQ	IPEQPLPQTRGGNPTDPKESKKEVASKTETDPCD	
MUTATED AAs	S S P D G E K E A F	
ISOLATE-E	IPEQPLPIIRGGNPTDPKESKKEVASKAETDPCD	
CONSENSUS-A	ipKQplPqtgq??ptgpkESkKkVeSKteTDrf?\$	95
CONSENSUS-B	Is---?s-pr-D-----rE---P?d?	99
CONSENSUS-C	-s-----r-d-----E-----p-D-	98
CONSENSUS-D	-----SS-pr-d-----?-A---p-Dw\$	99
CONSENSUS-F	V---IS-AR-N-----?-E---A??-P?--\$	96
CONSENSUS-O	V-?-S???-?RK.Q?RQE-QE??-K??GP?G?P????SC??CTR?S?Q\$	83
CONSENSUS-UP	---S--H--RV.S---E--E---A-----D-	101
CONSENSUS-CPZ	??-??-?????-..????K?-?-?-?????-D	52

FIGURE 7

11/216

		high-affinity binding site nls		/<- ->/	
		exon \ / exon			
		\ / 3' sj			
DESIGNED SEQ	MAGRSGSTDE ELL RAVRIINILYQSNPYPSSEG	TROTRKNRRRRWRARQQRQIRAI		SERILSTCLGRS	
MUTATED AAs	D K I K S A R E HS W NF P				
ISOLATE-E	MAGRSGSTDE ELL RAVRIINILYQSNPYPSSEG	TROTRKNRRRRWRARQQRQIRAI		SERILSTCLGRS	
CONSENSUS-A	MagRSG?sDE.eLL.KaIRIIKILYQSNPyPkPkG.SRQARKNRRRRWRARQQRQIDS1SeRILStCLGRP			66	
CONSENSUS-B	-----d-----tV-l--f-----p-s-e--T---R-----e-----r-i--w---y---s			67	
ISOLATE-C	MAGRSGSDSE ELL KAVRIIKILYQSNPYPTPEG	TRQARRNRRRRWRARQQRQIH		TL SERILSNFLGRP	
CONSENSUS-F	-----N-?T---.R-?-Y-----E--T---R-----?-R??-?-S-----			61	
CONSENSUS-O	-----E-...Q?-?Q--Q-----?-?-?-N-----R--A-V-?-A?-?-A-VVHG?			56	
CONSENSUS-U	-----DA-...RVV-----P-E--T--T-----RAI---F-----S			67	
CONSENSUS-CPZ	-----?E-?????-?-VK-----?-?-?-?-R-?-?-?-?-V-?-?-?-			41	
Leu-rich effector domain /<- ->/					
DESIGNED SEQ	AEPVPLQLPPLERLHLDCSEDCGTSQTQSQGTETGVGRPQISGESSVILGPGTKN				
MUTATED AAs	N SD N L AV S				
ISOLATE-E	TEPVPLQLPPLERLHLDCSEDCGTSQTQSQGTETGVGRPQISGESSVILGPGTKN				
CONSENSUS-A	AEPVPLQLPPLERLhLDCsEdcgTSgTQq?gg?etGVGrpOvsVEssavLGSgTkn			120	
CONSENSUS-B	-----t---?-----s---il---p---e---E\$			115	
ISOLATE-C	AEPVPLQLPPLERLHLDCSESDTSQTQSQGTTEGVGNP	PREMATURE TRUNCATED			
CONSENSUS-F	E-----?---?IN?---?E.Q-A?E.....S--T-G--H-----E\$			105	
CONSENSUS-O	Q?NN?VD-----Q-?IRDP-?D?L????TVDPRAEDN\$CL-NLCSCNT???????N\$			95	
CONSENSUS-U	-----I---C-----G-----P--T-----S-PI-G---TI-----E\$			123	
CONSENSUS-CPZ	PK-GD-E--E-DK-S-Q-V-TTQDV--SNTSQPQ-AT-ETVPAGGNYSI--K-A--			97	

FIGURE 8

12/216

		env cds ->									
		phos phos									
DESIGNED SEQ	MTPL	EIIAIVAFIVALIIAIVVWTIAYI EYRKLLRQR									
MUTATED AAs		L	L	VF	K	K	K	E	I		
CONSENSUS-A	mtPL???	eIcAIvGLiVALILAI	VVWTIVgI	eyKcllkqr	Kidrl?ikRIRERA	EDSGNES				57
CONSENSUS-B	-qs-	q-?--a-v--a-i-	-----f-?	-r-i-R-?	-----d-----					56
ISOLATE-C	MVDLLAKVDYRIVIVAFIVALIIAIVVWTIAYI	EYRKLLRQR				RIDRL IKRTRERA	EDSGNES				
CONSENSUS-D	-Q--	v-l---A-v---i-	-----f-	-ckr-kr-	-w--d-----?					57
CONSENSUS-F	-S??	LAIS?TA-----I-	-----Y-	-R--R-	-N--YE?--?--					51
CONSENSUS-O	-H??	?LL-?I??SAL??INV??-?	...F?..	LR?Y-?	??QDR?E?E-LE	R.LR--?-IR.D--DY--					42
CONSENSUS-U	-Q--	T-T-----V--F-A-----S--Y-	-R-IR--K.	LD-----						57
CONSENSUS-CPZ	--??	????L??????W?-CI???	I????-??YK???	??????-?.??I?????.???????						14
DESIGNED SEQ	EGDTEE	LSTM	VDM GNYDLGVDNNL								
MUTATED AAs	R	AL									
CONSENSUS-A	?GDT?E.L?kL....	VEM.GnydlgvdnNL\$									78
CONSENSUS-B	e--qe--sa-????--?	H?apwdvdD--									79
ISOLATE-C	DGDTEE	LSTM	VDM	GNLRLLDVNDL							
CONSENSUS-D	E--rE--sa-----	-HhAPwd?Ddm-									80
CONSENSUS-F	E--AE--A?-----	G--PFIP-DI?--									73
CONSENSUS-O	N?EE-QEVM?-----	??SH-F?NPM.FE??									59
CONSENSUS-U	D---E--ST-----	M---YFYILDND--									81
CONSENSUS-CPZ	-?EE--??-?????????	FANP?..????DE									23

FIGURE 9

```

      <- vpU cds
signal peptide / gp120

```

DESIGNED SEQ	MRVKETQMNNPNL WK	W	GTILGLVIIC	SA	SD	NLWVTVYVGVPVWRDADTLFLCAS	
MUTATED AAS	R	M	M	M	E	E T	
CONSENSUS-A	Mrvmgiq?nyq?l.wr??...	??W	gtmilg??i	lc.na??e	?.lWvtVyYGVPVWkdae	TLFLcAS	49
CONSENSUS-B	??--k--rk--h-?-----	????	--l--mlm--s-----	-----	e-t-----		53
CONSENSUS-C	--r--?x-w-gw-.i-----	-----	ILGFWmlm--v--g-n-----	-----	e-k-----		53
CONSENSUS-D	--?r--er--h-----	????	--L--mLM--sv.a??-----	-----	E-t-----		52
CONSENSUS-E	--Ket-m-wpn--k-----	-----	--l--lv--?s--Sd.N-----	-----	r-d-----		55
CONSENSUS-F	-?-R-M-R-W-H-.GK.....	-----	--LLF--il-----	-----	n-----	e-T-----	53
CONSENSUS-G	-?-k--x-N-H--k-----	-----	--L--LV--s--sn-n-----	-----	E-D-----		54
CONSENSUS-O	-t-tmKam?KrNr.Kl.....	-----	?lylamAlI-P--LS--??Q-YA--s-----	-----	E-?Pv-----		51
CONSENSUS-U	-?-?E?-R-??-?-?-?-----	-----	---??-?--?--?--?-----	-----	?.-??-?-----		36
CONSENSUS-CPZ	-??-??-??-??-?-??-?-?-----	-----	---??-??-??-??-??-?T-----	-----	?.-??-?-----	??-?P?-----	19

[illegible]

```
DESIGNED SEQ PLCVTLNCTNANLINVN      HYPERVARIABLE REGIONS 1/2
MUTATED AAS

CONSENSUS-A   PLCVTLC????????n?c????????n?c???????n????...????????.....m    126
CONSENSUS-B   -----n-.td-----?-?-????????-??-????-??..?????-    133
CONSENSUS-C   -----n-.-----?-?-????????-t--?..????-??    132
CONSENSUS-D   -----n-.t-----?-????????-t--?..??????????    131
CONSENSUS-E   -----n-.tna-----l-----nv-i-nvsnii-g-it.....??????    150
CONSENSUS-F   -----n-?t-a-----a-----t-?-?-g-----?tlkE    139
CONSENSUS-G   -----n-.t-----V-t-----?-?-Nct--?en--nNetv-----???    143
CONSENSUS-O   F---Qnn-.td-----l-----e-----    129
CONSENSUS-U   -----n-.t-----e-----    105
CONSENSUS-CPZ -?-???-?-?-?-?-?-?-P????-???    60
```

DESIGNED SEQ MUTATED AAs	HYPERVARIABLE REGIONS 1/2	
CONSENSUS-A	?..?e.....ikNCsfNmTtelrdkkqkvysLfYrldVvqi????????n?????.....n?????????	160
CONSENSUS-B	e??g-?????-i-si--v-e-a--k---p-d-----?-----????-----	169
CONSENSUS-C	-?-.....-a-?-?-A-----i-pl-----s-----	166
CONSENSUS-D	-?-g.....m-----i-?v--kq-ha--k-----s-----t-----	165
CONSENSUS-E	--d.....Vr-----hA--k-i-----s-----?....?	185
CONSENSUS-F	eP.ga.....Q-----v--Q?-Ha-----I-p-s-----ns-----??-----	177
CONSENSUS-G	--e.....m-----i--i--ktE-A--k-----p-n-----?ss-----sd-----	182
CONSENSUS-O	..n-??..m-?-?-V--V-k--E-KQA--Vs-L?k?N-ts-----T-----m-----	164
CONSENSUS-U	..??-?.....-i-?-?-kt?-a--k-----P-n-----n-----?-----	137
CONSENSUS-CPZ	??-?.....???-?-??-??-?-----?-----T-----	79

DESIGNED SEQ YRLINCNTSVIKQACPKVSFDPIPIHYCAPAGYAILKCNCKNFNGTGPKCNVSSVQCTHG IKPVVSTQL
MUTATED AAs S A T I T E F N K T T R

FIGURE 10
SUBSTITUTE SHEET (RULE 26)

14/216

CONSENSUS-D	-----t-----n-k-----r-----	234
CONSENSUS-E	-----V-K-----i-D-----t-y-----N-n-----S-----	254
CONSENSUS-F	-----?-T-----Wd-----Y-----N-k-----	245
CONSENSUS-G	-----v-T-K-----n-d-----r-n-----	251
CONSENSUS-O	-----?-t-----STt-----?-y-F-N?T-----l-?-itV-T-----T-----	228
CONSENSUS-U	-----?-k-----n-K-----	205
CONSENSUS-CPZ	-----????-T?-----?-?-?-?-?-?-?-D?-----?-?-?-?-?-H-----?-?-?-?-?-	120

<- V3 neutralization loop

DESIGNED SEQ LLNGSLAE EIIIRSENLTNNAKTIIVHLNESVEINCRTP NNNTR K HYPERVARIABLE REGION 3/4/5
MUTATED AAs VV P D V Q K V S T

CONSENSUS-A	LLnGSLAE???v?irSenitnNaktiiVql??pV?InCtRP.nnntr.ks???vri???gpGq??afya.	279
CONSENSUS-B	-----e.e-v-----f-d-----nes-e-----?-----ih-----r.-----t.	296
CONSENSUS-C	-----eii-----l-----v-----h-n-s-e-v-----t-----t-----t.	291
CONSENSUS-D	-----E.EiI-----l-----?-----n-----s-----y?-----qr.-tp-----?-----l-t?	288
CONSENSUS-E	-----e.eIi-----L-----h-NKs-e-----s-----t....it....v-r.	312
CONSENSUS-F	-----e.dii-----q-----sd-----h-Nes-q-----I?-----r-----.	302
CONSENSUS-G	-----e.eI-----?-----d-----v-----nksie-----I?-----f-----.	305
CONSENSUS-H	-----?-----D-T-N-----K-----?-----I?-----?-----?-----?	39
CONSENSUS-O	I---T-Skg.kIxrMgk.-?dsq-N---T-N?-i-mt-e--g?-v.Qe...i?-----m.-W-S.	279
CONSENSUS-U	-----E.E-i-----?-----d-----net-k-----?-----?-----v-----.	261
CONSENSUS-CPZ	-?-?-????-?-????K????V????E??-??-?-?-G?-?..??-?Q-----M.-T-N.	142

V3 neutralization loop ->

DESIGNED SEQ	HYPERVARIABLE REGION 3/4/5	
MUTATED AAs		
CONSENSUS-A	tgdi.....iG.dirqAhCnvsr?eWn?tlq?V....a?qLr?...f???nkt....??iIf?n.ssGGD	320
CONSENSUS-B	--?-???...-----i--ak-n--kqi...v-k-e??q-----v-nq?----	342
CONSENSUS-C	-----I-?-k-e-----?kK-ae.h-p-----k-?-?	334
CONSENSUS-D	-?r????..?-?-----i-?a?-k-q-...k-gd?.ll-----t---kp-----	331
CONSENSUS-E	-----k-y-EINGTk-e?-kq....tek-ke.H--n-----qp?p----	160
CONSENSUS-F	--?-----k-----gtq-----e-----?a?-ks.h-----?--k-ns-----	344
CONSENSUS-G	-----?em-n-----?--?-i-----?--?--t-ns.-a----	344
CONSENSUS-H	?-?-----?--I??-?--?--?-----?--?..H?....??-----?--P-----	65
CONSENSUS-O	M-.l????n?k???s?-Y-?YnaTd?ka-kqt....-eRYLe.Lv....?-???vvtm?-n?s-?---	321
CONSENSUS-U	-----i-t?-n-q-----k.y.n-?-----?-ns?-----	306
CONSENSUS-CPZ	?E??.....?-T-?-?--?N?T-?-?--?--?--?--?--?--?--?--?A-???-?..???-	157

CD4 * * * * *

DESIGNED SEQ	HYPERVARIABLE REGION 3/4/5
MUTATED AAs	
CONSENSUS-A	lEitthsFnCggef?FYCNts?lF.nstW???????...n?t.???????.??n?t????..???sndtI 355
CONSENSUS-B	p--vm-----tq--.....-????--?-.....-??-????- 374
CONSENSUS-C	-----r-----y---p---? -g-?-----?-.?-?...??-????- 366
CONSENSUS-D	p-----t-----????--??-?-.?-....??-????- 361
CONSENSUS-E	--m-h--r-----t---n-cig.....e-m...gc..g.....????- 398
CONSENSUS-F	--m----r-----? ?-----?-----? ?-----??-? 372
CONSENSUS-G	-----r-----g-?-?s?-----n?-----? ?-----??-??- 373
CONSENSUS-H	?-??-?-?-?-----?K-----??-?.N-?-?.-G-.....??- 92
CONSENSUS-I	?-v-hlh--H-----m..y-Fsc-----????-?-----n-----? -g-? 356
CONSENSUS-J	-----t-----?-----?d-----?-----??-??- 336
CONSENSUS-K	P-V??-?-?-?-?-----??-?-?-----?I-----G?? 175

★	CD4		★	***		CD4	***
---	------------	--	---	------------	--	------------	------------

DESIGNED SEQ	HYPERVARIABLE REGION 3/4/5	
MUTATED AAs		
CONSENSUS-A	t..lq.CrI.kqIvnm.wQrvqg.AmYapPIq.g?irb?sNITGllLTRDGg??...nns??...???	401
CONSENSUS-B	??-p.-----i-----e-k.-----?-q--s-----????-??-?-?----	419
CONSENSUS-C	---p.-----i-----e-r?-----?-n-t-k-----?-----??-???	411
CONSENSUS-D	---p.-----i-?-?-k.k-----e---s-----?...?-...?----	405

FIGURE 10 (Cont)
SUBSTITUTE SHEET (RULE 26)

15/216

		gp120 / gp41									
DESIGNED SEQ	TPRPGGGDIKDNWRSELYKYKVVKIEPLGVAPTR AKRRVV	EREKRA	VG	IGAMIFGFLGA							
MUTATED AAs	I NMR E K I K Q L FL										
CONSENSUS-A	?netFrPgGgdmdrDNWrsELYkYkVkiePlGvaPtr. akrRVV	EREKRA??vg.lGavflgflGa	462								
CONSENSUS-B	-t-i-----k-----q-----i-m-----	480									
CONSENSUS-C	-?-e-k-----?-----i-m-----	470									
CONSENSUS-D	-----r-----?-----I-----m-----	465									
CONSENSUS-E	-----NiK-----Q-----i-----I-Mif-----	508									
CONSENSUS-F	-?-n-k-----e-----q-----k-----l-----	478									
CONSENSUS-G	-----k-----R-----G-----?-----	481									
CONSENSUS-H	-?V-----??-?-?-?-?-?-?-?-?-?-?-?-?-?-?-?	187									
CONSENSUS-O	-?-l-----k-I-T-f-----rvK-FS-----ki-RP?Igt?t?H-----ML-v-S-----	462									
CONSENSUS-U	-?	435									
CONSENSUS-CPZ	-????-????-?-?-?-?-?-?-S-----??R????-?-Q-?-?-?-?-?-?-?-?-?	227									

DESIGNED SEQ	AGSTMGAASITLTVOARQLLSGIVQQSNLLRAIEAQOHLLOLTVNGIKQLQARVLAVERYLKD QKFLG										
MUTATED AAs	M L N M I QL										
CONSENSUS-A	AGSTMGAASITLTVOarqLLSGIVqqQsNllrAIEaQghlLkLTVNGIKQLQARVLAVERYLrD.QQLLG	531									
CONSENSUS-B	-----?-----n-----q-----k-----	548									
CONSENSUS-C	-----?-----m-----t-----i-----k-----	539									
CONSENSUS-D	-----?-----N-----Q-----k-----	533									
CONSENSUS-E	-----?-----Q-----K-----Kf-----	577									
CONSENSUS-F	-----?-----n-----O-----?-----	546									
CONSENSUS-G	-----?-----V-----Q-----?-----	549									
CONSENSUS-H	-----?-----?-----?-----?-----	227									
CONSENSUS-O	-----ATa-----tht-?K-----D-----Q-----R-S-----R-R-L-L-TliQN-----n	529									
CONSENSUS-U	-----??-??-?-?-?-?-?-?-N-----O-----ES-----	496									
CONSENSUS-CPZ	-----??-??-?-?-?-?-?-?-Q-S?-V-----?-----?-----?-----?	279									
* * *** *** *** ***											
DESIGNED SEQ	LWGCSGKIICCTnVPWNSSW	S NKSLEBIWNMTWMEWEREISNYTNQIYE ILTESQNOQ									
MUTATED AAs	I L N T F D IQ SL K										
CONSENSUS-A	INGCSGKIICCTnVPWNsSW.....S.Nks??dIWdnMTWlqWdKEIsnYT?iIY?LiEesqngQ	586									
CONSENSUS-B	-----a-----a-----?-----l-----?-----me-er-d-----l-t-----	603									
CONSENSUS-C	-----a-----a-----?-----q-----m-----r-----dt-r?-L-d-----	597									
CONSENSUS-D	-----h-----h-----r-L-e-?-mE-ER-d-Gl-s-----?	589									
CONSENSUS-E	L-----I-----A-----t-----r-fEE-n-----iE-eR-----Nq-e.ILT-----	636									
CONSENSUS-F	L-----L-----A-----?-----qEe-?-ME-e-----SnE-R-----?	603									
CONSENSUS-G	L-----t-----t-----InE-----Ie-eR-N-q-n.l-----?	606									
CONSENSUS-O	L---K---Y-S-K-?-t-?G.....??neS-?L-Q---qq-n-vSS?-e.e-Q?A-?-	580									
CONSENSUS-U	L-----T-----LVTLL-L-ME-R-----QV-G-L-D-K-----	555									
CONSENSUS-CPZ	L-???-??-?-T---N-?????????..??-?-?-?-Q?--?LV?-?-G?-?-?L?A??-?	312									
V 3'sj											
DESIGNED SEQ	DRNEQELLELOKMASLWNWFDITNWLNYIKIPIMIVGGLIGLRIVFAVLSIVNRVRCGYSPISFQTLIPA										
MUTATED AAs	KD A N SK V I I T										
CONSENSUS-A	EkNEqdLLaLDkWanLwnWpDIsnWLNyIriPimIVGGLIGLRIVfaVlsIInRVRqGYSPISFQtltp?	555									
CONSENSUS-B	-----e-----s-----?-----t-----k-----v-----v-----?l-a-----	671									
CONSENSUS-C	-----k-----s-----?-----t-----k-----i-----v-----n-----	664									
CONSENSUS-D	-----e-----s-----T-----k-----k-----lv-----l-a-----	657									
CONSENSUS-E	DR-K-e-s-T-----K-----i-----v-----p?Hh-----	705									
CONSENSUS-F	-----e-----s-----K-----v-----K-----?hiS-----	672									
CONSENSUS-G	-----?S-s-s-----k-----v-----?HH-----	674									
CONSENSUS-O	---K?-E-E-Si---l-TK---K-A-I---A---v-ViMI---NLVKNI---Q---L-IP??h	647									
CONSENSUS-U	---S-K---E---S---G-T---K-----T-F-----L-T-----	625									
CONSENSUS-CPZ	-?-???-?E-?-?-S-----T-----K-?-?-?-I?-----????-??R?-----?-----?-----?	355									

A <- tat cds
 DESIGNED SEQ PRG PDRPEGIEEGG EQDRDRSVRLVSGFLALAWDDLRLSLCLPSYHRLRLILILI A AR IVELLGHS
 MUTATED AAs LGR RG G N S N F V T R

FIGURE 10 (Cont)

SUBSTITUTE SHEET (RULE 26)

16/216

CONSENSUS-O q?E.agT-G-TG-g---e--p-Wtp-Pq---?-LYT---TII-Wt--L-SNLaSg.I.....qk 702
 CONSENSUS-U --G.---G-T-----E-MN--V--N-----E-----I-----L---V-----KG-R... 685
 CONSENSUS-CPZ Q?-.????E-?-?-.??--?-???-??-???-?-----N-GIW--QS-TSLACN.V.W-##LKT---L 398

<- rev cds

DESIGNED SEQ	SLRGLRRG	WEALKYL WNLLQYWQELKISAVSLLNATAIAVAEGTDRVIEVAQRAGRILHI	
MUTATED AAs	K Q	G W G L L N I GN I V W N	
CONSENSUS-A	slkgrlrg.....	weglkYL.wNLLlyWgrELK?SainLldtiAiavAgwtDRvIEigOrigRAilni	780
CONSENSUS-B	?...??-	-a--w--g--sq--n--vs--nat-----Eg-----vv--a?---h-	789
CONSENSUS-C	--r--qr-	-a-----Gs-vq--l--k--S-----EG--i--??---?--	787
CONSENSUS-DR-	-a-----q--?q--n--S-----Eg--?--?v--a?---v-h-	773
CONSENSUS-ER-	-G-----Q--I--S--naT-----VA-gaW---h-	832
CONSENSUS-F	.?R--R-	-A--l-.G--t---Q--N--s--N-T--v--Eg--?--?AL--?	787
CONSENSUS-G	i	-q--N--?-----N-----vv--aC-----	800
CONSENSUS-O	lI?y-g--LWILGQktIeaCR-c?Av?Q--LQ--qn--T-----?V--N--gi-lGi---?G---		767
CONSENSUS-UR-	-A-----G--V---Q--N--S--NAT--V--EG--I--V---C-----	741
CONSENSUS-CPZ	I-HS---L.....	R-R-CL-.GGIIQ--K--I--S--AT-----EG--I--AF-VTL-I-R--	460

DESIGNED SEQ	PRRIRQGLERALL	
MUTATED AAs	T F	
CONSENSUS-A	PrRIRQGLERaLl\$	793
CONSENSUS-B	-?-----	801
CONSENSUS-C	-----F-a--q-	800
CONSENSUS-D	-?-----	785
CONSENSUS-E	-----	845
CONSENSUS-F	-?-----?-----	798
CONSENSUS-G	-----	813
CONSENSUS-O	-----?---	779
CONSENSUS-U	-----F-----	754
CONSENSUS-CPZ	-----	473

FIGURE 10 (Cont)

17/216

DESIGNED SEQ	MGGKWSKSSIVGWPQVRERIRQT	PPAAEGVGAVSQD	LDKHGAITSSNTPA
MUTATED AAs	C P A RA	A AR	<u>Y</u> L A
ISOLATE-E	MGGKWSKSSIVGWPQVRERIRQT	PPAAEGVGAVSQD	LDKHGAITSSNM
CONSENSUS-A	MGGKWSKsSiVgNpEvrkRmRqT.....	?PtAAkGVGAvSQD.....	LDKhGAITSSNt??
CONSENSUS-B	-----?--?--?--e--ra????????????--	Bp--d-----r-----	e-----aa
ISOLATE-C	MGGTMSKCSFVGNPAIRERIRRA	APAAEGVGAAASRD	LDKYGALTSSNTPA
CONSENSUS-D	-----AI-E-I-x-?????-----	dP--D-----R-----	E-----as
CONSENSUS-O	--NA??-?KF?--??--?--R?-----	???P?-?PC-P--??-RE.....	-A?-R-G?-?-H-PQ
CONSENSUS-U	--?-----???--??-E-I-?-----	P???--?--?-----?--?--?--A-	
\vskip6pt			
	* SH3-binding SH3-binding		
DESIGNED SEQ	NNADCVWLK AQE E EG VGFPVRPQVPLRPMTYKGAFDLSFFLKEKGGLEGLVYSKKRQEIIDLNV		
MUTATED AAs	P A E E	A V L	D I Q D
ISOLATE-E	NNADCVWLK AQE E EG VGFPVRPQVPLRPMTYKGAFDLSFFLKEKGGLEGLVYSKKRQEIIDLNV		
CONSENSUS-A	tnpsCanLE?Aqe?.d.e?.VGFPVRPQVPLRPMTYKGAvDLSbFLKEKGGLDGLiYs?kRQEIIDLNV		110
CONSENSUS-B	--ad-----e??-e?-----a-?-----e-?-q--d-----		108
ISOLATE-C	NNPDCAWLE AQEE E EE VGFPVRPQVPLRPMTYKAAFDLSLFLKEKGGLEGLIYSKKRQEIIDLNV		
CONSENSUS-D	--ad-----ES.-E-----e-----E--W-K-----		115
CONSENSUS-O	N-AAL-P-?-SH?..?-----?--?--F-----?--H-A-----?		93
CONSENSUS-U	N-?-?-?-?-E?..E-----?--F-----?-----?-----?		83
\vskip6pt			
	* SH3-binding		
DESIGNED SEQ	YHTQGFFPDWNYTPGPGIRY PLTFGCWCFKLVPVDPREVE EINKGENNCLLHPMSQHGMEDEREVL I		
MUTATED AAs	N <u>Y</u> Q T	S A E	ICL D K
ISOLATE-E	YHTQGFFPDWNYTPGPGIRY PLTFGCWCFKLVPVDPREVE EINKGENNCLLHPMSQHGMEDEREVL I		
CONSENSUS-A	YnTOGIFFPDWNYTPGPGIRf.PLTFGCWCFKLVPvDPaEVR.eat?GenNSLLHPICQHGMdDe?revIm		176
CONSENSUS-B	-h-y-----?-y?-----e-ek-----ne-----msl-----pE-----?		174
ISOLATE-C	YNTQGFPPDWNQNYTPGPGVRY PLTFGCWCFKLVPVDPSEVE EINEGENNCLLHPASLHGMEDEDEVLK		
CONSENSUS-D	-----I-----I-Y-----e-----q-----E--t-c-----?-----E-pE-q--k		182
CONSENSUS-O	-?------?-----?-----L-----S?E-A-RLGNT?-?A?-----A-?-?-E?-H?-I-?		150
CONSENSUS-U	-H---?-----?-----?-----?-----N-----C-----S-----?--E-----?		138
\vskip6pt			
DESIGNED SEQ	WKFDsRLARRHRIARELRPEFY KDC		
MUTATED AAs	H L M H Y		
ISOLATE-E	WKFDsALARRHRIARELRPEFY KDC		
CONSENSUS-A	WkFDsRLalkhRa?ElHPEfY.KDCs		199
CONSENSUS-B	-r-----fh-m-r-----y-----?TSMCLOGTFRWGISREARLGGTGEWRALRCCI		230
ISOLATE-C	WKFDsHLARRHRIARELRPEfY KDC		
CONSENSUS-D	-R-N-----fE-K-R-m-----		206
CONSENSUS-O	-?-RS-G?T?-?-?-LF?--?		166
CONSENSUS-U	-----S-?-?-R-?-?-?-?		157

FIGURE 11
SUBSTITUTE SHEET (RULE 26)

18/216

GAG OVERLAPPING SEGMENTS

M G A R A S V L S G G K L D A W E K I R L R P G G K K Y ^(K)	Segment 1
atg ggc gcc agg gcc agc rtc ctc agm ggc ggc rag ctg gac gcc tgg gaa aag att agg ctc agg cct ggc gga aag aaa aag tat arg	
W E K I R L R P G G K K Y K M K H L V W A S R E L E R F A	Segment 2
tgg gag aaa atc aga ctg aga ccc gga ggc aaa aag aaa tac ara mtg aaa cac mtt gtg tgg gcc tcc agg gaa ctg gaa agg ttt gcc	
M K H L V W A S R E L E R F A L N P G L L E T A E G C Q Q I	Segment 3
mtg aag cat mtc gtc tgg gct agc aga gag ctg gag aga ttc gct ctg aat ccc rgc ctg ctg gag aca kcc gaa ggc tgt mag caa att	
L N P G L L E T A E G C Q Q I L E Q L Q S A L K T G S E E L	Segment 4
ctc aac cct rgc ctc ctg gaa acc kct gag gga tgt maa cag atc ctg gra cag ctg cag ycc gcc ctc mag aca ggc wcc gaa gag ctg	
L E Q L Q S A L K T G S E E L K S L Y N T I A T L W C V H Q	Segment 5
ctc grg caa ctg caa yct gct ctg maa acc gga wca gag gaa ctg arg tcc ctg twt aac aca rtc gct acc ctc tgg tgt gtg cat cag	
K S L Y N T I A T L W C V H Q R I E V K D T K E A L D K I E	Segment 6
ara agc ctc twc aat acc rtc gcc aca ctg tgg tgc gtc cac caa agg att gas gtc arg gac aca aag gaa gcc ctc gac aaa atc gaa	

FIGURE 12

19/216

R I E V K D T K E A L D K I E E E Q K K S Q Q K T Q Q A A A Segment 7
 D R
 aga atc gaw gtg ara gat acc aaa gag gct ctg gat aag att gag gag gwg caa aas aaa agc mag caa aag aca caa cag gct gcc gct
 E E Q K K S Q Q K T Q Q A A D T G S S S K V S Q N Y P I V Segment 8
 V N K
 gaa gwa cag aaw aag tcc maa cag aaa acc cag caa gcc gcc gcc gat aca ggc arc tcc agc mag gtc agc caa aac tat ccc att gtg
 D T G S S S K V S Q N Y P I V Q N A Q G Q M V H Q P L S P R Segment 9
 N Q L
 gac acc gga art agc tcc maa gtg tcc cag aat tac cct atc gtc cag aat syc caa ggc caa atg gtc cac caa scc mtc tcc ccc aga
 Q N A Q G Q M V H Q P L S P R T L N A W V K V I E E K G F N Segment 10
 L A I V A S
 caa aac syc cag gga cag atg gtg cat cag sct.mtt agc cct agg acc ctc aac gct tgg gtc aag gtc rtc gaa gag aaa gac ttt arc
 T L N A W V K V I E E K G F N P E V I P M F S A L S E G A T Segment 11
 V A S T
 aca ctg aat gcc tgg gtg aaa gtg rtc gag gaa aag gaa ttc art ccc gaa gtg att ccc atg ttt wcc gct ctg tcc gag gga gcc aca

FIGURE 12 (Cont)

P E V I P M F S A L S E G A T P Q D L N M M L N I V G H Q	Segment 12
cct gag gtc atc cct atg ttc wca gcc ctc agc gaa ggc gct acc ccc caa gac ctg aat ayg atg ctc aac ayc gtc ggc gga cac caa	
P Q D L N M M L N I V G H Q A A M Q M L K E T I N E E A A	Segment 13
cct cag gat ctc aac ayg atg ctg aat ayt gtc gga ggc cat cag gcc gct atg caa atg ctg aaa gag aca atc aat gag gaa gcc gct	
A A M Q M L K E T I N E E A A E W D R V H P V H A G P I P P	Segment 14
gct gcc atg cag atg ctc aag gaw acc att aac gaa gag gct gcc gag tgg gac aga rtc cat ccc gtc cat gcc gga ccc rtt acc cct	
E W D R V H P V H A G P I P P G Q M R E P R G S D I A G T T	Segment 15
gaa tgg gat agg rtt cac cct gtc cac gct ggc cct rtc sct ccc ggc caa ats aga gag cct agg gga agc gat atc gct ggc aca acc	
G Q M R E P R G S D I A G T T S T L Q E Q I G W M T N N P P	Segment 16
gga cag atr agg gaa ccc aga ggc tcc gac att gcc gga acc aca agc aca ctg caa gag caa atc gaa tgg atg aca arc aat ccc cct	
S T L Q E Q I G W M T N N P P I P V G D I Y K R W I I L G L	Segment 17
tcc acc ctc cag gaa cag att gac tgg atg aca art aac cct ccc rtc cct gtc gga gaa att tac aaa agg tgg att atc ctc ggc ctg	

FIGURE 12 (Cont)

21/216

I P V G D I Y K R W I I L G L N K I V R M Y Q P V S I L D I	Segment 18
V E	
rtt ccc gtg ggc gaw atc tat aag aga tgg atc att ctg gga ctc aac aaa atc gtg aga atg tat yma ccc gtc agc att ctg gat atc	
N K I V R M Y Q P V S I L D I R Q G P K E P F R D Y V D R F	Segment 19
S K	
aat aag att gtc agg atg tac yma cct ctc tcc atc ctc gac att arg caa ggc cct aag gaa ccc ttt agg gat tac gtc gac aga ttc	
R Q G P K E P F R D Y V D R F Y K T L R A E Q A T Q E V K N	Segment 20
K F	
ara cag gga ccc aaa gag cct ttc aga gac tat gtg gat agg ttt twc aaa acc ctc agg gct gag caa gcc wca cag gaw gtg aaa aac	
Y K T L R A E Q A T Q E V K N W M T E T L L V Q N A N P D C	Segment 21
F S D	
twt aag aca ctg aga gcc gaa cag gct wcc caa gas gtc aag aat tgg atg acc gas aca ctg ctc gtg caa aac gct aac cct gac tgc	
W M T E T L L V Q N A N P D C K S I L K A L G T G A T L E E	Segment 22
D T R P S	
tgg atg aca gaw acc ctc ctg gtc cag aat gcc aat ccc gat tgc aag wcc atc ctc arg gct ctg gga mcc gga gcc wca ctg gaa gag	
K S I L K A L G T G A T L E E M M T A C Q G V G G P S H K A	Segment 23
T R P S G	
aaa wca att ctg ara gcc ctc ggc mea ggc gct wcc ctc gag gaa atg atg aca gcc tgt cag gga ggc cct xgc cat aag gct	

FIGURE 12 (Cont)

22/216

M M T A C Q G V G G P S H K A R V L A E A M S Q A T H A N I Segment 24
 atg atg acc gct tgc caa ggc gtc ggc gga ccc rgt cac aaa gcc agg gtc ctg gca gag gct atg tcc cag gyg amc mac gct aac att
 V N N
 R V L A E A M S Q A T H A N I M M Q R G N F K G Q K R I I K Segment 25
 aga gtg ctg gcc gaa gcc atg agc caa gyc amc mat gcc aat atc atg atg cag aga ggc aat ttc ara ggc cna aag aga atc rtc aaa
 V N N R P V
 M M Q R G N F K G Q K R I I K C F N C G K E G H L A R N C R Segment 26
 atg atg caa agg gga aac ttt arg gga cmg aaa agg att rtc aag tgc ttt aac tgt gga aag gaa gcc cat mtc gct arg aat tgc aga
 I K
 C F N C G K E G H L A R N C R A P R K K G C W K C G K E G H Segment 27
 tgt ttc aat tgc ggc aaa gag gga cac mtt gcc ara aac tgc agg gcc cct aga aag aaa ggc tgt tgg aaa tgc gga arg gaa ggc cat
 I K R
 A P R K K G C W K C G K E G H Q M K D C T E R Q A N F L G K Segment 28
 gct ccc agg aaa aag gga tgc tgg aag tgt ggc ara gag gga cac cag atg aag gat tgc aca gag aga cag gct aac ttt ctg gga aag
 R
 Q M K D C T E R Q A N F L G K I W P S N K G R P G N F P Q S Segment 29
 H L
 S
 caa atg aaa gac tgt acc gaa agg caa gcc aat ttc ctg ggc aaa atc tgg ccc tcc mrc aaa ggc aga ccc gga aac ttt cyc caa agc

FIGURE 12 (Cont)

24/216

POL OVERLAPPING SEGMENTS

F F R E N L A F Q Q G K A R E F S S E Q T G A N S S A S R K	Segment 1
ttc ttt agg gaa anc T ctc gct ttc cmg caa ggc raa gcc aga gag ttt ycc agc gaa cag aca rga gcc aat agc ycc tcc tcc agg aaa	
F S S E Q T G A N S S A S R K L G D G G A E R Q G T S S	Segment 2
P R P T D	
ttc yct tcc gag caa aca xgg gct aac tcc yct tca agc aga aag ctg gga gac gga ggc gga gcc gas aga cag gga aca agc tcc agc	
L G D G G A E R Q G T S S F S F P Q I T L W Q R P L V T	Segment 3
ctc ggc gat ggc gga ggc gct gaw agg caa ggc acc tcc agc tcc ytc arc ttt ccc caa atc aca ctg tgg caa agg cct ctg gtc acc	
F S F P Q I T L W Q R P L V T I K I G G Q L K E A L L D T G	Segment 4
L N V I	
ytt art ttc cct cag att acc ctc tgg cag aga ccc ctc gtg aca rtc aaa atc ggc gga cag ctc awa gag gct ctg ctc gac aca ggc	
I K I G G Q L K E A L L D T G A D D T V L E D I N L P G K W	Segment 5
V I E M R	
rtt aag att gga ggc caa ctg awa gaa gcc ctc ctg gat aca gga gcc gat gac acc gtc ctg gaa gaw ata aat ctg cct ggc arg tgg	
A D D T V L E D I N L P G K W K P K M I G G I G G F I K V R	Segment 6
E M R	
gct gac gat aca gtg ctc gag gas ata aac ctc ccc gga ara tgg aag cct aag atg att ggc gga atc ggc gga ttc att aag gtg aga	

FIGURE 12 (Cont)

25/216

K P K M I G G I G G F I K V R Q Y D Q I L I E I C G K K A I Segment 7
 I
 H
 aaa ccc aaa atg atc gga ggc att gga ggc ttt atc aaa gtc agg cag tat gac caa atc mtt atc gaa atc tgt gga mas aag gct atc
 Q Y D Q I L I E I C G K K A I G T V L V G P T P V N I I G R Segment 8
 I
 H
 caa tac gat cag att mtt att gag att tgc ggc mas aaa gcc att ggc aca gtg ctc gtg gga cct acc cct gtg aat atc att ggc aga
 G T V L V G P T P V N I I G R N M L T Q I G C T L N F P I S Segment 9
 L
 R
 gga acc gtc ctg gtc ggc ccc aca ccc gtc aac att atc gga agg aac mtg ctg aca cag mtt ggc ygc acc ctc aac ttt ccc att agc
 N M L T Q I G C T L N F P I S P I D T V P V K L K P G M D G Segment 10
 L
 R
 E
 aat mtg ctc acc caa mtc gga ygc aca ctg aat ttc cct atc tcc ccc att gas aca gtg cct gtg aaa ctg aaa ccc gga atg gat ggc
 P I D T V P V K L K P G M D G P K V K Q W P L T E E K I K A Segment 11
 E
 cct atc gaw acc gtc ccc gtc aag ctc aag cct ggc atg gac gga ccc aaa gtg aaa cag tgg ccc ctc acc gaa gag aaa atc aaa gcc
 P K V K Q W P L T E E K I K A L T E I C K E M E E G K I S Segment 12
 A
 T
 K
 Q
 cct aag gtc aag caa tgg cct ctg aca gag gaa aag att aag gct ctg aca gmg att tgc ana gag atg gag vaa gag gga aag att agc

FIGURE 12 (Cont)

26/216

L T E I C K E E E G K I S K I G P E N P Y N T P V F A I Segment 13
 A T K Q
 ctc acc gmG atc tgt ama gaa atg gaa vaa gaa ggc aaa atc tcc arg att ggc cct gag aat ccc tat aac aca ccc rtc ttt gcc att
 K I G P E N P Y N T P V F A I K K K D S T K W R K L V D F R Segment 14
 R I
 arg atc gga ccc gaa aac cct tac aat acc cct rtc ttc gct atc aag aaa aag gac tcc acc aaa tgg aga aag ctc gtg gat ttc aga
 K K K D S T K W R K L V D F R E L N K R T Q D F W E V Q L G Segment 15
 aaa aag aaa gat agc aca aag tgg agg aaa ctg gtc gac ttt agg gag ctc aac aaa agg aca cag gat ttc tgg gag gtc cag ctc ggc
 E L N K R T Q D F W E V Q L G I P H P A G L K K K S V T V Segment 16
 gaa ctg aat aag aga acc caa gac ttt tgg gaa gtg caa ctg gga atc cct cac cct gct gga ctg aaa aag aaa aag tcc gtg aca gtg
 I P H P A G L K K K S V T V L D V G D A Y F S V P L D E S Segment 17
 K D
 G
 att ccc cat ccc gcc ctc aag aaa aag agc gtc acc gtc ctg gat gtg gga gac gct tac ttt agc gtc ccc ctc gac raa rrc

FIGURE 12 (Cont)

27/216

L D V G D A Y F S V P L D E S F R K Y T A F T I P S I N N E
 Segment 18
 ctc gac gtc ggc gat gcc tat ttc tcc gtg cct ctg gat raa rrc ttc aga aug tat acc gct ttc aca atc cct agc aya aac aat gag
 K D T
 F R K Y T A F T I P S I N N E T P G I R Y Q Y N V L P Q G W
 Segment 19
 ttt agg aaa tac aca gcc ttt acc att ccc tcc ayc aat aac gaa acc cct ggc att agg tat cag tat aac gtc ctg cct cag gga tgg
 T
 T P G I R Y Q Y N V L P Q G W K G S P A I F Q S S M T K I L
 Segment 20
 aca ccc gga atc aga tac caa tac aat gtg ctc ccc caa ggc tgg aag gga tcc ccc ecc att ttc caa agc tcc atg mcc maa atc ctc
 P Q
 K G S P A I F Q S S M T K I L E P F R I K N P E M V I Y Q Y
 Segment 21
 aaa ggc agc cct sct atc ttt cag tcc agc atg mca mag att ctg gag cct ttt agg ava maa aac cct gas atg gtc atc tat cag tat
 P Q K Q D
 E P F R I K N P E M V I Y Q Y M D D L Y V G S D L E I G Q H
 Segment 22
 gaa ccc ttc aga ava mag aat ccc gav atg gtg att tac caa tac atg gac gat ctg tat gtg gga agc gat ctg gaa atc gga cag cat

FIGURE 12 (Cont)

28/216

M D D L Y V G S D L E I G Q H R T K I E E L R A H L L R W G Segment 23
 A E K
 atg gat gac ctc tac gtc ggc tcc gac ctc gag att ggc caa cac agg rcc aaa atc gaa gag ctc agg sma cac ctc ctg ara tgg gga
 Q
 R T K I E E L R A H L L R W G F T T P D K K H Q K E P P F L Segment 24
 A E K
 aga rca aag att gag gaa ctg aga smg cat ctg ctc ara tgg ggc ttc aca acc cct gac aaa aag cat cag aaa gag cct ccc ttt ctg
 Q
 F T T P D K K H Q K E P P F L W M G Y E L H P D R W T V Q P Segment 25
 ttt acc aca ccc gat aag aaa cac caa aag gaa ccc cct ttc ctc tgg atg gga tac gaa ctg cat ccc gat agg tgg acc gtc cag cct
 W M G Y E L H P D R W T V Q P I E L P E K D S W T V N D I Q Segment 26
 V E
 tgg atg ggc tat gag ctc cac cct gac aga tgg aca gtc caa ccc atc swg ctc ccc gaa aag gaa tcc tgg aca gtc aat gac att cag
 Q
 I E L P E K D S W T V N D I Q K L V G K L N W A S Q I Y A G Segment 27
 V E P
 att swg ctg cct gag aaa gaw agc tgg acc gtc aac gat atc caa aag ctc gtc gga aag ctc aac tgg gcc tcc cag att tac acc gga

FIGURE 12 (Cont)

29/216

K L V G K L N W A S Q I Y A G I K V K Q L C K L L R G T K A Segment 28
 aaa ctg gtc ggc aaa ctg aat tgg gct agc caa atc tat sct ggc atc aaa gtg arg caa ctg tgt aag ctc ctg aga ggc rcc aaa gcc
 I K V K Q L C K L L R G T K A L T D I V P L T E E A E L E L Segment 29
 att aag gtc ara cag ctc tgc aaa ctg ctc agg gga rca aag gct ctg aca gas att gtg mca ctg aca gag gaa gcc gaa ctg gaa ctg
 L T D I V P L T E E A E L E E N R E I L R E P V H G V Y Segment 30
 ctc acc gaw atc gtc mca ctc acc gaa gag gct gag ctc gmg gaa aac aga gag att ctg arg gaa ccc gtc cac gga gtg tat
 E E N R E I L R E P V H G V Y Y D P S K D L V A E V Q K Q G Segment 31
 gmg gag aat agg gaa atc ctc ara gag cct gtg cat ggc gtc tac tac gat ccc tcc aag gat ctg rtc gct gaa rtc caa aag caa ggc
 Y D P S K D L V A E (V) Q K Q G Q D Q W T Y Q I Y Q E P F K N Segment 32
 tat gac cct agc aaa gac ctc rtt gcc gag rtt cag aaa cag gga cag grt cag tgg aca twt cag att twc caa gag cct ttc aaa aac
 Q D Q W T Y Q I Y Q E P F K N L K T G K Y S R K R S A H T N Segment 33
 caa gtc caa tgg acc twc caa atc twt cag gaa ccc ttt aag aat ctg aaa acc gga aag tat kcc aga awg aga tgc gct cac aca aac

FIGURE 12 (Cont)

30/216

L K T G K Y S R K R S A H T N D V R Q L T E V V Q K I A T E Segment 34
 ctc aag acc ggc aaa tac kct agg awg agg rgt gcc cat acc aat gac ctc arg caa ctg aca gmg gyt gtg caa aag rtt gcc aca gag
 A M G K A A (V)
 D V R Q L T E V V Q K I A T E S I V I W G K T P K F R L P I Segment 35
 K A A V K
 gat ctg ara cag ctc acc gma gyc gtc cag aaa rtc gct acc gaa agc att gtg att tgg gga aag aca ccc aaa ttc ara ctg. cct atc
 S I V I W G K T P K F R L P I Q R E T W E T W M E Y W Q A Segment 36
 K K A T D
 tcc atc gtc atc tgg ggc aaa acc cct aag ttt arg ctc ccc att cag ara gag aca tgg gaa rcc tgg tgg ayg gas tat tgg caa gcc
 Q R E T W E T W M E Y W Q A T W I P E W E F V N T P P L V Segment 37
 K A T D
 caa arg gaa acc tgg gag rct tgg tgg ayg gam tac tgg cag gct acc tgg atc cct gag tgg gag ttt gtg aat acc cct ctc ctc gtg
 T W I P E W E F V N T P P L V K L W Y Q L E K D P I V G A E Segment 38
 aca tgg att ccc gaa tgg gaa ttc gtc aac aca ccc cct ctg gtc aag ctc tgg tat cag ctc gag aaa gas cct atc gyt ggc gyt gag
 K L W Y Q L E K D P I V G A E T F Y V D G A A S R E T K L G Segment 39
 E A V N
 aaa ctg tgg tac caa ctg gaa aag gam ccc att gyc gga gyc gaa acc ttt tac gtc gac gga gcc gct arc aga gag aca aag ctc ggc

FIGURE 12 (Cont)

Segment 40
T F Y V D G A A S R E T K L G K A G Y V T D R G R Q K V I S
N I V
aca ttc tat gtg gat ggc gct gcc art agg gaa acc aaa ctg gga aag gct ggc tat gtg aca gac aga ggc aga cag aaa rtc rtt agc

Segment 41
K A G Y V T D R G R Q K V I S L T E T T N Q K T E L H A I H
I V D Q
aaa gcc gga tac gtc acc gat agg gga agg caa aag rtt ttc ctg aca gaa aca acc aat cag aaa acc gaa ctg caw gcc att cam

Segment 42
L T E T T N Q K T E L H A I H L A L Q D S G S E V N I V T D
D Q L
ctc acc gam acc aca aac aag aca gag ctc cam gct atc caw ctg gct ctg caa gac tcc ggc tya gag gtc aac att gtg aca gac

Segment 43
L A L Q D S G S E V N I V T D S Q Y A L G I I Q A Q P D R S
L K
ctc gcc ctc cag gat agc gga tyg gaa gtg aat atc gtc acc gat agc caa tac gct ctg gga atc att cwg gct cag cct gac ara agc

Segment 44
S Q Y A L G I I Q A Q P D R S E S E V V S Q I I E E L I K K
L K L N K Q
tcc cag tat gcc ctc ggc att atc cwa gcc caa ccc gat arg tcc gag tcc gag stc gtg art cag att atc gaa vag ctc atc aaa aag

Segment 45
E S E V V S Q I I E E L I K K E K V Y L S W V P A H K G I G
L N K S R A
gag tcc gag stc gtg art cag att atc gaa vag ctc atc aaa aag gaa arg gtc tac ctc kcc tgg gtg cct gcc cac aag gga atc gga

FIGURE 12 (Cont)

32/216

E K V Y L S W V P A H K G I G G N E Q V D K L V I S G I R K Segment 46
 R A
 gag ara gtg tat ctg kct tgg gtc ccc gct cat aaa ggc att ggc gga aac gaa cag gtc gac aaa ctg gtc akc kct ggc att agg aaa
 G N E Q V D K L V I S G I R K V L F L D G I N K A Q E E H E Segment 47
 S A D
 ggc aat gag caa gtg gat aag ctc gtg akt kcc gga atc aga aag gtg ctc ttc ctc gac gga atc rat aag gct cag gaa gag cac gaa
 V L F L D G I N K A Q E E H E R Y H S N W R T M A S D F N L Segment 48
 D K
 gtc ctg ttt ctg gat ggc att rac aaa gcc caa gag gaa cat gag arg tat cac tcc aac tgg agg aca atg gct arc gam ttc aat ctg
 (R) Y H S N W R T M A S D F N L P P I V A K E I V A N C D K C Segment 49
 K N E P S C
 ara tac cat agc aat tgg aga acc atg gcc art gas ttt aac ctc ccc cct atc gtc sct aag gaa atc gtc gcc wrt tgc gat aag tgt
 P P I V A K E I V A N C D K C Q L K G E A M H G Q V D C S P Segment 50
 P S C I N
 cct ccc att gtg scc aaa gag att gtg gct wrt tgt gac aaa tgc cag ctc aag gga gag gct atk cac gga cag gtc rac tgt agc cct

FIGURE 12 (Cont)

33/216

Q L K G E A M H G Q V D C S P G I W Q L D C T H L E G K V I Segment 51
 I N
 caa ctg aaa ggc gaa gcc atc cat ggc caa gtc rat tgc tcc ccc ggc att tgg caa ctg gat tgc aca cac ctc gag gga aag rtt atc
 G I W Q L D C T H L E G K V I L V A V H V A S G Y I E A E V Segment 52
 I
 gga atc tgg cag ctc gac tgt acc cat ctg gaa ggc aaa rtc att ctg gtc gcc gtc cac gtc gcc tcc ggc tac att gag gct gag gtc
 L V A V H V A S G Y I E A E V I P A E T G Q E T A Y F L L K Segment 53
 I
 ctc gtc gct gtc cat gtc agc gga tat atc gaa gcc gaa gtc gtc cct gcc gaa acc gga cag gaa acc gct tac ttt mtc ctc aag
 I P A E T G Q E T A Y F L L K L A G R W P V K V I H T D N G Segment 54
 I R T
 att ccc gct gag aca ggc caa gag aca gcc tat ttc mtt ctg aaa ctg gct ggc aga tgg cct gtg ara ryc att cac aca gac aat ggc
 L A G R W P V K V I H T D N G S N F T S A A V K A A C W W A Segment 55
 R T T
 ctc gcc gga agg tgg ccc gtc arg rya atc cat acc gat aac gga agc aat ttc aca agc rct rcc gtc aag gct gcc tgc tgg tgg gct
 S N F T S A A V K A A C W W A N I K Q E F G I P Y N P Q S Q Segment 56
 T T G Q
 tcc aac ttt acc tcc rct rct gtc aaa gcc gct tgt tgg tgg gcc rrt atc maa cag gaa ttc gga atc cct tac aat ccc caa agc caa

FIGURE 12 (Cont)

34/216

N I K Q E F G I P Y N P Q S Q G V V E S M N K E L K K I I G Segment 57
 G Q
 xrc att mag caa gag ttt ggc att ccc tat aac cct cag tcc cag ggc gtc gtc gaa agc atg aac aaa gag ctc aag aaa atc att ggc
 G V V E S M N K E L K K I I G Q V R E Q A E H L K T A V Q M Segment 58
 D
 gga gtc gtc gag tcc atg aat aag gaa ctg aaa aag att atc gga cag gtc agg gam cag gct gag cat ctg aaa acc gct gtc caa atg
 Q V R E Q A E H L K T A V Q M A V F I H N F K R K G I G G Segment 59
 D R
 caa gtc aga gaa caa gcc gaa cac ctc aag aca gcc gtc cag atg gcc gtc ttc att cac aat ttc aaa agg ara ggc gga atc gga ggc
 A V F I H N F K R K G G I G G Y S A G E R I I D I I A T D I Segment 60
 R V S
 gct gtc ttt atc cat aac ttt aag aga arg gga ggc att ggc gga tac tcc gcc gga gag aga atc rtt gac att atc gct aac gat atc
 Y S A G E R I I D I I A T D I Q T K E L Q K Q I T K I Q N F Segment 61
 V S N L
 tat agc gct ggc gaa agg att rtc gat atc att gcc wcc gac att cag tat aag gaa ctg caa aas caa atc mya aag att cag aat ttc
 Q T K E L Q K Q I T K I Q N F R V Y R D S R D P I W K G P Segment 62
 N L L
 caa tac aaa gag ctc cag aam cag att myc aaa atc caa aac ttt agg gtc tac tat agg gat agc aga gac cct mtc tgg aag gga ccc

FIGURE 12 (Cont)

35/216

R V Y R D S R D P I W K G P A K L L W K G E G A V V I Q D Segment 63
 L
 aga gtg tat tac aga gac tcc agg gat ccc mtt tgg aaa ggc cct gcc aaa ctg ctc tgg aaa ggc gaa ggc gct gtg gtc atc caa gac
 A K L L W K G E G A V V I Q D N S D I K V V P R R K A K I I Segment 64
 gct aag ctc ctg tgg aag gga gag gcc gtc gtg att cag gat aac tcc gac att aag gtc gtg cct agg aga aag gct aag att atc
 N S D I K V V P R R K A K I I R D Y G K Q M A G D D C V A G Segment 65
 A
 aat agc gat atc aaa gtg gtc ccc aga agg aaa gcc aaa atc att agg gat tac gga aag caa atg gct ggc gmt gac tgt gtg gct xgc
 R D Y G K Q M A G D D C V A G R Q D E D Segment 66
 A
 agg gat tac gga aag caa atg gct ggc gmt gac tgt gtg gct xgc agg caa gac gaa gac

FIGURE 12 (Cont)

36/216

VIF OVERLAPPING SEGMENTS

M E N R W Q V M I V W Q V D R M R I R T W N S L V K H H M Y	Segment 1
atg gaa aac aga tgg caa gtg atc gtc tgg caa gtg gat agg atg arg att agg aca tgg aaw agc ctc gtg aaa cac cat atg yat	H
M R I R T W N S L V K H H M Y I S K K A K G W F Y R H H Y E	Segment 2
atg ara atc aga tac tgg aas acc ctg gtc aag cat cac atg yac atc tcc aag aaa gcc aaw ggc tgg ttc tat agg cat cac twt gas	F D
I S K K A K G W F Y R H H Y E S Q H P K V S S E V H I P L G	Segment 3
att agc aaa aag gct aas gga tgg ttt tac aga cac cat twc gaw agc cra cac cct aag gtc agc tcc gag gtc cac att ccc ctc ggc	
S Q H P K V S S E V H I P L G E A R L V I R T Y W G L Q T G	Segment 4
tcc crg cat ccc aaa gtg tcc agc gaa gtg cat atc cct ctg gga gas gct agg ctc rtc att arg aca tac tgg ggc ctc caa aca ggc	H
E A R L V I R T Y W G L Q T G E K D W Q L G H G V S I E W R	Segment 5
gaw gcc aga ctg rtt atc ara acc tat tgg gga ctg caw acc gga gag ara gac tgg cas ctc ggc caw ggc gtc agc att gag tgg agg	

FIGURE 12 (Cont)

37/216

E K D W Q L G H G V S I E W R Q K R Y S T Q V D P D L A D Q Segment 6
 R H Q L S K
 gaa arg gat tgg caw ctg gga caa gga gtg tcc atc gaa tgg aga mwg aaa aga tat agc aca cag gtc gac cct grc ctc gcc gat caa
 Q K R Y S T Q V D P D L A D Q L I H L Q Y F D C F S D S T I Segment 7
 L S K H G H Y H A A
 mwg aag agm tac tcc acc caa gtg gat ccc grt ctg gct gac caw ctg att cac ctc yas tat ttc gat tgc ttt kcc gat agc rca atc
 L I H L Q Y F D C F S D S T I R R A I L G Q I V R R R C E Y Segment 8
 H Y A A H R S
 ctc atc cat ctg yaw tac ttt gac tgt ttc kct gac tcc rcc att agg aga gcc att ctg gga caa aka gtg agm agg aga tgc gaa tac
 R R A I L G Q I V R R R C E Y P S G H N K V G S L Q Y L A L Segment 9
 H R S Q A
 aga agg gct atc ctc ggc caw aka gtc aga aga agg tgt gag tat cmg kcc gga cac aat aag gtc ggc tcc ctg caa tac ctc gcc ctc
 P S G H N K V G S L Q Y L A L K A L I T P K K I R P P L P S Segment 10
 Q A T K
 cma kct ggc cat aac aaa gtg gga agc ctc cag tat ctg gct ctg amg gct ctg att amg cct aag aaa atc ara' ccc cct ctg cct agc

FIGURE 12 (Cont)

38/216

Segment 11

K A L I T P K K I R P P L P S V K K L T E D R W N K P Q K I
T K K

ama gcc ctc atc ama ccc aaa aag att arg cct ccc ctc tcc gtc aaa aag ctc acc gaa gac ara tgg aat rag cct caa aag aya

Segment 12

V K K L T E D R W N K P Q K I K G H R E N H T M N G H
K E T R G

gtc aag aaa ctg aca gag gat arg tgg aac raa ccc cag aaa ayc aag gga ctc aga gra aat cac aca atg aat ggc cat

FIGURE 12 (Cont)

39/216

VPR OVERLAPPING SEGMENTS

M E Q A P E D Q G P Q R E P Y N E W A L E L L E L K Q E A	Segment 1
S S T H	
atg gaa cag gct ccc gaa gac caa xgc yct cag aga gag cct tac aat gag tgg rcc ctc gag ctc ctg gaa gag ctc aag mam gag gct	
N E W A L E L L E L K Q E A V R H F P R P W L H N L G Q Y H	Segment 2
T H N G S	
aac gaa tgg rca ctg gaa ctg ctc gag gaa ctg aaa maw gaa gcc gtg aga cac ttt ccc aga ccc tgg ctg cat rrc ctc ggc caa yac	
V R H F P R P W L H N L G Q Y I Y E T Y G D T W S G V E A L	Segment 3
G H S	
gtc agg cat ttc cct agg cct tgg ctc cac rrc ctg gga cag yac atc tat gag aca tac gga gac aca tgg kmg gga gtg gaa gcc ctc	
I Y E T Y G D T W S G V E A L I R T L Q Q L M F I H F R I G	Segment 4
E I L V	
att tac gaa acc tat ggc gat acc tgg kma ggc gtc gag gct ctg atc aga ayc ctc cag caa ctg mtg ttt rtc cat ttc aga atc gga	

FIGURE 12 (Cont)

40/216

I R T L Q Q L M F I H F R I G C Q H S R I G I L R Q R R A R
I L V
att agg ayc ctg caa cag etc mtg ttc rtt cac ttt agg att ggc tgc crg cac tcc agg att ggc att myc aga cag aga agg gsc aga
C Q H S R I G I L R Q R R A R N G A S R S
R G S
tgt cra cat agc aga atc gga atc myc agg caa agg aga gat agg aac gga kcc tcc agg tcc

Segment 5
G
I
T
Segment 6

FIGURE 12 (Cont)

42/216

Segment 6

Q T R G N P T D P K E S K K E V A S K T E T D P C D

P D G E K E A F

caa mcc aga ggc grt aac cct acc grt ccc raa gag tcc aag aaa rag gtc gmg tcc aag rca gag aca gac cct tkt gac

* different

FIGURE 12 (Cont)

REV OVERLAPPING SEGMENTS

M A G R S G S T D E E L L R A V R I I N I L Y Q S N P Y P S T Segment 1

atg gct ggc aga agc gga rrc aca gac gaa gag ctc ctg arg gct rtc aga atc att aas att ctg tat cag tcc aac cct tac cct wcc

Segment 2

V R I I N I L Y Q S N P Y P S S E G T R Q T R K N R R R W
I K T A R
rtt agg att atc aaw atc ctc tac caa agc aat ccc tat ccc wca agc gaa gcc wcc agg caa rcc aga arg aat agg aga agg aga tgg

Segment 3

S E G T R Q T R K N R R R R A R Q R Q I R A I S E R I L
S A R E H S W
tcc gag gga wca aga cag rct agg ara eac aga agg aga tgg agg gmg agg caa agg caa atc crc kcc atc tcc gag wgg att ctg

Segment 4

R A R Q R Q I R A I S E R I L S T . C L G R S A E P V P L Q L
E H S W N F P

aga gma aga cag aga cag att crt kct att agc gaa wgg atc ctc agc amc tkc ctc ggc aga ycc gct gag cct gtc cct ctg caa ctg

Segment 5

S	T	C	L	G	R	S	A	E	P	V	P	L	Q	L	P	P	L	E	R	L	H	L	D	C	S	E	D	C	G
N	F						P												N								S	D	
tcc	amc	tkt	ctg	gga	agg	yct	gcc	gaa	ccc	gtc	ccc	cag	ctc	ctc	ccc	cct	ctg	gaa	agg	ctc	mac	ctc	gac	tgt	agc	gaa	gac	wgt	gic

43/216

FIGURE 12 (Cont)

P P L E R L H L D C S E D C G T S G T Q Q S Q G T E T G V G
 N S D
 cct ecc ctc gag aga ctg mac ctg gat tgc tcc gag gat wgc grt acc tcc ggc aca cag caa agc caa ggc aca gag aca gga gtc gga
 T S G T Q Q S Q G T E T G V G R P Q I S G E S S V I L G P G
 N L A V S
 aca agc gga acc caa cag tcc cag gga acc gaa acc ggc gtc ggc mrc cct cag att tyg gga gag tcc agc gyt rtc ctc ggc ycc gga
 R P Q I S G E S S V I L G P G T K N
 L A V S
 mrc ccc caa atc tya ggc gaa agc tcc ggc rtt ctg gga yct ggc acc aaa aac
 S

44/216

FIGURE 12 (Cont)

VPU OVERLAPPING SEGMENTS

M T P L E I I A I V A F I V A L I I A I V V W T I A Y I E Y	Segment 1
<div>[S] [Q] [R] L V F</div>	
atg aca ycc ctc eag ara atc gct atc gtc gcc ytt atc gtc gcc ctc atc mta gcc att gtc gtc tgg aca atc gyc twc att gag tat	
L I I A I V V T I A Y I E Y R K L L R Q R R I D R L I K R	Segment 2
<div>L V F K K K E</div>	
ctg att mtc gct atc gtc tgg acc att gyg twt atc gaa tac arg aaa ctg ctc arg caa agg ara atc gat agg ctc atc raa agg	
R K L L R Q R R I D R L I K R T R E R A E D S G N E S E G D	Segment 3
<div>(K) K K I E I</div>	
ara aag ctc ctg ara cag aga arg att gac aga ctg att rag aga ayc aga gag aga gcc gaa gac tcc ggc aat gag tcc gag gga gac	
T R E R A E D S G N E S E G D T E E L S T M V D M G N Y D L	Segment 4
<div>I R A L</div>	
aya agg gaa agg gct gag gat agc gga aac gaa agc gaa ggc gat asa gaa gag ctc agc rca wtg gtc gac atg ggc aat tac gat ctg	
T E E L S T M V D M G N Y D L G V D N N L	Segment 5
<div>R A L</div>	
asa gag gaa ctg tcc rcc wtg gtg gat atg gga aac tat gac ctc ggc gtc gac aat aac ctc	

FIGURE 12 (Cont)

46/216

ENV OVERLAPPING SEGMENTS

M R V K E T Q M N W P N L W K W G T L I L G L V I I C S A S	Segment 1
atg aga gtc aaa gag aca cag atg aac tgg ccc aat ctg tgg arg tgg ggc aca mtg att ctg gga mtg gtc ats att tgc tcc gcc tcc	
W G T L I L G L V I I C S A S D N L W V T V Y G V P V W R	Segment 2
tgg gga acc wtg atc ctc ggc wtg gtc atx atc tgt agc gct agc gas aat ctg tgg gtc aca gtc tat tac gga gtc cct gtc tgg agg	
D N L W V T V Y G V P V W R D A D T T L F C A S D A K A H	Segment 3
gam aac ctc tgg gtc acc gtc tac tat ggc gtc ccc gtc tgg aga gas gct xmc aca acc ctc ttc tgt gcc tcc gac gct aag gct yac	
D A D T T L F C A S D A K A H E T E V H N V W A T H A C V P	Segment 4
gam gcc xmt acc aca ctg ttt tgc gct agc gat gcc aaa gcc yat gas aca gag gtc cac aat gtc tgg gcc aca cac gct tgc gtc ccc	
E T E V H N V W A T H A C V P T D P N P Q E I H L E N V T E	Segment 5
gam acc gaa gtc cat aac gtc tgg gct acc cat gcc tgt gtc cct acc gat ccc aat ccc caa gag rtt swc ctc gag aat gtc aca gag	
T D P N P Q E I H L E N V T E N F N M W K N N M V E Q M Q E	Segment 6
aca gac cct aac cct cag gaa rtc swt ctg gaa aac gtc acc gaa aac ttt aac atg tgg aaa aac rat atg gtc gas caa atg caw gag	

FIGURE 12 (Cont)

47/216

N F N M W K N N M V E Q M Q E D V I S L W D Q S L K P C V K Segment 7
D D H I
aat ttc aat atg tgg aag aat rac atg gtg gam cag atg cam gaa gac rtt atc tcc ctg tgg gac caa agc ctc aag cct tgc gtc aag
D V I S L W D Q S L K P C V K L T P L C V T L N C T N A N L Segment 8
I
gat rtc att agc ctc tgg gat cag tcc ctg aaa ccc tgt gtg aaa ctg aca ccc ctc tgc gtc acc ctc aac tgt acc aat gcc aat ctg
L T P L C V T L N C T N A N L I N V N Segment 9
ctc acc cct ctg tgt gtg aca ctg aat tgc aca aac gct aac ctc atc aat gtg aat

FIGURE 12 (Cont)

48/216

GAP IN SEGMENTS DUE TO HYPERVARIABLE REGIONS 1 AND 2

Y R L I N C N T S V I K Q A C P K V S F D P I P I H Y C T P	Segment 1
tac aga ctg att arc tgt aac aca agc gyt atc ama cag gct tgc cct aag rtt asc ttt gas cct atc cct atc cat tac tgt rcc cct	A
P K V S F D P I P I H Y C T P A G Y A I L K C N D K N F N G	Segment 2
I T E	N K
ccc aaa rtc wcc ttc gam ccc att ccc att cac tat tgc rct ccc gcc gga twc gct atc ctc aag tgt aac rat aag amm ttc aat ggc	T
A G Y A I L K C N D K N F N G T G P C K N V S S V Q C T H G	Segment 3
F N K T	T
gct ggc twt gcc att ctg aaa tgc aat rac aaa ama ttt aac gga acc gga ccc tgt amg aat gtg tcc asc gtc cag tgt acc cat ggc	
T G P C K N V S S V Q C T H G I K P V V S T Q L L L N G S L	Segment 4
aca ggc cct tgc ama aac gtc agc wcc gtg caa tgc aca cac gga atc ara ccc gtc gtg tcc acc caa ctg ctc ctg aat ggc tcc ctg	R
I K P V V S T Q L L L N G S L A E E I I I R S E N L T N N	Segment 5
att arg cct gtg gtc agc aca cag ctc ctg ctc aac gga agc ctc gcc gaa gag gaa rtc rtt atc aga agc gaa aac ytt acc rat aac	V F D

FIGURE 12 (Cont)

49/216

A	E	E	I	I	I	R	S	E	N	L	T	N	N	A	K	T	I	I	V	H	L	N	E	S	V	E	I	N	Segment 6
			(V)	(V)					F	D					V				Q			K			V				
gct gag gaa gat rtt rtc att agg tcc gag aat ytc aca rac aat gyc aaa acc att atc gtc cam ctc aac raa agc gtc gwg att aac																													
A	K	T	I	I	V	H	L	N	E	S	V	E	I	N	C	T	R	P	N	N	T	R	K					Segment 7	
V					(Q)				K		V				S							T							
ggt aag aca atc att gtg caw ctg aat rag tcc gtg gva atc aat tgc aca agg cct arc aat aac aca agg ama																													

FIGURE 12 (Cont)

50/216

GAP IN SEGMENTS DUE TO HYPERVARIABLE REGIONS 3,4 AND 5

T F R P G G D I K D N W R S E L Y K Y K V V K I E P L G V	Segment 1
I N M R	
ayc ttt agg cct ggc gga ggc rat ats ara gac aat tgg aga agc gaa ctg tat aag gtc gtg rag att rag cct ctg gga rtc	
E L Y K Y K V V K I E P L G V A P T R A K R R V V E R E K R	Segment 2
E K I K Q	
gag ctc tac aaa tac aaa gtg gtc raa atc raa ccc ctc ggc rtt gcc cct acc ara gcc aaa agg aga gtg gtc sag aga gag aaa agg	
A P T R A K R R V V E R E K R A V G I G A M I F G F L G A A	Segment 3
K Q L F L	
gct ccc aca arg gct aag aga agg gtc gtg saa agg gaa aag aga gcc gtc ggc mtt ggc gct atg wtt ytc gga ttc ctc ggc gct gcc	
A V G I G A M I F G F L G A A G S T M G A A S I T L T V Q A	Segment 4
L F L M	
gct gtg gga mtc gga gcc atg wtc ytt ggc ttt ctg gga gcc gct ggc tcc acc atg ggc gct gcc tcc ats aca ctg aca gtg caa gcc	
G S T M G A A S I T L T V Q A R Q L L S G I V Q Q Q S N L L	Segment 5
M L N	
gga agc aca atg gga gcc gct agc atk acc ctc acc gtc cag gct agg cwa ctg ctc agc gga atc gtc cag caa cag arc aat ctg ctc	
R Q L L S G I V Q Q Q S N L L R A I E A Q Q H L L Q L T V W	Segment 6
L N M	
aga cwg ctc ctg tcc ggc att gtg caa cag caa art aac ctc ctg agg gct atc gaa gcc caa cag cat mtg ctc cag ctc acc gtc tgg	

FIGURE 12 (Cont)

51/216

R A I E A Q Q H L L Q L L T V W G I K Q L Q A R V L A V E R Y Segment 7
 M
 aga gcc att gag gct cag caa cac wtg ctg caa ctg aca gtg tgg ggc att aag caa ctg caa gcc aga gtg ctc gcc rtt gag aga tac
 G I K Q L Q A R V L A V E R Y L K D Q K F L G L W G C S G K Segment 8
 I
 gga atc aaa cag ctc cag gct agg gtc ctg gct rtc gaa agg tat ctg aaa gac caa mag ytt ctg gga mtc tgg ggc tgt agc gga aag
 Q L I
 L K D Q K F L G L W G C S G K I I C T T A V P W N S S W S N Segment 9
 L
 ctc aag gat cag maa ytc ctc ggc mtt tgg gga tgc tcc ggc aaa mtc att tgc aca acc rmt gtg cct tgg aac agc wcc tgg tcc aac
 I I C T T A V P W N S S W S N K S L E E I W N N M T W M E W Segment 10
 N
 mtt atc tgt acc aca rmc gtc ccc tgg aat tcc asc tgg agc aat aag tcc ytc gaa gag att tgg rat aac atg acc tgg atg aaa tgg
 F
 K S L E E I W N N M T W M E R E I S N Y T N Q I Y E I L Segment 11
 D
 aaa agc ytt gag gaa atc tgg rac aat atg aca tgg atk sag tgg gag aga gag att agc aat tac aca arc cwa atc tat rag att ctg
 I Q
 E R E I S N Y T N Q I Y E I L T E S Q N Q Q D R N E Q E L L Segment 12
 S L K
 gaa agg gaa atc tcc aac tat acc art cwg att tac raa atc ctc acc gaa agc caa aac cag gat agg aat gag maa gas ctc ctg
 K D

FIGURE 12 (Cont)

52/216

T E S Q N Q Q D R N E Q E L L E L D K W A S L W N W F D I T Segment 13
 K D A N S
 aca gag tcc cag aat cag caa gac aga aac gaa mag gam ctg ctc gmg ctc gac aaa tgg gct agc ctc tgg aat tgg ttt rac att asc

 E L D K W A S L W N W F D I T N W L W Y I K I F I M I V G G Segment 14
 A N S K
 gma ctg gat aag tgg gcc tcc ctg tgg aac tgg ttc rat atc wcc aas tgg ctg tgg tac att aag att ttc att atg att gtg gga ggc

 N W L W Y I K I F I M I V G G L I G L R I V F A V L S I V N Segment 15
 K V I I
 aam tgg ctc tgg tat atc aaa atc atg atc gtc ggc gga ctg rtt ggc ctc agg att rtc ttt gcc gtc ctg tcc atc rtt aac

 L I G L R I V F A V L S I V N R V R Q G Y S P L S F Q T L L Segment 16
 V I I T
 ctc rtc gga ctg aga atc rtt ttc gct gtg ctc agc att rtc aat agg gtc agg caa ggc tat agc cct ctg tcc ttc caa acc ctc myc

 R V R Q G Y S P L S F Q T L L P A P R G P D R P E G I E E E Segment 17
 T L G R
 aga gtg aga cag gga tac tcc ccc ctc agc ttt cag aca ctg myg ccc gct ccc aga ggc cct gac aga cgc gra agc att gag gaa gag

 P A P R G P D R P E G I E E E G G E Q D R D R S V R L V S G Segment 18
 L G R R G G N
 cct gcc cct agg gga ccc gat agg cyg gzg tga atc gaa gag gaa ggc gga gag cra ggc aga gtc aga agc gtc agc ctc gtg art ggc

FIGURE 12 (Cont)

54/216

I A V A E G T D R V I E V A Q R A G R A I L H I P R R I R Q
G W I V W T
att gcc gtc gcc gra kgg aca gac aga rtc att gag gtc gyc caa agg gct kgg aga gcc att ctg mat atc cct asa aga atc aga cag

R A G R A I L H I P R R I R Q G L E R A L L
W N T F
aga gcc kgg agg gct atc ctc mac att ccc asg agg att agg caa ggc ytt gag aga gcc ctc ctg

Segment 25

Segment 26

FIGURE 12 (Cont)

55/216

NEF OVERLAPPING SEGMENTS

M G G K W S K S S L V G W P E V R E R I R Q T P P A A E G V Segment 1
 C P A R A A
 atg gga ggc aaa tgg tcc aag wgc tcc cgc gtc gga tgg ccc gma gtg aga gag aga atc aga crg rca acc cct gcc gct gag gga gtg
 V R E R I R Q T P P A A E G V G A V S Q D L D K H G A I T S Segment 2
 R A A A R Y L
 gtc agg gaa agg att agg cra rcc set ccc gct gcc gaa ggc gtc ggc gct gyc tcc crg gat ctg gat aag kac gga gcc mtc acc tcc
 G A V S Q D L D K H G A I T S S N T P A N N A D C V W L K A Segment 3
 A R Y L A P A E
 gga gcc gyg agc cra gac ctc gac aaa kat ggc gct mtt aca agc tcc aat acc set gcc aat aac act gac tgt gyc tgg ctc rag gct
 S N T P A N N A D C V W L K A Q E E E G V G F P V R P Q V P Segment 4
 A P A E
 agc aac aca ecc gct aac aat scc gat tgc gyg tgg ctg raa gcc cag gaa gag gaa gra gtg gga ttt cct gtg aga ccc caa gtg cct
 Q E E G V G F P V R P Q V P L R P M T Y K G A F D L S F F Segment 5
 E A V L
 caa gag gaa gag grg gtc ttc ccc gtc agg cct cag gtc ccc ctg aga cct atg acc tac aaa gaa gcc rtc gat ctg tcc ytc ttc
 L R P M T Y K G A F D L S F L K E K G G L E G L V Y S K K Segment 6
 A V L D I Q
 ctc agg ccc atg aca tat aag gac gct rtt gac ctc agc ytg ttt ctg aaa gag aaa ggc gga ctg gaw ggc ctc rtc tat agc mag aaa

FIGURE 12 (Cont)

56/216

L K E K G G L E G L V Y S K K R Q E I L D L W V Y H T Q G F Segment 7
 ctg aag gaa aag gga ggc ctc gaa gga ctg rtt tac tcc maa aag agg caa gaa att ctg gat ctg tgg gtg tat mac aca cag gga twc
 R Q E I L D L W V Y H T Q G F F P D W H N Y T P G P G I R Y Segment 8
 (D) N Y Q T V
 aga cag gaw atc ctc gat ctc tgg gtc tac mat acc caa ggc twt ttc cct gac tgg cas aat tac aca ccc gga ccc gga ryc aga tac
 F P D W H N Y T P G P G I R Y P L T F G W C F K L V P V D P Segment 9
 Q T V
 ttt ccc gat tgg caw aac tat acc cct ggc cct ggc rya agg tat ccc ctc acc ttt ggc tgg tgc ttt aag ctc gtg cct gtg gat ccc
 P L T F G W C F K L V P V D P R E V E E I N K G E N N C L L Segment 10
 S A E
 cct ctg aca ttc gga tgg tgt ttc aaa ctg gtc ccc gtc gac cct ags gaa gtc gaa gag ryc aac raa ggc gaa aac aat tgc ctc ctg
 R E V E E I N K G E N N C L L H P M S Q H G M E D E R E V Segment 11
 S A E I C L D
 agw gag gtc gag gaa ryc aat rag gga gag aat aac tgt ctg ctc cac cct ats rgt cwg cat ggc atg gaa gac gaa gaa aga gag gtc

FIGURE 12 (Cont)

57/216

H P M S Q H G M E D E R E V L I W K F D S R L A R R H I A	Segment 12
I C L	
cat ccc ats tgc cwa cac gga atg gag gat gag gaw agg gaa gtg ctg awa tgg aaa ttc gat agc crt ctg gct ckc agg cat ats gct	
L I W K F D S R L A R R H I A R E L R P E F Y K D C	Segment 13
K	
ctc awa tgg aag ttt gac tcc crc ctc gcc ckg aga cat ats gcc agg gaa ctg crt ccc gaa twc tac aaa gac tgc	

FIGURE 12 (Cont)

59/216

The Genetic Code- First and Second Most Frequently Used Codons

K	M	P	S	T	W	Y	V	L
Lys	Met	Phe	Pro	Thr	Trp	Tyr	Val	Leu
AAG/AAA	ATG/	TTC/TTT	CCC/CCT	ACC/ACA	TGG/	TAC/TAT	GTC/GTC	CTG/CTC

The Genetic Code- First and Second Most Frequently Used Degenerate Codons For TWO or More Amino Acids

TWO BASES AT A SINGLE POSITION

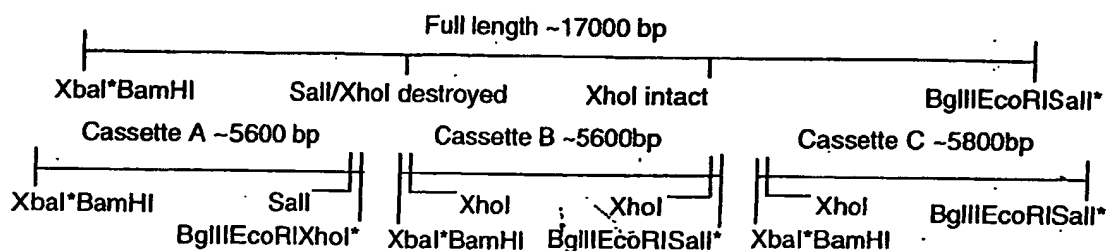
KM	ANG/	MR	AKT/	FC	TKC/TKT	PQ	CMG/CMA	SN	TSQ/	TM	AYG/	WR	MGQ/YGG	YN	WAC/WAT	VM	RTG/	LM	MYG/WTG
KN	AAS/AAM	MI	ATS/ATK	FI	WTC/WTI	PH	CMC/CMT	SN	ARC/ART	TN	AMC/AMT	WG	KGG/	YD	KAC/KAT	VD	GWC/GWT	LN	TKG/
KQ	MAG/MAA	ML	MTG/MTG	FL	YTC/YTT	PA	BGC/BCT	SL	TYG/TYA	TK	ANG/ANA	WS	TSQ/	YC	YAC/YAT	VE	GMG/GWA	LS	TYG/TYA
KE	RAG/RAA	MK	ANG/	FS	TYC/TTY	PR	CSC/CST	SC	MGC/MGT	TI	ATC/AT	WL	TKG/	YH	TAC/TAT	VF	KTC/KTT	LQ	CWG/CWA
KR	ARG/RAA	MT	ANG/	FY	TWC/TWT	PL	CYC/CYG	SP	TYC/TTY	TR	RCC/RCT	WC	TGS/TGK	YS	TWC/TWT	VI	RTC/RTT	LH	CWC/CWT
KT	ANG/ANA	MV	RTG/	FV	KTC/KTT	PS	YCC/YCT	SI	TMC/TMT	TS	ASA/ASG				TMC/TMT	VG	GTC/GTT	LP	YTC/TTY
KI	ANA					PT	MCC/MCT	SA	AKC/ACT		ASC/WCC					VL	GKG/GKC	LI	MTG/MTT
								SG	KCC/KCT								STG/STC	LV	CYC/CYG
								SP	RGC/RGT									LR	STG/STC
								ST	YCC/YCT										CKG/CKC
								SR	ASC/WCC										
									MGC/MGT										

Single letter code

R = A or G
Y = C or T
K = G or T
S = C or G
W = A or T
H = A or C or T
B = C or G or T
V = A or C or G
D = A or G or T
N = A or C or G or T

FIGURE 13 (cont)

60/216



Full length construction after cloning the cassettes into pBS.
 Sites marked with a "*" are in the pBS MCS

Cassette Extras (Can be removed from cassette ends)

A (37bp)	BamHI/Kozak Start	SalI	Stop	BglII	EcoRI	
	5' gc ggaaccacc atg.....gtcgac	tga	agatct	gaattc	gc 3'
B (43bp)	BamHI/Kozak Start XhoI	XhoI	Stop	BglII	EcoRI	
	5' gc ggaaccacc atg ctcgag...ctcgag	tga	agatgt	gaattc	gc 3'
C (37bp)	BamHI/Kozak Start XhoI		Stop	BglII	EcoRI	
	5' gc ggaaccacc atg ctcgag...tga	agatct	gaattc	gc 3'	

FIGURE 14

61/216

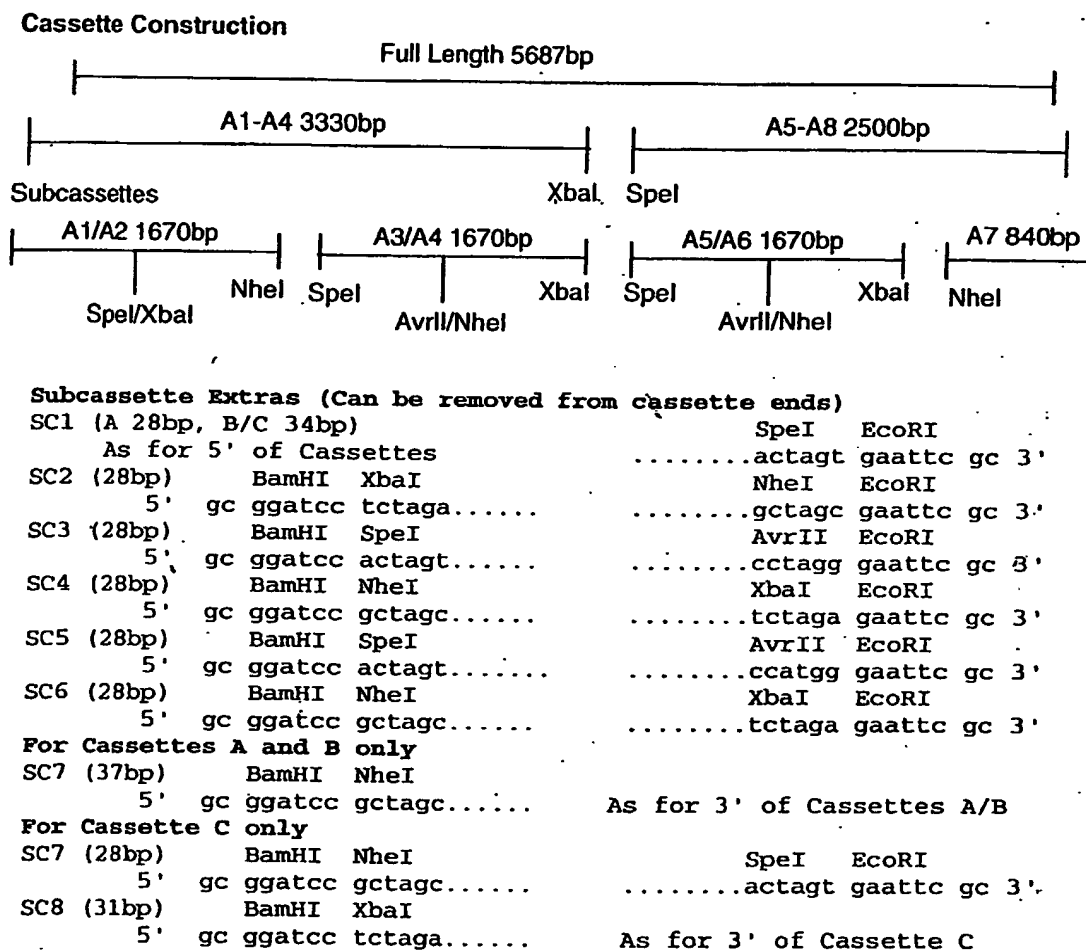


FIGURE 14 (Cont)

62/216

HIV SAVINE CONSTRUCTION

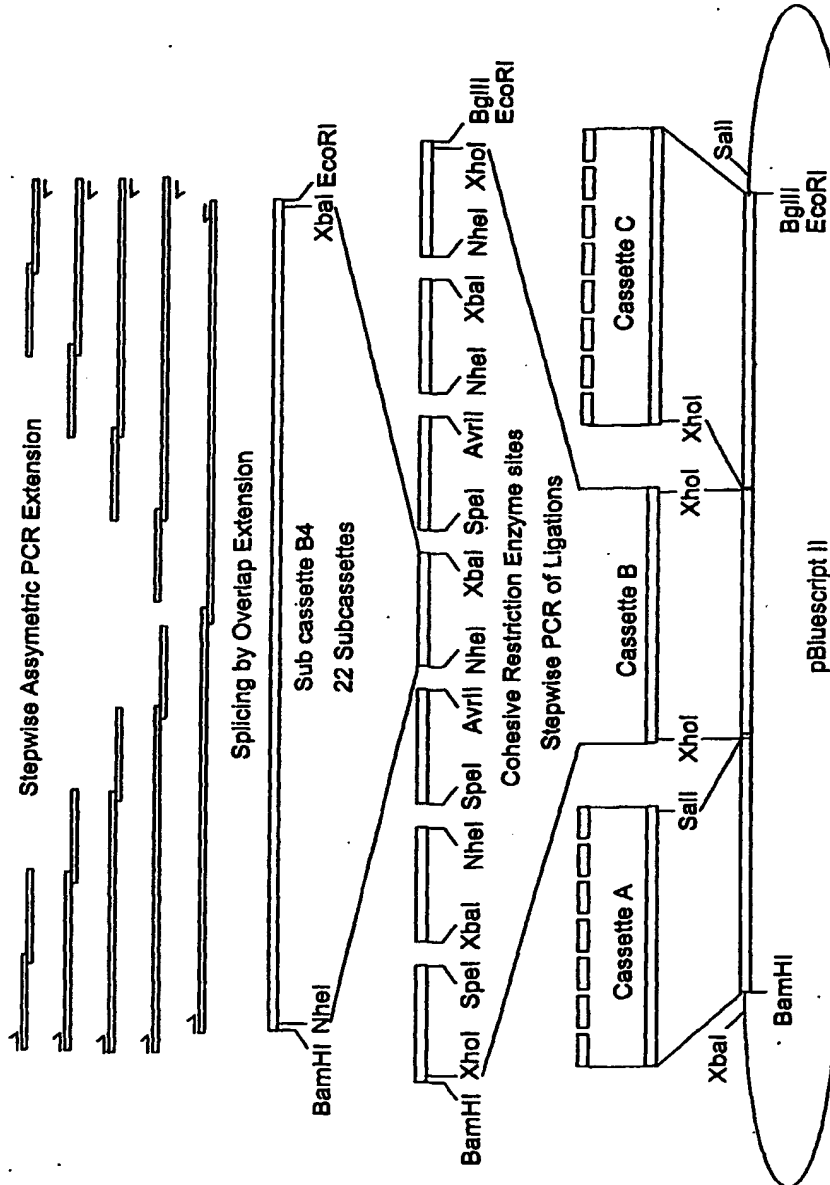


FIGURE 14 (Cont)

63/216

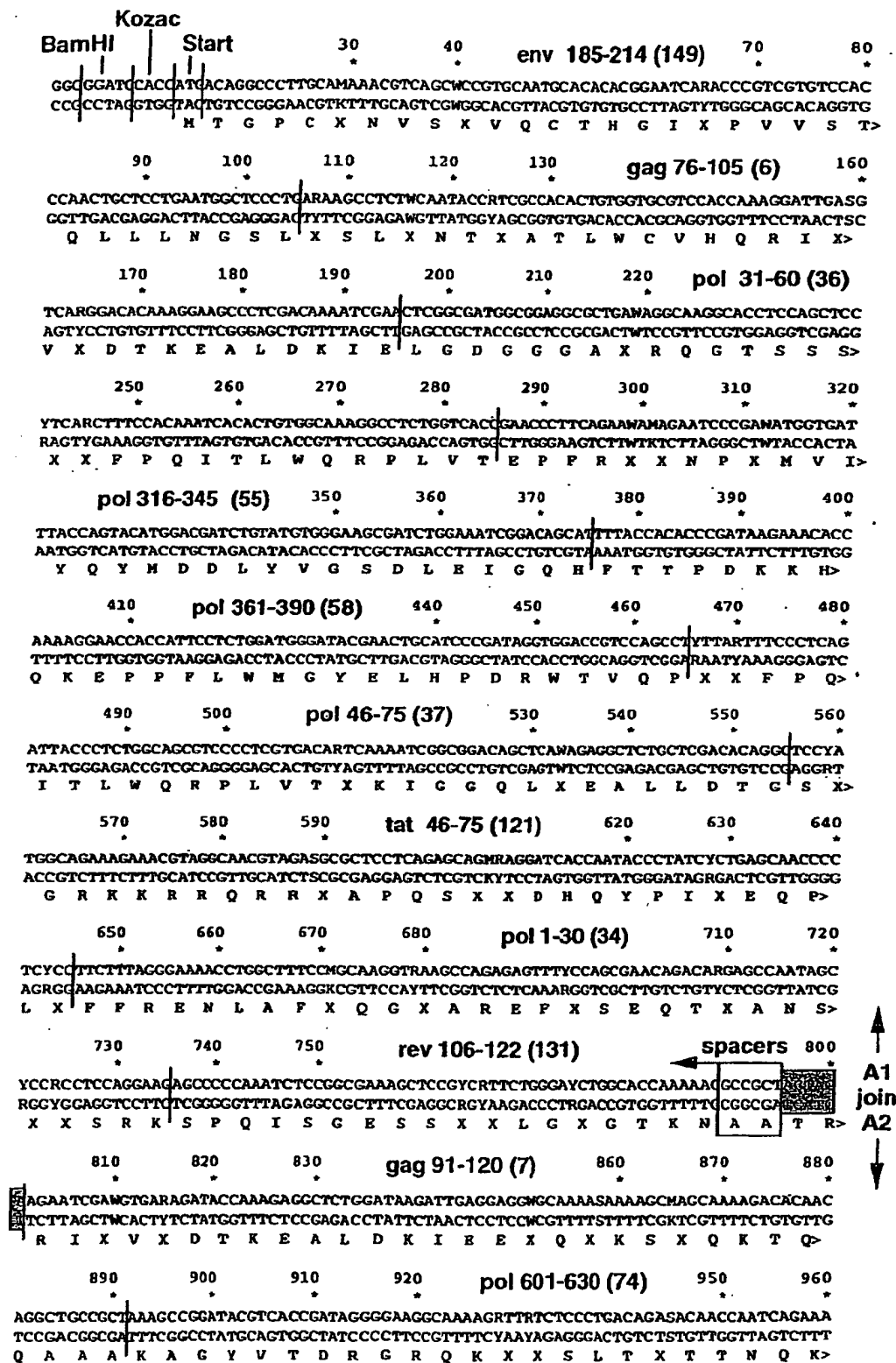


FIGURE 15

SUBSTITUTE SHEET (RULE 26)

1970 980 990 1000 1010 1020 1030 1040
ACCGAACTGCAGGCCATTTCAMGAGCCRMATACCACACTGTTTTCGCCACGCGATGCCAAAGCCYATGASACAGAGGTCCA
TGGCTTGACGTWCGGTAACTKCTKCGYKATGGTGTGACAAAACGCGTTCGCTACGGTTTCGGRTACTSTCTCTCCAGGT
T E L X A I X X A X T T L F C A S D A K A X X T E V H>

1050 1060 1070 1080 1090 pol 76-105 (39) 1120
CAATGTGTGGGCCACACACCGTTGCGTCCCGTCTGACGATACAGTCTGAGGASATSAACCTCCCCGGAARATGGAAGC
GTTACACACCCGGTGTGTGCGAACGAGGGCCGACTCTATGTCAGACCTCTTASTTGGAGGGCCCTTATACCTTCG
N V W A T H A C V P A D D T V L E X X N L P G X W K>

1130 1140 1150 1160 1170 1180 1190 1200
CTAAGATGATTGGCGGAATCGCGGATTCTAATAGGTGAGTARGATCGGACCCGAAACCTTACAATACCCARTCTTC
GATTCTACTAAACGCTTAGCCGCTAAGTAATTCACCTCTTCTAGCCTGGGCTTTTGGGAATGTTATGGGGTYAGAAG
P K M I G G I G G F I K V R X I G P E N P Y N T P X F>

pol 196-225 (47) 1230 1240 1250 1260 1270 1280
GCTATCAAGAAAAGGACTCCACCAATGGAGAAAGCTCGTGGATTTCAGTCTTAGGATTATCAAAATCCTCTACCAAG
CGATAGTCTTTTCTGAGGTGGTTACCTCTTTTCGAGCACCTAAAGTCTYAATCTTAATAGTTWTAGGAGATGGTTTC
A I K K K D S T K W R K L V D P R X R I I X I L Y Q S>

1290 rev 16-45 (125) 1320 1330 1340 1350 1360
CAATCCCTATCTAGCTCCGAAGGCWCCAGGCAARCCAGAARGAATAGGAGAAGGAGATGGGAGGCCAACRGGRTAGGG
GTTAGGGATAGGATCAGAGCTTCCGWWGTCGGTCTTCTATCTCTCTCTCTAGCTCTCCGCTTGCCYATCC
N P Y P S S E G X R Q X R X N R R R R W G G E X X R>

1370 1380 env 525-554 (171) 1410 1420 1430 1440
ATAGGTCCGTGAGACTGGTCARCGGATTCTYAGCCCTCGGCTGGGACGATCTGAGAARCTCTGCGCTCTTGAMAACCTC
TATCCAGGCACTCTGACCAGTYGCCTAAGARTCGGGAGCGGACCTGCTAGACTCTTTCGAGACGGAGAGCTTCTGGAG
D R S V R L V X G F X A L A W D D L R X L C L F X N L>

1450 1460 1470 env 31-60 (139) 1500 1510 1520
TGGGTACCGTCTACTATGGCGTCCCGTCTGGAGAGAGGCTTTCACCAACCTCTCTGTGCTCCGACCTAAGCGTYA
ACCCAGTGGCAGATGATACCGCAGGGGCAGACCTCTCTSCGAYKGTGTTGGGAGAAGACCGGACCTCCGATTCGART
N V T V Y Y G V P V W R X A X T T L F C A S D A K A X>

spacers 1550 1560 rev 1-30 (124) 1590 1600
CGCTGCTATGGCTGGCAGAAAGCGGCRRCAGACGAAGAGCTCTGARGGCTRTCAGAATCATTAASATCTGTATCAGT
CGGACGTACCGACCTCTTCGCGYGTGCTGCTCTTCGAGGACTYCGAYAGTCTAGTAATTTAAGACATAGTCA
A A M A G R S G X T D E E L X A X R I I X I L Y Q>

1610 1620 1630 1640 1650 vif 16-45 (101) 1680
CCAACCTTACCCTTCCATGARAATCAGAACCTGGAASAGCCTGGTCAAGCATCACATGYACATCTCCAAGAAA
GGTTGGGAATGGGAAGCTTACTYTTAGTCTTGGACCTTSTCGGACAGTTCGTAGTGTACRTTAGAGGTTCTTT
S N P Y P S A S M X I R T W X S L V K H H M X I S K K>

1690 1700 1710 1720 1730 1740 1750 1760
GCCAAWGGCTGGTCTATAGGCGATCACTWTGASAGTCCGAGSTCGTGARTCAGATTATCGAAGVAGCTCATCAAAAAGGA
CGGTTWCCGACCAAGATATCCGTAGTGAWACTCTCAGGCTCSAGCACTYAGTCTAATAGCTTBTGAGTAGTCTTTTCT
A X G W F Y R H H X X E S E X V X Q I I E X L I K K E>

pol 661-690 (78) 1790 1800 1810 1820 1830 1840
AARGGTCTACCTAKCATGGGTACCAGCCCAAGGGAATCGGCAAAACCAAGAGCTCCAGAACAGATTMYCAAAATCC
TTYCCAGATGGATGATACCAATGGTCGGGTGTTCCCTTAGCTCTTTGGTTCTCGAGTCTTGTGCTAAKRGTTTTAGG
X V Y L X W C V P A G H K T I G Q T K E L Q X Q I X K I>

1850 1860 1870 1880 1890 1900 1910 1920
AAAACTTTAGGGTCTACTATAGGGATACAGAGACCTTCTTGGAAAGGACCCAAAAGCTTTCAGGAAATCTGGRACAAT
TTTTTGAATCCCAAGATGATATCCCTATCGTCTCTGGGAKAGACCTTCCCTGGGTTTTTCGAACTCCTTTAGACCTGTTA
D N F R V Y Y R D S R P D P X K G P K S X E E I W X N>

FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

65/216

1930 env 405-434 (163) 1960 1970 1980 1990 2000
ATGACATGGATKSAGTGGGAGAGAGAGATTAGCAATTACACAARCCWAATCTATRAGATTCTGACACCCGAACCCACAGC
TACTGTACCTAMSTCACCCCTCTCTCTCTAATCGTTAATGTGTTTGGWTTAGATAYTCTAAGACTTGTGGGCTTGGGTGTCG
M T W X X W E R E I S N Y T X X I Y X I L X F E P T A>

2010 2020 gag 451-480 (31) 2050 2060 2070 2080
CCCTCCCGCTGAGARTTTCRGATTCCGTGAGGAACTACACCCCTCCMAAAGCAAGAGCMAAAGGATAAGGACCAATACG
GGGAGGGCGGACTCTYAAAGYCTAAGCCACTCCTTTGATGTGGGAGGGKTTTCGTTCGRITTCCTATTCCTGTATATGC
P P A E X F X F G E E T T P S X K Q E X K D K E Q Y>

2090 2100 2110 pol 106-135 (41) 2140 2150 2160
ATCAGATTMTTATGAGATTTCGCCAAGAAAGCTATTGGTACAGTCTCGTGGGACCTACCCCTGTGAATATCATTTGGC
TAGTCTAAKAATAACTCTAAACGCCCTTCTTTGATAACCATGTCTACGAGCACCCCTGGATGGGGACACTTATAGTAACCG
D Q I X I E I C G K K A I G T V L V G P T P V N I I G>

2170 2180 2190 2200 vpr 46-75 (115) 2230 2240
AGATTTTACGAAACCTATGGCGATACCTGGGAGGGCGTCGAGGCTCTGATCAGAACTCCAGCAACTGHTGTTTTRCCA
TCTTAAATGCTTTGGATACCGCTATGGACCTCCCGCAGCTCCGAGACTAGTCTTGGAGGTCGTTGACKACAAAYAGGT
R I Y E T Y G D T W E G V E A L I R X L Q Q L X F X H>

2250 2260 2270 2280 2290 tat 31-61 (120) 2320
TTTCAGAAATCGGATGTTTTCATTGCAASTGTGTTTCTCACCAAGGTCTCGGCATTAGCYACGGAAGGAAAAAGAGAA
AAAGTCTTAGCTTACAAGAGTAACGGTTSACACAAAAGAGTGGTTTCCAGAGCCGTAATCGRTGCCTTCTTTTCTCTT
F R I G C X H C Q X C F L T K G L G I S X G R K K R>

2330 2340 spacers 2370 2380 tat 1-30 (118)
RACAGAGAAGSGAGCTCCCAAGCTGCCATGGACCCCGTGGACCCCAASCTGGAGCCTTGGAAWCAACCTGGCTCCCAAG
YTGCTCTCTCCSCTCGAGGGCTTCGACGGTACCTCGGGCACCCTGGGCTTSGACCTCCGAACCTTWTGCGGACCGAGGGTC
X Q R R X A P Q A A M D P V D P X L E P W X H P G S Q>

2410 2420 2430 2440 2450 2460 2470 2480
CCTAMGACAGCCTGTWMCAAATGCTATTGCAAAAAGTGAAGAGACAACCCCTAGCCMGAAACAGGAACMGAA
GGATKCTGTGCGACAWKGTTTACGATAACGTTTTCACCTCTCTCTGTTGGGGATCGGKCTTTGTCTTGTGKCTT
P X T A C X K C Y C K K C P S E E T T P S X K Q E X K>

gag 466-495 (32) 2510 2520 2530 2540 2550 2560
AGACAAAGAACWCTACCCCTTAYGCCAGCCTCAAGTCCCTGTTTGGCAATGAAATTTCAATATGTGGAAGAATRACA
TCTGTTCTTGGGATGGGGGAARTCGGTCGGAGTTCAGGGACAAACCGTTACTTTAAAGTTATACACCTCTTAYTGT
D K E X Y P P X A S L K S L F G N D N F N M W K N X>

2570 env 91-120 (143) 2600 2610 2620 2630 2640
TGGTGGAMCAGATGCAMGAAGACRTATCTCACTATGGGACCAAGCCTCAAGCCTTGGCTCAACCTCGACCTCGGGGAT
ACCACCTFKGTCTACGTCTCTCTGYAATAGAGTGATACCCCTGGTTTCGGAGTTCGGAACCGAGTTGAGCTGCAGCCGCTA
M V X Q M X E D X I S L W D Q S L K P C V K L D V G D>

2650 2660 pol 256-285 (51) 2690 2700 2710 2720
GCCTATTTCCTCGTGCCTCTGGATRAARRCTTCAGAAAGTATACCGCTTTCACAATCCCTAGCAYAAACAATGACCAACT
CGGATAAAGAGGCACGGAGACTAYTTTYYGAAGTCTTTCATATGGCGAAAGTGTAGGGATCGTRTTTGTACTGTTGA
A Y F S V P L D X X F R K Y T A P T I P S X N N E Q L>

2730 2740 2750 pol 751-780 (84) 2780 2790 2800
GAAAGCGCAAGCCATSCATGECGAAGTGRATTGCTACACGAGCATTTGGCAACTGGATTGCACACACCTCGAGGGGAAAGR
CTTCCGCTTCGGTASGTACTGGTTCACYTAAACAGTGGTCCGTAAACCGTTGACCTAACGTTGTGACCTCCCTTTCY
K G E A X H G Q V X C S P G I W Q L D C T H L E G K>

2810 2820 2830 2840 pol 166-195 (45) 2870 2880
TTATCCTTAAGGTCAAGCAATGGCCTCTGACAGAGGAAAGATTAAAGCTCTGACTGMAATTTCAMAGAGATGGAGVAA
AATAAGGATTCCAGTTCGTACCGGAGACTGTCTCTTTCTAATTCGAGAGCTGACKCTAAACGTTCTCTACCTCBTT
X I P K V K Q W P L T E E K I K A L T X I C X E M E X>

A3
Join
A4FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

66/216

2890 2900 2910 pol 331-360 (56) 2940 2950 2960
GAGGGAAGATTAGATGGATGACCTCTACGTCGGCTCCGACCTGGAGATTGGCCAACTAGGRCCAAAATCGAAGAGCT
CTCCCTTTCTAATCTTACCTACTGGAGATGCAGCCGAGGCTGGACCTCTAACCGGTTGTATCCYGGTTTTAGCTTCTCGA
E G K I S M D D L Y V G S D L E I G Q H R X K I E E L>

2970 2980 2990 3000 pol 616-645 (75) 3030 3040
CAGGSMACCTCTCGARATGGGGCTCACCGAMACCACAAACCAAAAGACTGAGCTCCAMGCTATCCAWCTGGCTCTGC
GTCCSKTGTGGAGGACTTACCCCTGAGTGGCTGTGGTGTTTGGTTTTCTGACTCGAGGTCGATAGGTWAGCCGAGACG
R X H L L X W G L T X T T N Q R T E L X A I X L A L>

3050 3060 3070 3080 3090 pol 796-825 (87) 3120
AAGACTCCGGCTYAGAGGTCAACATTGTGACAGATTTCCCGCTGAGACTGGTCAAGAGACCGCTATTTCMTTCTGAAA
TTCTGAGGCGGARTCTCCAGTTGTAAACACTGTCTCTAAGGGCGACTCTGACCACTTCTCTGGCGGATAAAGKAAGACTTT
Q D S G X E V N I V T D I P A E T G Q E T A Y F X L R>

3130 3140 3150 3160 3170 3180 3190 3200
CTGGCTGGCAGATGGCTGTGARARYCATTACACAGACAATGGAGGACAAAGATTGAGGAACAGAGASHGCATCTGCT
GACCGACCGCTTACCGGACACTTGTGTAGTGTCTGTCTTACCTTCTGTCTTAACTCTTGACTCTSKCGTAGACGA
L A G R W P V X X I H T D N G R T K I E E L R X H L L>

pol 346-375 (57) 3230 3240 3250 3260 3270 3280
CARATCGGCTTACAAACCCCTGACAAAAAGCATCAGAAAGAGCTCCCTTTCTGTCTCAAGAACTGACAGAGG
GTCTACCCCGAAGTGTGGGGACTGTCTTCTGAGTCTTTCTCGAGGGAAGAGAGTCTCAGTTCTTTGACTGTCTCC
X W G F T T P D K K H Q K E P P F L S S V K K L T E>

3290 vif 166-192 (111) 3320 3330 spacers 3360
ATARGTGGAACRAACCCAGAAAAAYCAAGGGACRCAGAGRAAATCACACAATGAATGGCCATGCTGCCACAGAGTCCAG
TATYCACCTGTGTTGGGGTCTTTTGTCTTCTGCTCTCTTCTAGTGTGTACTTACCGGTACGACGGTGTCTACCGGTC
D X W N X P Q K X K G X R X N H T M N G H A A T E S Q>

3370 3380 env 435-464 (165) 3410 3420 3430 3440
AATCAGCAAGACAGAAACGAAMAGGAMCTGCTGGMGCTCGACAAATGGGCAAGCCTCTGGAATTGGTTTRACATTASCA
TTAGTCTGTCTGTCTTGTCTTCTGACGACCKCGAGCTGTTTACCCGTTCCGAGACCTTAACCAAAATGTAAATSCCT
N Q Q D R N E X X L L X L D K W A S L W N W F X I X D>

3450 3460 3470 gag 121-150 (9) 3500 3510 3520
CACCGBAARTAGCTCCMAAGTGTCCAGAAATTACCCTATCGTCCAGAATSYCCAAGGCCAAATGGTCCACCAASCCTCT
GTGGCCTTATCGAGGKTTACAGGGCTTAATGGGATACGAGCTCTASRGCTTCCGGTTTACCAGGTGGTTSGGKAGA
T G X S S X V S Q N Y P I V Q N X Q G Q M V H Q X X>

3530 3540 3550 3560 env 480-509 (168) 3590 3600
CCCCAGCTCTCTCGGACTGAGAAATCTTTTCGCTGTGCTCAGCATTTCAATAGGGTCAGGCAAGGCTATAGCCCTCTG
GGGGTCTGAGYAGCCTGACTCTTAGYAAAAGCGACAGAGTCTGTAAYAGTTATCCAGTCCGTTCCGATATCGGGAGAC
S P R L X G L R I X F A V L S I X N R V R Q G Y S P L>

3610 3620 3630 3640 3650 vif 106-135 (107) 3680
TCCTTCCAAACCTCMYCTCATCCATCTGYAWTACTTTGACTGTTTCKCTGACTCCRCCATTAGGAGAGCCATCTGGG
AGGAAGGTTTGGGAGKRCGAGTAGGTAGACRTWATGAACTGACAAAGMGACTGAGGYGGTAATCTCTCGGTAGGACCC
S F Q T L X L I H L X Y F D C F X D S X I R R A I L G>

3690 3700 3710 3720 3730 3740 3750 3760
ACASAKAGTGAGHAGGAGATGCGAATACTGCTGTGGGAMTCGGAGCCATGWTCTYTTGGCTTTCTGGGTGCCGCTGGCTCCA
TGTSTMTCACTCKTCTCTACGCTTATCGACACCCCTAGCCTCGGTACWAGRAACCGAAAGACCCACGGCGACCGAGGT
X X V X R R C E Y A V G X G A M X X G P L G A A G S>

env 300-329 (156) 3790 3800 3810 3820 3830 3840
CCATGGGCGCTGCCCTCCATSACTGACAGTCAAGCCTATGACCTAGCAAGACCTCTTGTCTGAGATTAGAAACAG
GGTACCCGCGAGGAGTASTGTGACTGTACGTTCCGATACCTGGATCGTTCTGGAGYAAAGACTCTAAGTCTTTGTC
T M G A A S X T L T V Q A Y D P S K D L X A E I Q K Q>

A4
join
A5

FIGURE 15 (Cont)

SUBSTITUTE SHEET (RULE 26)

67/216

pol 466-495 (65) 3870 3880 3890 3900 3910 3920
GGTCAGGRTCACTGGACATWTCAGATTTCAGAAAGAGCCTTTCAAAAAGGAAACCGTCCTGGTCGGCCCTACACCCGTCAC
CCAGTCCYAGTCACCTGTAWAGTCTAAAWGGTTCTCGGAAAGTTTTCCTTGGCAGGACCAGCCGGGATGTGGGCAGTT
G Q X Q W T X Q I X Q E P F K N G T V L V G P T P V N>

3930 pol 121-150 (42) 3960 3970 3980 3990 4000
CATCATCGGAAGGAACMTGCTGACACAGMTTGGCYGCACCTCAACTTTCCCATAGCAAGGCAGCCCTGCTATCTTTC
GTAGTAGCCTTCTTGKACGACTGTGTCKAACCGRCGTGGGAGTTGAAAGGGTAATCCTTCCGTCGGGACGATAGAAAG
I I G R N X L T Q X G X T L N P P I S K G S P A I F>

4010 4020 pol 301-330 (54) 4050 4060 4070 4080
AGTCCAGCATGMCAMAGATTCTGGAGCCTTTTAGGAWAMAAAACCTGASATGCTCATCTATCAGTATCTCTCTG
TCAGGTCGTACKGTRTCTAAGACCTCGGAAAATCCTWTCTTTGGGACTSTACCACTAGATAGTCATCTCTCTGAGAC
Q S S M X X I L E P F R X X N P X M V I Y Q Y P S P L>

4090 4100 4110 nef 136-165 (188) 4140 4150 4160
ACATTCGGATGGTGTTCAAACTGGTCCCGTGGACCCAGSGAAGTGGAGAGRYCAACRAGGGCGAAAACAAATTGCCT
TGTAAGCCTACCAACAAGTTTGACCAGGGGCACTGGGGTCTCTCACTCTCTYRGTGTGTCCCGCTTTGTAAACGGA
T F G W C F K L V P V D P X E V E E X N X G E N N C L>

4170 4180 4190 4200 pol 271-300 (52) 4230 4240
CCTCTTTAGGAAATACACAGCCTTTACCATTCCCTCCAYCAATAACGAAACCCCTGGCATTAGGTATCAGTATAACGTC
GGACAAATCCTTTATGTCTCGGAAATGTAAGGGAGGTGTGTTATGCTTTGGGGACCGTAATCCATAGTCATATTCAGG
L F R K Y T A F T I P S X N N E T P G I R Y Q Y N V>

4250 4260 4270 4280 4290 env 315-344 (157) 4320
TGCCTCAGGATGGGGAAGCACAATGGGAGCGCCAGCATKACCCTCACCGTCCAGGCTAGGCWACTGCTCAGCGGAATC
ACGGAGTCCCTACCTCTGTGTACCTCGCGGCTCGTAMTGGGAGTGGCAGGTCCGATCCGWTGACGAGTCCGCTTAG
L P Q G W G S T M G A A S X T L T V Q A R X L L S G I>

4330 4340 4350 4360 4370 pol 451-480 (64) 4400
GTCCAGCAACAGARCAATCTGCTGCGGAGAAATAGGGAAATCCTCARAGAGCCTGTGCATGGCCTCTACTACGATCCCTC
CAGGTCTGTGTCTGTGTAGACGACCKCTCTTATCCCTTTAGGAGTYTCTCGACACGTACCGCAGATGCTAGGAG
V Q Q Q X N L L X E N R E I L X E P V H G V Y Y D P S>

4410 4420 4430 4440 4450 vpu 61-81 (136) 4480
CAAGGATCTGRTCGCTGAARTCCAAAAGCAAGGASAGAGGAACGTCTCCRCWTGGTGGATATGGGAACTACGACCTCG
GTTCCTAGACYAGCGACTTAYAGGTTTCTGTTCCCTSTCTCTTGCAGGYGCAACCTATACCTTTGATGCTGGAGC
K D L X A E X Q K Q G X E E L S X X V D H G N Y D L>

spacers 4510 4520 4530 vpr 61-90 (116) 4560
GAGTGGACAATAAATCTGCCGCTATTAGAACTGCAACAGCTCTGTCTCTTCACTTTAGGATTGGCTGCCRCGACTCC
CTCACCTGTATTGAGACCGCGCTAATCTTGGACGTTGTGAGKACAAGYAAGTGAATCTTAACCGAGCGGCTGAGG
G V D N N L A A I R X L Q Q L X F X H F R I G C X H S>

4570 4580 4590 4600 4610 gag 406-435 (28) 4640
AGGATTGGCATCHMYCCGTAGAGAAGGGSCAGTCTCCAGGAAAAAGGGATGCTGGAAGTGTGGCARAGAGGACACCA
TCCTAACCGTAGKRGCGACTCTCTCCSGTCTCGAGGGTCTTTTCCCTACGACCTTCACACCGTCTCTCCCTGTGGT
R I G I X R Q R R X R A P R K K G C W K C G X E G H Q>

4650 4660 4670 4680 4690 4700 4710 4720
GATGAAGGATTGCACTGAGAGACAGGCTAACTTTCTGGGAAAGCAAGCCAGACTGRTTATCARAACCTATTGGGGACTGC
CTACTTCTAACGTACTCTCTGTCGATTGAAAGACCTTTCTWCGGTCTGACYAATAGTYTTGGATAACCCCTGACG
M K D C T E R Q A N P L G K X A R L X I X T Y W G L>

vif 61-90 (104) 4750 4760 4770 4780 4790 4800
ATACCGGTGAGAGAGACTGGCASCCTCGGCCAWGGCGTCAGCATTGAGTGGAGGAYAAAGGGAAGGGCTGAGGATACCGGC
TATGGCCACTCTCTCTGACCGTSGAGCCGGTWCAGCAGTCTGAACCTACCTCTTTTCCCTTTCCGACTCTATCGCCG
H T G E R D W X L G X G V S I E W R X R E R A E D S G>

A5
join
A6

FIGURE 15 (Cont)

SUBSTITUTE SHEET (RULE 26)

68/216

vpu 46-75 (135) 4830 4840 4850 4860 4870 4880
 AACGAAAGCGAAGGCGACASAGAAGAGCTCAGCRCATGGTGGACATGGGCAATTACGATCTGCTAGGCTGCCCCAG
 TTGCTTTTCGCTTCGCTGTSTCTTCTCGAGTCGYGTWACCACCTGTACCCGTTAATGCTAGACGAGCGGGGTC
 N E S E G D X E E L S X X V D M G N Y D L S S P A P R>

4890 env 510-539 (170) 4920 4930 4940 4950 4960
 GGGACCCGATAGGCGYGRGGAATCGAAGAGGAAGCCGAGAGCAGRCAGAGCAGAAGCGTCAGGCTCGTGARTGGCA
 CCCGCGGCTATCCGRCYCYCTAGCTTCTCTCCGCTCTCGYTCYGTCTTCGCGAGTCCGAGCACTYACCT
 G P D R X X X I E E E G G E X X R X R S V R L V X G>

4970 4980 nef 151-180 (189) 5010 5020 5030 5040
 GWCAGGTCGAGGAARYCAATRAGGGAGAGAATACTGTCTGCTCCACCTATSRGTCWACATGGCATGGAAGACGAAGAS
 CWCCTCAGCTCCTTYRGTTAYTCCCTCTCTTATTGACAGACGAGGTGGGATASYCAGWTGTACCGTACCTTCTGCTTCT
 X E V E E X N X G E N N C L L H P X X X H G M E D E X>

5050 5060 5070 pol 961-990 (98) 5100 5110 5120
 AGAGAGGTGAATAGCGATATCAAAGTGGTCCCGAGAAAGCCAAATCATTAGGGATTACGGAAAGCAAATGGCTGG
 TCTCTCCATTATCGCTATAGTTTACCAGGGGCTTCTCTTCGGTTTGTAGTAATCCCTAATGCCCTTCTGCTTACCGACC
 R E V N S D I K V V P R R K A K I I R D Y G K Q M A G>

5130 5140 5150 5160 pol 16-45 (35) 5190 5200
 CGMTGACTGTGTGGCCRGTTCTCTCCGAGCAACARGGGCTAATCCYCTCAAGCAGAAAGCTGGGAGACGGAGGGCG
 GCKACTGACACACCGGYCAAGRAAGGCTCGTTTCTYCCGATTGAGRGAYTTCGTCTTTCGACCTCTGCTCCCGC
 X D C V A X F X S E Q T X A N S X X S R K L G D G G>

5210 5220 5230 5240 5250 gag 390-420 (27) 5280
 GAGCCGASAGACAGGCAACAGCTCCAGTGTTCATTCGCGCAAGAGGGACACMTTGCCARAACTGTAGGGCCCTT
 CTCGGCTSTCTGCTCCCTTCTCGAGGTTCACAAAGTTAAGCGCTTCTCCCTGTGKAACGGTYYTTTGACATCCCGGGA
 G A X R Q G T S S S C F N C G K E G H X A X N C R A P>

5290 5300 5310 5320 5330 5340 5350 5360
 CGCAAGAAAGGTTGTGGAAATGCGGAARGAAGGCCATCAATGAAAGACTGTACCGAAAGCAAGCCAAATTCCTCGG
 GCGTCTTTCCAACAACCTTTACGCCCTTYCCTCCGGTGTGTACTTTCTGACATGCTTTCGGTTCGGTTAAAGGAGCC
 R K K G C W K C G X E G H Q M K D C T E R Q A N F L G>

gag 421-450 (29) 5390 5400 5410 5420 5430 5440
 CAAAATCTGGCCCTCMHCAAGGCGAGACCCGGAACCTTTCYCCAAGCAATGGCTCTGGTATATCAAAATCTTTATCA
 GTTTTAGACGGGAGGKYGTTCCTGCTGCGGCTTTGAAAGRGTTTCCTTACCGAGACCATATAGTTTAAAGATAGT
 K I W P S X K G R P G N F X Q S X W L W Y I K I P I>

5450 env 465-494 (167) 5480 5490 5500 5510 5520
 TGATCGTCGGTGGACTGRTTGGCTCAGGATRTCTTTGCGCTCTGTCCATCTTAAGGAGCCGYGAGCCRAGACCTC
 ACTAGCAGCCACCTGACYAACCGAGTCTTAAYAGAAACCGCAGGACAGGTAGTAATTCCTCGGCRCCTCGGYTCTGGAG
 M I V G G L X G L R I X F A V L S I X N G A X S X D L>

5530 5540 nef 31-60 (181) 5570 5580 spacers
 GATAACATGGCGCTMTTACAAGCTCCAATAACCSCTGCCAATAACSTGACTGTGYCTGGCTGRAGGCTGCTGCCATGAC
 CTATTTGTACCGCAKAATGTTGAGGTATGSSGACGGTATTGSGACTGACACRAGCCGACTCCGTCGACGGTACTG
 D K H G A X T S S N T X A N N X D C X W L X A A A M T>

5610 5620 5630 vpu 1-30 (132) 5660 5670 5680
 ACCCTCGAGATCATCGCTATCGCTCGCYTTATCGTCCGCTCATCTAGCCATTGTTGGTCTGGACAAATCGYCTWCATTG
 TGGGACCTCTAGTAGCATAGCAGCGGAAATAGCAGCGGAGTAGKATCGGTAACACCAGACCTGTTAGCRGANGTAAC
 P L E I I A I V A X I V A L I X A I V V W T I X X I>

5690 5700 5710 5720 pol 136-165 (43) 5750 5760
 AGTAATGCTCACCCTCAATTCGGAGCAGACTGAATTCCTATCTCCCCATTCASACAGTCCCTGTGAAA
 TCATTAACGAGTGGGTTKAGCCTRCGTGTCACTTAAGGGATAGCGGGTAAGTSTGTACGGACACTTT
 E Y V E N X L T Q X G X T L N P P I S P I X T V P V K>

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 A6
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 A7
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 A7
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FIGURE 15 (Cont)
 SUBSTITUTE SHEET (RULE 26)

69/216

5770 spacers 5800 5810 env 255-284 (153) 5840

CTGAAACCCGGAATGGATGGCGCCGCCAYCTTTAGGCCTCGCCGAGGCRATATSARAGACAATTGGAGAAGCGAACTGTA
GACTTTGGGCTTACCTACCCCGCCGCTRGAATCCGACCGCCTCCGYTATASTYTTCTGTAACTCTTCGCTTGACAT
L K P G M D G A A X F R P G G G X X X D N W R S E L Y>

5850 5860 5870 5880 5890 5900 5910 5920

TAAGTATAAGGTCGTGRAGATTAGCCCTCTGGGARTACATGGATTCCCGAATGGGAGTTCGTCAACACACCCCACTGG
ATTCATATTCCAGCACYTCTAAYTCGGAGACCCCTYAGTGTACCTAAGGGCTTACCCCTCAAGCAGTTGTGTGGGGGTGACC
K X K V V X I X P L G X T W I P E W E F V N T P P L>

pol 556-585 (71) 5950 5960 5970 5980 5990 6000

TCAAGCTATGGTATCAGCTCGAGAAAGASCCATCTCYTGGCGYTGGCTCAGGATCTCAACAYGATGCTGAATAYTCTGA
AGTTCGATACCATAGTCGACCTCTTTCTSGGATAGCRACCGCRACCTGGAGTCTAGAGTTCTCTACGACTTATACAT
V K L W Y Q L E K X P I X G X E P Q D L N X M L N X V>

6010 gag 181-210 (13) 6040 6050 6060 6070 6080

CGAGCCATCAGGCCGCTATGCAATGCTGAAAGASACAATCAATGAGGAAGCCGCTGTCTCTTTCTGGATGGCATTRA
CCTCCGGTAGTCCGGCGATACGTTTACGACTTTCTSTGTTAGTTACTCTCTCGGCGACAGGACAAAGACCTACCGTAAYT
G C H Q A A M Q M L K X T I N E E A A V L F L D G I X>

6090 6100 pol 706-735 (81) 6130 6140 6150 6160

CAAAGCTCAAGAGGAACATGAGARGTATCACTCCAACCTGGAGGACAAATGGCCARCGAMTTTAATCTCTMTGAAGCATMTGG
GTTCTCGAGTTCTCTCTGACTCTYCATAGTGGAGTTGACCTCTCTGTACCGGTGCTKAAATTAGACKACTCTGTAKAGC
K A Q E E H E X Y H S N W R T M A X X P N L X K H X>

6170 6180 6190 gag 31-60 (3) 6220 6230 6240

TCTGGGCTCTAGGGAGCTGGAGAGATTGCTCTGAATCCCGCTGCTGGAGACAKCCGAAGGCTGTAGCAAAATCTCT
AGACCCGGAGATCCCTCGACCTCTCTAAGCGAGACTTAGGGVCGGACGACCTCTGTHGGCTTCCGACARTCGTTTAAAGGA
V W A S R E L E R F A L N P X L L E T X E G C X Q I A>

6250 6260 6270 6280 env 215-244 (151) 6310 6320

GAGGAAGAGATTATCATTAGGTCGAGAAATYTCACARACAATGYCAAAACCAATTATCTCCANCTCAACRAAAGCGTCGW
CTCCTTCTCTAATAGTAACTCAGGCTCTTARAGTGTGTGTACRGTTTGGTAATAGCAGGTGAGTTGTYTTTCCGACGW
E E E I I I R S E N X T X N X K T I I V X L N X S V X>

6330 6340 6350 6360 6370 gag 1-30 (1) 6400

GATTAACTATGGGCTAGGGCTAGTGTCTCAGMGCCGCRAGCTGGACGCTGGGAAAAGATTAGGCTCAGGCTCGCG
CTAATTGTACCGCGATCCCGATCACAGGACTCKCCCGGYTCGACCTCCGACCCCTTTCTAATCCGAGTCCGACCGC
I N M G A R A S V L X G G X L D A W E K I R L R P G>

6410 6420 6430 6440 6450 nef 91-120 (185) 6480

CAAAGAAAACATATAGGCTCAAGGAGAGGGAGGCTGGAGGACTGRTTACTCCMAAAGAGGCAAGASATTCTGGAT
CTTTCTTTTTCATATCCGAGTCTCTTCCCTCCGACCTSCCTGACYAATGAGGKTTTCTCCGTTCTSTAAGACCTA
G K K K Y R L K E K G G L X G L X Y S X K R Q X I L D>

6490 6500 6510 6520 6530 6540 6550 6560

CTGTGGGTGTATACACACAGGGATTCTGTTGTTGGGAACCTGATCTCTGGCWTGGTGATKATCTGTAGCGCCAGCGA
GACACCCACAPAKTGTGTCTCTAAGCTGTTACCCCTTGGWACTAGGAGCCGWACCCTAATAGACATCGCGGTGCT
L W V Y X T Q G F T R W G T X I L G X V X I C S A S X>

env 16-45 (138) 6590 6600 6610 6620 6630 6640

SAATCTGTGGGTGACAGTGTATTACGGAGTGCCTGTGTGGAGGAGACWGTCTCTGTCGGCATTTGCAACAGCAAARTA
STTAGACACCCACTGTACATAATGCTTCACGGACACACCTCTCTGWCAGGACAGGCCGTAACACGTTGTCTTTAT
N L W V T V Y Y G V P V W R R X L L S G I V Q Q Q X>

6650 env 330-359 (158) 6680 6690 6700 6710 6720

ACCTCTGAGGGCTATCGAAGCCCAACAGCATCTGCTCCAGCTCACCCTCTGCTGTCAGGCATTTCCCAAGCCCTTGGCTC
TGGAGGACTCCCGATAGCTTCGGGTGTCTGTAGACGAGGTGAGTGGCAGACCCAGTCCGTAAGGGGTCCGGAACCGAG
N L L R A I E A Q Q H L L Q L T V W V R H P P R P W L>

B1
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FIGURE 15 (Cont)

SUBSTITUTE SHEET (RULE 26)

70/216

vpr 31-60 (114) 6750 6760 6770 6780 6790 6800
CACRRCTGGGACAGYACATCTATGAGACATACGGAGACATGCKMGGGAGTGGAGGCCCTGAMAGCCCTCATCAMACC
GTGYGGACCCTGTCRTGTAGATACTCTGTATGCTCTGTGTACCMKCCCTCACCTTCGGGAGTKTCGGGAGTAGTKTGG
H X L G Q X I Y E T Y G D T W X G V E A L X A L I X P>

6810 vif 151-180 (110) 6840 6850 6860 6870 6880
CAAAAAGATTARGCCTCCCTCCCATCCGTGAAAAAGCTCACCGAAGACARATGGAATRAGCCTCAAAAGAYATATAGCG
GTTTTTCTAATYCGGAGGGGAGGGTAGGCACTTTTCGAGTGGCTCTGTATTACCTTAYTCGGAGTTTTCTRTATATCGC
K K I X P P L P S V K K L T E D X W N X P Q K X Y S>

6890 6900 pol 901-930 (94) 6930 6940 6950 6960
CTGGCGAAAGGATRTTCGATATCATTGCAWCCGACATTGAGCTAAGGAACCTGCAAAASCAAATCHYAAAGATTTCAGAAAT
GACCCGCTTTCTAAYAGCTATAGTAACGTWGGCTGTAGTCTGATTCCCTTGACGTTTTSGITTAGKRTTCTTAAGCTTTA
A G E R I X D I I A X D I Q T R E L Q X Q I X K I Q N>

6970 6980 6990 pol 886-915 (93) 7020 7030 7040
TTCTGCTGTCTTATCCATAACTTTAAGAGGAAGGGAGGCTTGGCGGCTACTCCGCCGGAGAGAGAATCRTTGACATTAT
AAGCGACACAAATAGGTATTGAATCTCTCTCCCTCCGTAAACCGCCGATGAGGCGGCCCTCTCTCTAGYAACTGTAATA
P A V F I H N F K R K G G I G G Y S A G E R I X D I I>

7050 7060 7070 7080 gag 256-285 (18) 7110 7120
CGCCASCAGATATCTTCCCGTGGCGGAWATCTATAAGAGATGATCATTTCTCGGACTCAACAAAATCGTGAGAAATGTATY
GCGGTSGGTATAGYAAAGGCACCCGCTWTAGATATTCTCTACCTAGTAAGACCCCTGAGTTGTTTTAGCACTCTTACATAR
A X D I X P V G X I Y K R W I I L G L N K I V R M Y>

7130 7140 7150 7160 7170 env 495-524 (169) 7200
MACCCGTCAGCATTTCTGGATATCAGAGTGAGACAGGGAATCTCCCCCTCAGCTTTCAGACACTGMYGCCCGCTCCAGAG
KTGGGCACTCGTAAGACCTATAGTCTCACTCTGTCCCTATGAGGGGGAGTGGAAAGTCTGTGACRKGCGGCGAGGGCTCT
X P V S I L D I R V R Q G Y S P L S F Q T L X P A P R>

7210 7220 7230 7240 7250 7260 7270 7280
GGCCCTGACAGACYCGRASGCATTGAGGAAGACTCCAGSCAGGACCATCAGTATCCCATTYCCGAACAGCCCTCTGYCTCA
CCGGGACTGTCTGRGCTTSCGTAACCTCTCTCAGGTCGCTCTGCTAGTCATAGGGTAARGGCTTGTCCGAGACRGAGT
G P D R X X X I E E E S X Q D H Q Y P I X E Q P L X Q>

tat 61-90 (122) 7310 7320 7330 7340 7350 7360
GMCAAGGGGAGRCAATCCACAGRCCCTFRAGAAAGCAAAAAGGGAGTGGTCCGACTCCATGAATAAGCAACTGA
CRGTTCCCTCTYGTAGGGTGTCTGGGAYTCTCTTCGTTTTTCTCCTCACCAGCTCAGGTACTTATCTCTGACT
X R G X N P T X P X E S K K A S G V V E S M N K E L>

7370 pol 856-885 (91) 7400 7410 7420 7430 7440
AAAAGATTATCGGACAGGTCAGGGAMCAGGCTGAGCACCTGAAAACCGCTGTGCAAAATGCTGCCATGCAGATGCTCAAG
TTTTCTAATAGCTCTGTCAGTCCCTGTGCTCCGACTCGTGGACTTTTGGCGACACGTTTACGACGGTACGCTACAGGTC
K K I I G Q V R X Q A E H L K T A V Q M A A M Q M L K>

7450 7460 gag 196-225 (14) 7490 7500 7510 7520
GAWACCATTAAACGAAGAGGCTGCCGAGTGGGACAGARTCCATCCGCTCCATGCCGGACCCRTTSCCCCTTCACCGMGAT
CTWTGGTAAATGCTTCTCCGACGGCTCACCTGTCTYAGGTAGGGCAGGTACGGCTGGGYAASGGGAGAGTGGCKCTA
X T I N E E A A E W D R X H P V H A G P X X P L T X I>

7530 7540 7550 pol 181-210 (46) 7580 7590 7600
TTGTAMAGAAATGGAAVAAGAAGGCAAAATCTCCARGATTGGCCCTGAGAAATCCCTATAACACACCCRTCTTTGCCATT
AACATKICTTTACCTTBTCTCTCCGTTTTAGAGGTYCTAACCGGACTCTTAGGGATATTGTGTGGGYAGAAACGGTAG
C X E M E X E G K I S X I G P E N P Y N T P X F A I>

7610 7620 7630 7640 pol 871-900 (92) 7670 7680
AAGTGAGAGASCAAGCCGAACACCTCAAGACAGCCGCTCCAGATGGCAGTCTTCATTACAAATTTCAAAGGARAGGCGGA
TTCACCTCTCTSGTTCCGCTTGTGGAGTCTGTCCGAGGTCTACCGTCAGAAAGTAAGTGTAAAGTTTTCTTCCGCTT
Q V R X Q A E H L K T A V Q M A V P I H N F K R X G G>

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B3
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FIGURE 15 (Cont)

SUBSTITUTE SHEET (RULE 26)

71/216

7690 7700 7710 pol 211-240 (48) 7740 7750 7760
ATCGGAGGCAAAAAGAAAGATAGCACAAAGTGGAGGAACTGGTAGACTTTAGGGAGCTCAACAAACGTACACAGGATTT
TAGCCTCCCTTTTCTTCTATCGTGTTCACCTCCTTTGACCATCTGAAATCCCTCGAGTTGTTTGCATGTGCTCTAAA
I G G K K K D S T K W R K L V D F R E L N K R T Q D F>

7770 7780 7790 7800 env 540-569 (172) 7830 7840
CTGGGAGGTCCAGCTCGGTTTFTYGGCTCTGGCTTGGGATGACCTCAGGAGCCTGTGTCTGTTACAGTATCACAGACTGA
GACCTCCAGGTCGAGCCAAAARCCGAGACCGAACCTTACTGGAGTCTCGGACACAGACAAGTCGATAGTCTCTGACT
W E V Q L G F X A L A W D D L R S L C L F S Y H R L>

7850 7860 7870 7880 7890 vpr 76-96 (117) 7920
GAGACTTATCCTCATCGYTGCCAGAAATGCCRACATAGCAGAATCGGCATCACTAGGCAACGTAGAGTAGGAACGGC
CTCTGRAATAGGATAGCRACGCTCTTTCACGGYTGATCGTCTTAGCCGTAGTGATCCGTTGCATCTC SATCCTTGCCG
R D X I L I X A R X C X H S R I G I T R Q R R X R N G>

spacers 7950 7960 7970 env 155-184 (147) 8000
KCCTCCAGGTCGCTGCCCCAAARTCWCCTTCGAMCCATTCCCATTCATCTATTGCGCTCCCGCTGGCTWCCTATCCT
HGGAGCTCCAGTCGACGGGGGTTTAYAGWGAAGCTKGGGTAAAGGTAAAGTATAACCGAGGGCGACCGAWCCATAGGA
X S R S A A P K X X F X P I P I H Y C A P A G X A I L>

8010 8020 8030 8040 8050 vif 76-105 (105) 8080
CAAGTGTAAACRATAAGAMTTCAATGGGAAARAGGATTGGCAWCTGGGACASGGAGTGTCATCGAATGGAGAMWGA
GTTACATCTGTATTCTTKAAGTTACCGCTTTTCCTAACCGTGAACCTGTSCCTCACAGGTAGCTTACCTCTKMTTTT
K C N X K X F N G E X D W X L G X G V S I E W R X K>

8090 8100 8110 8120 8130 gag 481-499 (33) 8160
GSTATAGCACACAGGTGGACCTGRCCTCGCCGATCACTCTATCCTCCCTYAGCTTCCCTGAAAAGCCTCTTC
CSATCTCTGTCTCCACCTGGGACCTGGGACCTAGTCTGAGATAGCAGGGARTCGAAGGGACTTTTCGGAGAAG
X Y S T Q V D P X L A D Q P S L Y P P X A S L K S L F>

8170 spacers 8200 8210 vif 121-150 (108) 8240
GGAAACGATCCCTYATCCCAAGCCGCTAGAAGGGCTATCCTCGGCCAWAKAGTCAGSAGAAGGTGTGAGTATCMKCCGG
CCTTTGCTAGGGARTAGGGTTCGGCGATCTTCCGATAGGAGCCGGTWTMTCACTCTCTTCCCACTCATAGCKMGGCC
G N D P X S Q A A R R A I L G X X V X R R C E Y X X G>

8250 8260 8270 8280 8290 8300 8310 8320
ACACAATAACGTCGGCTCCCTGCAATACCTCGCACTAGCCAAACCCAMAACCGTTGCMWCAAGTGTACTGTAAAGAA
TGTGTTATTCCAGCCGAGGGACGTTATCGAGCGTGAATCGGTTGGGTATTGGCGAACGKGTTCACAATGACATTCTTTA
H N K V G S L Q Y L A L S Q P X T A C X K C Y C K K>

tat 16-45 (119) 8350 8360 8370 pol 976-995 (99) 8400
GTTGCTWCCACTGTCTAGSTCTGCTTCTCTGAMGAAGGACTGGGAATAGGGATTACGGAAGCAAATGCTGGCGMTGAC
CAACGAWGGTGACAGTCSAGACGAAGGACTKCTTCCCTGACCTTACTCCCTAATGCCTTTCGTTTACCGACCGCACTG
C C X H C Q X C F L X K G L G I R D Y G K Q M A G X D>

8410 spacers 8440 8450 pol 721-750 (82) 8480
TGTGTGGCCRGACAGGCAAGACGAAGAGCGACCAAGTACCATAGCAATTGGACAACCATGGCCARTGASTTTAACTTCC
ACACACCGGYCGTCCGTTCTGCTTCTCGTCCGTTTCATGGTATCGTTAACTCTTGGTACCCTGACTSAAATTGGAGGG
C V A X R Q D E D A A K Y H S N W R T M A X X F N L P>

8490 8500 8510 8520 8530 8540 8550 8560
CCCTATCGTCSCTAAGGAAATCGTCGCAWRTTGGGATAAGTGAACGAATCGRCACCTGGAACTGCTGGAGGAACGAAAM
GGGATAGCAGSGATTCTTTAGCAGCGTWAACCGTATTACATTTGCTTACCCTGACCTTGACGACCTCTTGACTTTK
P I V X K E I V A X C D K C N E W X L E L L E E L K>

vpr 16-45 (113) 8590 8600 8610 8620 8630 8640
ANGAAGCCGTGAGACACTTTCCAGACCTGGCTGCATGGCCTCGGTCAACAGATRTCAATTAGCCTCTGGGATCAGTCC
TWTCTCGGCATCTGTGAAAGGGTCTGGGACCGACGTACCGGACCGCAGTTGTCTAYAGTAATCGGAGACCTTAGTCAGG
X E A V R H F P R P W L H G L G Q H D X I S L W D Q S>

B3
join
B4

FIGURE 15 (Cont)

SUBSTITUTE SHEET (RULE 26)

72/216

8650 env 106-144 (144) 8680 8690 8700 8710 8720
CTGAAACCTGTGTGAACTGACACCCCTCTGCGTCACCCCTCAACTGTACCAATGCCAATCTGGAAGAGMTACTCCAC
GACTTTGGGACACACTTTGACTGTGGGGAGACGCACTGGGAGTTGACATGGTTACGGTTAGACATCTCTCKATGAGGTG
L K P C V K L T P L C V T L N C T N A N L X K X Y S T>

8730 8740 vif 91-120 (106) 8770 8780 8790 8800
CCAAGTGGACCCCGRTCTGGCTGACCAWCTGATTACCTCCACTATTTCCGATTGCTTTKCCGATAGCRCAATCATCCCCA
GGTTCACCTGGGGCYAGACCCGACTGGTGAATAAGTGGAGGTGATAAAGCTAACGAAAHGGCTATCGVGTAGTAGGGT
Q V D P X L A D X L I H L H Y F D C F X D S X I H P>

8810 8820 8830 nef 166-195 (190) 8860 8870 8880
TSRGCWACACGGAATGGAGGATGAGGAWAGGGAAGTCTGAWATGGAATTCGATAGCCRTCTGGCTCKCAGCCATATS
ASYCGGWTGTGCCTTACCTCTACTCTCTTCCCTTCACGACTWTACCTTTAAGCTATCGGYAGACCGAGMTCCGTATAS
X X X H G M E D E X R E V L X W K F D S X L A X R H X>

8890 8900 8910 8920 pol 151-180 (44) 8950 8960
GCTATCGAWACCGTCCCCGTCAAGCTCAAGCTGGCATGGACGGACCCAAAGTGAAACAGTGGCCCCCTCAC
CGATAGCTWTGGCAGGGGCACTTCGAGTTCGGACCGTACCTGCCTGGGTTTCACTTTGTACACCGGGAGTG
A S S P I X T V P V K L K P G M D G P K V K Q W P L T>

8970 8980 8990 9000 9010 gag 436-465 (30) 9040
CGAAGAGAAATCAAGCTATTGGCCTAGCMRCAAGGGAAGGCTGGCAATTTCCYGCAGTCCARGCCTGAGCCTACCG
GCTTCTCTTTTAGTTCGTAACCGGATCGKYGTTCCTTCCGGACCGTTAAAGGRCGTACAGTTCGGACTCGGATGGC
E E K I K A I W P S X K G R P G N F X Q S X P E P T>

9050 9060 9070 9080 9090 vif 31-60 (102) 9120
CACCCCCAGCCGAGARCTTTTGATTCGGCTATTAGCAAAAAGGCTAAAGGATGGTTTTACAGACACCATTTWCGAWAGCCRA
GTGGGGGTCCGCTCTYGAAYCTAAGCCCTAATCGTTTTTCCGATTSCCTACCAAAATGCTGTGGTAAMGCTTTCGGYT
A P P A E X P X F G I S K K A X G W F Y R H H X X S X>

9130 9140 9150 9160 9170 9180 9190 9200
CACCTAAGCTCAGCTCCGAGGTCCACATTCCCCCTCGGCTATGATGACCGCTTGCCAAGGCGTGGCGGACCCRCACAA
GTGGGATTCCAGTCCGAGGTCCAGGTGTAAGGGGAGCCCTACTACTGGCGAAGCGTTCCGACGCCCTGGGYCAGTGTT
H P K V S S E V H I P L G M M T A C Q G V G G P X H K>

9230 9240 9250 9260 9270 9280
gag 346-375 (24)
AGCCAGGCTACTGGCAGAGGCTATGTCCAGGYGAMCMACGCTAACATTCTCCCATTTGTGSCAAAGAGATTGTGGCAN
TCGGTCCCATGACCGTCTCCGATACAGGGTCCRCCTGKTGCGATTGTAGGGAGGTAACACSGGTTTCTTAACACCGTW
A R V L A E A M S Q X X X A N I P P I V X K E I V A>

9290 9320 9330 9340 9350 9360
pol 736-765 (83)
RCTGTGACAAATGCCAGCTCAAGGGTGAGGCTATKACGGACAGGTGACTGTAGCCCTTCCGAGGGAWCAAGACAGRCT
YGACACTGTTTACGGTCCAGTTCCTCCGATAGTGCCTGTCCACYTGACATCGGGAAGCTCCCTGCTTCTGCTCYGA
X C D K C Q L K G E A X H G Q V X C S P S E G X R Q X>

9370 9380 rev 31-60 (126) 9410 9420 9430 9440
AGGARGAACAGACGTAGAAGGTGGCGTGMGAGGCAAGGCAAAATCCRCCKCATCTCCGAGWGGATTCTGGACAGATRAG
TCCTYCTTGTCTGCATCTTCCACCGCACKCTCCGTTTCGTTTAGGYGMGGTAGAGGCTCWCCTAAGACCTGTCTAYTC
R X N R R R R W R X R Q R Q I X X I S E X I L G Q X R>

9450 9460 9470 gag 226-255 (16) 9500 9510 9520
GGAACCCAGAGGCTCCGACATTGCTCGGTACCAAGCACACTGCAAGAGCAAAATCCSATGCGATGACAAACATCCCCCTR
CCTTGGGCTCTCCGAGGCTGTAACGGCCATGTTGTTGCTGTGACGTTCTCGTTTAGCSTACCTACTGTTTGTAGGGGAY
E P R G S D I A G T T S T L Q E Q I X W M T X N P P>

9530 9540 9550 9560 pol 841-870 (90) 9590 9600
RCATTAGCAAGAGTTTGGCATTCCTTATAACCTCAGTCCAGGGCGTGGTGGAAAGCATGAACAAAGAGCTCAAGAAA
YGTAAKTCGTTCTCAAACCGTAAGGGATATTGGGAGTCAGCGTCCCGCAGCACCTTTCGTACTTGTCTCTGAGTCTTT
X I X Q E F G I P Y N P Q S Q G V V E S M N K E L K K>

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FIGURE 15 (Cont)

SUBSTITUTE SHEET (RULE 26)

73/216

9610 9620 9630 **nef 106-135 (186)** 9660 9670 9680
ATCATTGGGAGACAGGAGATCCTCGATCTCTGGGTCTACMTACCCAAGGCTWTTTCCCTGACTGGCASAATTACACACC
TAGTAACCTCTGTCTCTAGGAGCTAGAGACCCAGATGKTATGGGTCCGAWAAAGGGACTGACCGTSTTAATGTGTGG
I I G R Q E I L D L W V Y X T Q G X P P D W X N Y T P>

9690 9700 9710 9720 **rev 46-75 (127)** 9750 9760
CGSACCCGGARYCAGATAGAGAGAGACAGAGATTCRTKCTATTAGCGAANGGATTCTCAGCANCTKCC
GCCTGGGCTTYRGTCTATCTCTCKTCTGTCTCTGTCTAAGYAMGATAATCGCTTWCTTAAGAGTCGTGKAMGG
G P G X R Y P S R X R Q R Q I X X I S E X I L S X X>

9770 9780 9790 9800 9810 **gag 301-330 (21)** 9840
TCGGCAGAYCCGCTGAGCCTGTGCTCTGCAACTGTWTAAGACACTGAGAGCCGAACAGGCTWCCAAAGASGTCAAGAAT
AGCCCGCTCTRGGCGACTCGGACACGGAGACGTTGACANATTCTGTGACTCTCGGCTTGTCGANGGGTTCTSCAGTTCTTA
L G R X A E P V P L Q L X K T L R A E Q A X Q X V K N>

9850 9860 9870 9880 9890 9900 9910 9920
TGGATGACCGASACACTGCTCGTGCAAAACGCTAACCTGACTGTGAGARAGTGTATCTGKCTTGGGTCCCGCTCATAA
ACCTACTGCTCTGTGACGAGCACGTTTGGCATTGGGACTGACACTCTTTCACATAGACMGAAACCCAGGGCGAGTATT
W M T X T L L V Q N A N P D C E X V Y L X W V P A H K>

pol 676-705 (79) 9950 9960 9970 9980 9990 10000
AGGCATTGGCGGAAACGAGGTGGACAAACTGGTCAKCKCTGGCATTAGGAAPACAGACCCCTAACCTCAGGAARTCS
TCCGTAACCGCTTTGCTTGTCCACCTGTTTGACCACTGAGGACCGTAACTCTTGTCTGGGATTGGGAGTCCCTTYAGS
G I G G N E Q V D K L V X X G I R K T D P N P Q E X>

10010 **env 76-105 (142)** 10040 10050 10060 10070 10080
WTCTGGAAAACGTCACCGAGAAGCTTTAACAATGTGGAAAAACRATATGGTGGASCAATGCAWAGAGCTGGCTWTGCCATT
WAGACCTTTTGCAGTGGCTCTTGAATTTGTACACCTTTTGYTATACCACCTSGTTTACGTWCTCGACCGAWACGGTAA
X L E N V T E N F N M W K N X M V X Q M X E A G X A I>

10090 10100 **env 170-199 (148)** 10130 10140 10150 10160
CTGAAATGCAATRACAAAAMSTTCAACGGAAGTGGACCCCTGTANGAATGTCTCCASCCTCCAGTGTACCCATGGCTWAGA
GACTTTACGTTATTTGTTTSAAGTTGCTTGAACCTGGGACATCTTACACAGGTSGCAGGTACATGGGTACCGTCT
L K C N X K X F N G T G P C X N V S X V Q C T H G X E>

10170 10180 10190 **env 600-629 (176)** 10220 10230 10240
GCTCAAGANTAGCGCTRTCTCCCTGCTCAACGCTACCGCTATCGCTGTGGCTGRGKGGACCGATAGGRTTATCGAAGTGG
CGAGTTCTWATCGGAYAGAGGGACGAGTTGCGATGGCGATAGCGACACCGACYMCTGCTATCCYAATAGCTTCACC
L K X S A X S L L N A T A I A V A X X T D R X I E V>

10250 10260 10270 10280 **vif 46-75 (103)** 10310 10320
YTCATCCCRGCATCCCAAAGTGTCCAGCGAAGTGCATATCCCTCTGGGAGAGCGTAGGCTCRTCATTARGACATACTGG
RAGTACGGGCGTAGGGTTTACAGGTCGCTTACGCTATAGGGAGACCTCTSCGATCCGAGYACTAATYCTGTATGACC
X Q S X H P K V S S E V H I P L G X A R L X I X T Y W>

10330 **spacers** 10360 10370 **nef 1-30 (179)** 10400
GGCCTCCASACAGGCTGCTATGGGCGGTAAATGGTCCAAGWGCTCCCYCGTGGATGGCCCGMAGTGAGAGAGAGAAT
CCGGAGGTSTGTCCCGACGTTACCCGCCATTTACCAGGTTTCWCGAGGGRGACGCTACCGGGCKTCACTCTCTCTTA
G L X T G A A M G G K W S K X S X V G W P X V R E R I>

10410 10420 10430 10440 10450 **pol 496-525 (67)** 10480
CACACRGRCASCCCTGCGCTGAGGGAGTCTCAAGACCGGCAAGTACKCTAGGAWAGGRTGCCCATACCAATGACG
GTCTGYCYGTSCGGGACGGCGACTCCCTCAGAGTTCTGGCGGTATGAGATCTTCTCCYACGGGTATGGTTACTGC
R X X X P A A E G V L K T G K Y X R X R X A H T N D>

10490 10500 10510 10520 10530 10540 10550 10560
TCARGCAACTGACAGHGGYTGTCAAAAGATTGCCACAGAGTGGAGGSGTCTGAAATACTKKGGAATCTGCTC
AGTYCGTTGACTGTCKCCACACGCTTTCTAACGGTGTCTGAGGACCTCCSAGACTTTATGAMCMCTTAGACGAG
V X Q L T X X V Q K I A T E S S W E X L K Y X X N L L>

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B6
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B7

FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

74/216

env 585-614 (175) 10590 10600 10610 10620 10630 10640
CWGTACTGGGGCCWGGAACTGAAAACWCTCCGCCRTACGCCCTCTGAATGCCACAGCCATTSMGCTGCCTGAGAAAGAWAG
GWCATGACCCCGGNCCTTGACTTTTWGAGCGGAGTCCGAGGACTTACGGTCTCGGTAASWCGACGGACTCTTCTWTC
X Y W G X E L K X S A X S L L N A T A I X L P E K X S>

10650 pol 391-420 (60) 10680 10690 10700 10710 10720
CTGGACCGTCAACGATATCCAAAAGCTCGTGGGAAAGCTCAACTGGGCATCCAGATTACSCCGGAGAGCCATTGAGG
GACCTGGCAGTTGGATAGCTTTTCGAGCACCCCTTCGAGTTGACCCGTAGGGTCTAAATGSGGCCCTCTCGGTAACCTC
W T V N D I Q K L V G K L N W A S Q I Y X G R A I E>

10730 10740 env 345-374 (159) 10770 10780 10790 10800
CTCAGCAACACWTGCTGCAACTGACAGTGTGGGGCATTAAAGCACTGCAAGCCAGAGTGTCTGCCRTTGAGAGATATCTC
GAGTCGTTGTGACGAGCTTGACTGTACACCCCGTAATTCGTTGACGTTCCGGTCTCAGGAGCGGAACTCTCTATGAG
A Q Q H X L Q L T V W G I R Q L Q A R V L A X E R Y L>

10810 10820 10830 pol 631-660 (76) 10860 10870 10880
GCCCTCCAGGATAGCGGATYGGAAAGTGAATATCGTCACCGATAGCCAAATACGCTCTAGGCATCATTGCGGCTCAGCCTGA
CGGAGGTCCTATCGCCTARCTTCACTTATAGCAGTGGCTATCGGTTATGCGAGATCCGTAGTAAGWCCGAGTCGGACT
A L Q D S G X E V N I V T D S Q Y A L G I I X A Q P D>

10890 10900 10910 10920 env 420-449 (164) 10950 10960
CARAAGCGAAAGGGAAATCTCCAATATACCARTCWGATTACRAGATCCTCACCGAATCTCAAAATCAACAGGATAGGA
GTCTTCGCTTTCCCTTTAGAGGTTGATATGGTYAGWCTAAATGYTCTAGGAGTGGCTTACAGTTTATGTTCTCTATCT
X S E R E I S N Y T X X I Y X I L T E S Q N Q Q D R>

10970 10980 10990 11000 11010 env 285-314 (155) 11040
ATGAGMAAGASCTCCTGCTCCCAARGGCTAAGAGAGGGCTCGTCSAAAGGAAAAGCGTCCGCTCGGCTTTGGCGCT
TACTCTCTGAGGAGCGAGGGTGTTCGATTTCTCTCCAGCACSTTTCCCTTTTCGACGGCAGCGCAACCGCGA
N E X X L L A P T X A K R R V V X R E K R A V G X G A>

11050 11060 11070 11080 11090 pol 91-120 (40) 11120
ATGWTCTTCGATCTCTCGGCGCTGCCAAACCCAAAATGATCGGAGGCATTGGAGGCTTTATCAAAAGTCAGGCAATGA
TACWAARAGCCTAAGGAGCCCGACCGTTTCGGTTTACTAGCCTCCGTAACCTCCGAAATAGTTTCAGTCCGTCATACT
M X X G F L G A A K P K M I G G I G G F I K V R Q Y D>

11130 11140 11150 11160 11170 11180 11190 11200
CCAAATCTTTATCGAAATCTGTGGAMASAAAGGCTATCTCTACCATAGGCTCAGGGAATTTCTCTGATCGYCGCTAGGA
GGTTTAGAATAGCTTTAGACACCTKTSTTCCGATAGGATGGTATCCGAGTCCCTAAAGTAAGACTACGCGGATCTCT
Q I X I E I C G X K A I S Y H R L R D F I L I X A R>

env 555-584 (173) 11230 11240 11250 11260 11270 11280
YTGTGGAATGCTCGGCCRTAGCTCCCTGARAGGCCCTCRGAGAGGACACTGAATGCCTGGGTGAAAGTGRTTGAGGAA
RACACCTTGACGAGCCGGYATCCAGGGACTYTCGGGAGGYCTCTCCCTGTGACTTACGGACCCACTTTTCACYAATCCTT
X V E L L G X S S L X G L X R G T L N A W V K V X E E>

11290 gag 151-180 (11) 11320 11330 11340 11350 11360
AAGGSATTCARTCCCGAAGTGATCCCATGTTTWCCTCTGTCCGAGGAGCCACAGCAACACASCCGCTAA
TTCCSTAAGTYAGGGCTTCACTAAGGGTACAAANGGCGAGACAGGCTCCCTCGGTGAGCAATCGTGTGSGGCGATT
K X F X P E V I P M F X A L S E G A T L E S N T X A N>

11370 11380 nef 46-75 (182) 11410 11420 11430 11440
CAATSCCGATTCCGYCTGGCTGTAAGCCCAAGAGGAGAGTGGATTTCCTGTGAGACCCCAAGTGCCTAGAGCK
GTTASGGCTAAGCGRCACCGACTTCGGGTCTCTCTCTTCACCTAAAGGACACTCTGGGGTTACGGATCTCGGM
N X D C X W L X A Q E E E X V G F P V R P Q V P R A>

11450 env 630-651 (178) 11480 11490 spacers 11520
GGAGGGCTATCTCMACATTCACASGAGGATTAGGCAAGGCYTTGAGAGAGCCCTCTGCGCGCGAATGGGATAGGRTT
CCTCCGATAGGAGRTGTAAGGCTCTCCTAATCCGTTCCGAACTCTCTCGGAGGATCGGCGGCTTACCTATCCYAA
X R A I L X I P X R I R Q G X E R A L L A A E W D R X>

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FIGURE 15 (Cont)

SUBSTITUTE SHEET (RULE 26)

75/216

11530 11540 gag 211-240 (15) 11570 11580 11590 11600
CACCTGTGCACCGCTGGCCCTRTCTCCCGCCAAATAGAGAGCCAGGGGAAGCGATATCGCTGGCACAACCTCAG
GTGGGACACGTCGACCGGGAYAGSGAGGGCCGGTTTASTCTCTCCGGTCCCTTCGCTATAGCGACCGTGTTCGAGTC
H P V H A G P X X P G Q X R E P R G S D I A G T T L R>

11610 11620 11630 nef 76-105 (184) 11660 11670 11680
GCCCATGACATATAAGGSCGCTRTTGACCTCAGCYTGTTCGAAAGAGAAAGCGGACTGGAWGGCCTCCTCTATAGCM
CGGGTACTGTATATCCSGCGAYAACTGGAGTCGRACAAAGACTTCTCTTCCGCTGACCTWCCGGAGYAGATATCGK
P M T Y K X A X D L S L F L K E K G G L X G L X Y S>

11710 11720 vpr 1-30 (112) 11750 11760
spacers
AGAAAGCTGCTATGGAACAGCGCTCCCGAAGACCAARGCYCTCAGAGAGCGCTTACAATGAGTGGRCCTCGAGCTCCTG
TCTTCGACGTACCTTGTCCGAGGCTTCTGTTTCGRGAGTCTCTCTCGGAATGTTACTCACCYGGGACCTCGAGGAC
X K A A M E Q A P E D Q X X Q R E P Y N E W X L E L L>

11770 11780 11790 11800 11810 pol 481-510 (66) 11840
GAAGAGCTCAAGMAMGAGGCTCAAGRCCAATGGACCTWCCAAATCTWTCAGGAACCTTTAAGAATCTGAAAACCGGAAA
CTTCTCGAGTCTCKTCTCCGAGTTCYGGTTACCTGGAWGTTTAGAWAGTCTTGGAAATCTTAGACTTTGGCCTTT
E E L K X E A Q X Q W T X Q I X Q E P F K N L K T G K>

11850 11860 11870 11880 11890 11900 11910 11920
GTATKCCAGAAMGAGARGCGCTCACACAAATGGATGACAGAWACCTCCTGGTCCAGAAATGCCAATCCCGATTGCAAGW
CATAMGGTCTTCTCTYCGGAGTGTGTTTACCTACTGCTCTWGGGAGGACAGGTCTTACGGTTAGGGCTAACGTTCTW
Y X R X R X A H T N W M T X T L L V Q N A N P D C K>

11950 11960 11970 11980 11990 12000
gag 316-345 (22)
CCATCTCARGGCTCTGGGAMCCGAGCCWCACTGGAAGAGCCTGAGGTCTATCCCTATGTTTCWAGCCCTCAGCGAAGGC
GGTAGGAGTTCGAGACCTTGGCCTCGGNGTGACCTTCTGGACTCCAGTAGGAGATACAAGWTCGGGAGTCCGCTTCCG
X I L X A L G X G A X L E E P E V I P M F X A L S E G>

12010 gag 166-195 (12) 12040 12050 12060 12070 12080
GCTACCCCCAAGACCTGAATAYGATGCTCAACAYCGTCGGCGGACACCAATCCACCTCCAGGAACAGATTGSCCTGGAT
CGATGGGGGGTCTGGACTTATCTACGAGTGTGRGACCGCCCTGTGGTGGGAGGCTCTTGTCTAACSGACCTA
A T P Q D L N X M L N X V G G H Q S T L Q E Q I X W M>

12090 12100 gag 241-270 (17) 12130 12140 12150 12160
GACAARTAACCTCCCTCTGTCGGAGASATTTACAAAGGTGGATTATCTCGGCTCTATCCCCATCCCG
CTGTTTATGGGAGGGYAGGGACAGCCTCTSTAAATGTTTCCACCTAATAGGAGCCGGAGTAGGGGGTAGGGC
T X N P P X P V G X I Y K R W I I L G L T R I P H P>

12170 12180 12190 pol 241-270 (50) 12220 12230 12240
CCGGCCTCAAGAAAAAGAAAGCGTCACCGTCTGGATGTGGGAGACGCTTACTTCAGCGTCCCTCCGACRAARRCAA
GGCCGGAGTCTTTTCTTTTCGAGTGGCAGGACCTACACCTCTGCGAATGAAGTCCGAGGGGAGCTGYTTYTGTT
A G L K K K K S V T V L D V G D A Y F S V P L D X X Q>

12250 12260 12270 12280 pol 541-570 (70) 12310 12320
ARGGAAACCTGGGAGRCTTGGTGGAYGGAMTACTGGCAGGCTACCTGGATTCTGAGTGGGAGTTTGTGAATACCCCTCC
TYCCTTTGGACCTCYGAACCACTRCCTKATGACCGTCCGATGGACCTAAGGACTCACCTCAAACACTTATGGGGAGG
X E T W E X W W X X Y W Q A T W I P E W E F V N T P P>

12330 12340 12350 12360 12370 nef 121-150 (187) 12400
CCTCGTCTTCCCGATTGGCANAACTATACCCCTGGCCCTGGCRYAAGGTATCCCTCACCTTTGGATGGTGTCTTAAGC
GGAGCAAAAGCGCTAACCGTWTGATATGGGACCGGGACCGYRTCCATAGGGAGTGGAAACCTACCACGAATTCG
L V F P D W X N Y T P G P G X R Y P L T P G W C F K>

12410 12420 12430 12440 12450 pol 571-600 (72) 12480
TCGTGCTGTGGACCCCAAACTGTGGTACCACTGGAAAAGGAMCCCATTTGYCGGAGYCGAAACCTTTACGTGGACGGA
AGCACGGACACCTGGGTTTGACACCATGGTGACCTTTCTKGGGTAACRGCTCRGCTTTGGAATGCACCTGCCT
L V P V D P K L W Y Q L E K X P I X G X E T F Y V D G>

FIGURE 15 (Cont)

SUBSTITUTE SHEET (RULE 26)

76/216

12490 12500 12510 12520 gag 136-165 (10) 12550 12560
 GCCGCCARCAGAGAGACAAAGCTCGG|CAAAACSYCCAGGGACAGATGGTGCATCAGSCTMTTAGCCCCAGGACCCTCAA
 CGGCGGTGTCTCTCTGTTTCGAGCC|GTTTGSRRGGTCCCTGTCTACCACGTAGTCSGAKAATCGGGTCTCTGGGAGTT
 A A X R E T K L G Q N X Q G Q M V H Q X X S P R T L N>

12570 12580 12590 12600 12610 env 61-90 (141) 12640
 CGCTTGGCTCAAGGTCRTCGAAGAGAAAGSCTTTAR|GAMACCGAAGTGCATAACGTCTGGGCTACCCATGCTGTGTGC
 GCGAACCCAGTTCCAGYAGCTTCTTTCSGAAATY|CTRTGGCTTACGTATTGCAGACCCGATGGGTACGGACACACG
 A W V K V X E E K X F X X T E V H N V W A T H A C V>

12650 12660 12670 12680 12690 12700 12710 12720
 CTACCCGATCCCAATCCCAAGAGRTTSWCTGGAGAATGTGACAGAG|CTCAAGGATCAGMAAYTCTCGGCMTTTGGGGA
 GATGGCTAGGGTTAGGGGTTCTCYAASNGGACCTCTTACACTGTCT|GAGTTCCTAGTCTTTRAGGAGCCGKAAACCCCT
 P T D P N P Q E X X L E N V T E L K D Q X X L G X W G>

env 375-404 (161) 12750 12760 12770 12780 12790 12800
 TGCTCCGGCAAAATCATTTGCACAACCRMTGTGCTTGGAAACAGCWCTGGTCCAA|CNAKCTGGCCATAACAAAGTGGG
 ACGAGGCCGTTTGAATAACGTGTTGGYKACACGGAACCTTGTGCGGGACAGGTT|GKTHGACCGGTATTGTTTACCCC
 C S G K X I C T T X V P W N S X W S N X X G H N K V G>

12810 vif 136-165 (109) 12840 12850 12860 12870 12880
 AAGCTCCAGTATCTGGCTCTGAMGGCTCTGATTAMGCTAAGAAAATCARACCCCTCTGCTAG|GYTAAGACAATCA
 TTCGGAGGTATAGACCGAGACTKCCGAGACTAATKCGGATTTCTTTAGTYTGGGGGAGACGGATC|CRATTCTGTAGT
 S L Q Y L A L X A L I X P K K I X P P L P S X K T I>

12890 12900 env 230-254 (152) 12930 spacers 12960
 TTGTGCATCTGAATRAGTCCGTGGWAATCAATTGCACAAGCCCTARCAATAACACAAGGAMA|GCCGCGGGAAGWA
 AACACGTAGACTTAYTCAGGCACCTTAGTTAACGTGTTCCGGATYGTATTTGTTCTCT|CGGCGGGAAGTCTCWT
 I V H L N X S V X I N C T R P X N N T R X A A A S E X>

12970 12980 12990 gag 106-135 (8) 13020 13030 13040
 CAGAAWAAGTCCMAACAGAAAACCCAGCAAGCCGCGCCGATACAGGCARCTCCAGCMAGGTACGCCAAAATATCCCAT
 GTCTTWTTCAGGKTTGTCTTTTGGGTCGTTCCGGCGCGGCTATGTCCTGTYGAGGTGKTCAGTCGCTTTTGATAGGGTA
 Q X K S X Q K T Q Q A A D T G X S S X V S Q N Y P I>

13050 13060 13070 13080 pol 826-855 (89) 13110 13120
 TGTGTCCAACTTTACCTCCRCRCTGTGAAAGCCGCTTGTGGTGGGCCRRTATCMAACAGGAGTTTGGAAATCCCTTACA
 ACAGAGGTTGAAATGGAGGYGGYACACTTTCCGCGAACAACCCCGGYATAGKTTGTCTCAAACTTTAGGGAATGT
 V S N P T S X X V K A A C W W A X I X Q E P G I P Y>

13130 13140 13150 13160 13170 pol 586-615 (73) 13200
 ATCCCCAAAGCCATACATTCTATGTGCATGCGCTGCCARTAGGGAAACAAACTGGGAAAGGCTGGCTATGTGACAGAC
 TAGGGGTTTCGTTTGTAAAGATACACTACCGGACGGTYATCCCTTTGGTTTGACCCCTTCCGACCGATACACTGTCTG
 N P Q S Q T P Y V D G A A X R E T K L G K A G Y V T D>

13210 13220 13230 13240 13250 pol 766-795 (85) 13280
 AGAGGCAGACAGAAARTCTTAGCGGAATCTGCAGCTCGACTGTACCCATCTCGAAGGCAAARTATTCTGTAGCCGT
 TCTCCGTCTGTCTTYYAGYAATCCCTTAGACCGTCGAGCTGACATGGGTAGACCTTCCGTTTYYAGTAAGACCATCGGCA
 R G R Q K X X S G I W Q L D C T H L E G K X I L V A V>

13290 13300 13310 13320 13330 13340 13350 13360
 CCACGTCGCCCTCCGGCTACATTGAGGCTGAGGT|GGCAATGAGCAAGTGGATAAGCTCGTGAKTCCGGAATCAGAAAGG
 GGTGACGCGGAGGCGGATGTAACCTCCGACTCCAG|CCGTTACTCGTTCACTATTTCGAGCACTMAMGGCTTAGTCTTTCC
 H V A S G Y I E A E V G N E Q V D K L V X X G I R K>

pol 691-720 (80) 13390 13400 13410 13420 13430 13440
 TGCTATTCTCGACGGAAATCRATAAGGCTCAGGAAGAGCACGAG|GTCAGGGAAGGATTAGGCRARCCCTCCCGCTGCT
 ACGATAAGGAGCTGCCCTTAGYTATCCGAGTCTTCTCGTGCT|CACTCCCTTTCTTAATCCGYTYGSGAGGGCGACGA
 V L F L D G I X K A Q E E H E V R E R I R X X X P A A>

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FIGURE 15 (Cont)
 SUBSTITUTE SHEET (RULE 26)

77/216

nef 16-45 (180) 13470 13480 13490 13500 13510 13520
GAAGGCGTCGGCGCTGYCTCCCRGGATCTGGATAAGKACGGAGCCMTACCTCCACAAGCGGAACCCAACAGTCCCAGGG
CTTCCGCAGCCCGACRAGAGGGYCTAGACCTATTCTGCTCGGKAGTGGAGTGTTCGCCCTGGGTGTCTAGGGTCCC
E G V G A X S X D L D K X G A X T S T S G T Q Q S Q G>

13530 rev 91-120 (130) 13560 13570 13580 13590 13600
AACTGAAACTGGCGCTCGGCMRCCCTCAGATTYYGGGAGTCCAGCGYTRCTCTCGGCYCCGGTCCCATCGTCATCTGGG
TTGACTTTGACCGCAGCCCGYGGGAGTCTAAARCCCTCTCAGGTCGCRA YAGGAGCCGCGCCGAGGTAGCAGTAGACCC
T E T G V G X P Q I X G E S S X X L G X G S I V I W>

13610 13620 pol 526-555 (69) 13650 13660 spacers
GTAAACCCCTAAGTTTARGCTCCCCATTGAGARAGAGACATGGGAARCCCTGGTGGAYGGASTATTGGCAAGCGCTGCT
CATTTTGGGGATTCAAATYCGAGGGGTAAGTCTTCTCTGTACCTTYGGACCACTTCCTTSATAACCGTTCCGCGACGA
G K T P K F X L P I Q X E T W E X W W X X Y W Q A A A>

13690 13700 13710 env 140-169 (146) 13740 13750 13760
TACAGACTGATCARCTGTAAACAAGCGYTATCAMACAGGCTTGCCCTAAGTTTASCTTTGASCCATATCCCTATCCATTA
ATGCTCTGACTAGTYGACATTGTGTTCGCRATAGTGTGTCCGAACGGGATTCTAATSGAAACTSGGATAGGGATAGGTAAT
Y R L I X C N T S X I X Q A C P K X X F X P I P I H Y>

13770 13780 13790 13800 pol 376-405 (59) 13830 13840
CTGTGCCCCCTGGATGGGCTATGAGCTCCACCCTGACAGATGGACAGTGAACCCATC SWGCTCCCCGAAAAGG
GACACCGGGACCTACCCGATACCTCGAGGTGGGACTGTCTACCTGTACGTTGGGTAGSWGAGGGGCTTTTCC
C A P P S W M G Y E L H P D R W T V Q P I X L P E K>

13850 13860 13870 13880 13890 gag 331-360 (23) 13920
ASTCTCGACAGTGAATGACATTCAAAAWCAATTCTGARAGCCCTCGGCMCAGGCGCTWCCCTGGAGGAAATGATGACA
TSAGGACCTGTCACTTACTGTAAGTCTTTWGTAAAGACTYTCGGGAGCCGKGTCCGCGAWGGGACCTCTTTACTACTGT
X S W T V N D I Q K X I L X A L G X G A X L E E M M T>

13930 13940 13950 13960 13970 13980 13990 14000
GCATGTCAGGGAGTGGGAGGCCCTRGCCATAAGGCTAGAGTGTATTACAGAGACTCCAGGCACCCCTTTTGGAAAGGCC
CGTACAGTCCCTCACCCTCGGGAYCGGTATTCCGATCTCAATAATGCTCTGAGGTCCCTGGGGKAAACCTTTCCGGG
A C Q G V G C P X H K A R V Y Y R D S R D P X W K G P>

pol 931-960 (96) 14030 14040 14050 14060 14070 14080
TGCCAAACTGCTCTGGAAGGCGAAGGCGCTGTGGTCATCCAAGACTTAAGATTGGAGGCCAACTGAWAGAAGCCCTCC
ACGTTTGGACGAGACCTTCCGCTTCCGCGACACAGTAGGTTCTGYAATTTCTAACCTCCGGTTGACTTCTTCCGGGAGG
A K L L W K G E G A V V I Q D X K I G G Q L X E A L>

14090 pol 61-90 (38) 14120 14130 14140 14150 14160
TGGATACAGGAGCCGATGACACCGTCTGGAAGAWATSAATCTGCTTGGCARGTGGGAATCAACAGCTCCAGGCTAGG
ACCTATGTCTCGGCTACTGTGGCAGACCTCTWTASTTAGACCGACCGTYCACCTCTTACTTTCTCGAGGTCGATCC
L D T G A D D T V L E X X N L P G X W G I K Q L Q A R>

14170 14180 env 360-389 (160) 14210 14220 spacers
GTCCTGGCTRTCGAGAGTATCTGAAAGATCAAMAGYTTCTGGGAMTCTGGGGCTGTAGCGGAAAGCTGCTATGGAAAA
CAGGACCGAYAGCTCTCCATAGACTTTCTAGTTKTCRAAGACCCCTKAGACCCGACATCGCCTTTCCGACGATACCTTTT
V L A X E R Y L K D Q X X L G X W G C S G K A A M E N>

14250 14260 14270 vif 1-30 (100) 14300 14310 14320
CAGATGGCAAGTCHTGTATCTGCTGCAAGTGGACACCGATGARGATTAGGACATGGAAGAGCTCTGTAACACCATATGY
GTCTACCGTTTACACACTAGCAGACCGTTACCTGTCTACTYCTAATCTGTACCTTWTGCGGACACTTTGTGGTATACR
R W Q V X I V W Q V D R M X I R T W X S L V K H H M>

14330 14340 14350 14360 env 390-419 (162) 14390 14400
ATTTATCTGTACACARMCGTCCCTGGAATCCASCTGGAGCAATAAGTCCYTCGAAGAGATTGGRATAACATGACC
TTKAAATAGACATGGTGTGKACGGGACCTTGAGGTSACCTCGTTATTACAGGAGCTTCTTAAACCTTATTGTACTGG
X X I C T T X V P W N S X W S N K S X E E I W X N M T>

C3
join
C4FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

[illegible]

↑
C4
join
C5
↓

FIGURE 15 (Cont)
SUBSTITUTE SHEET (RULE 26)

79/216

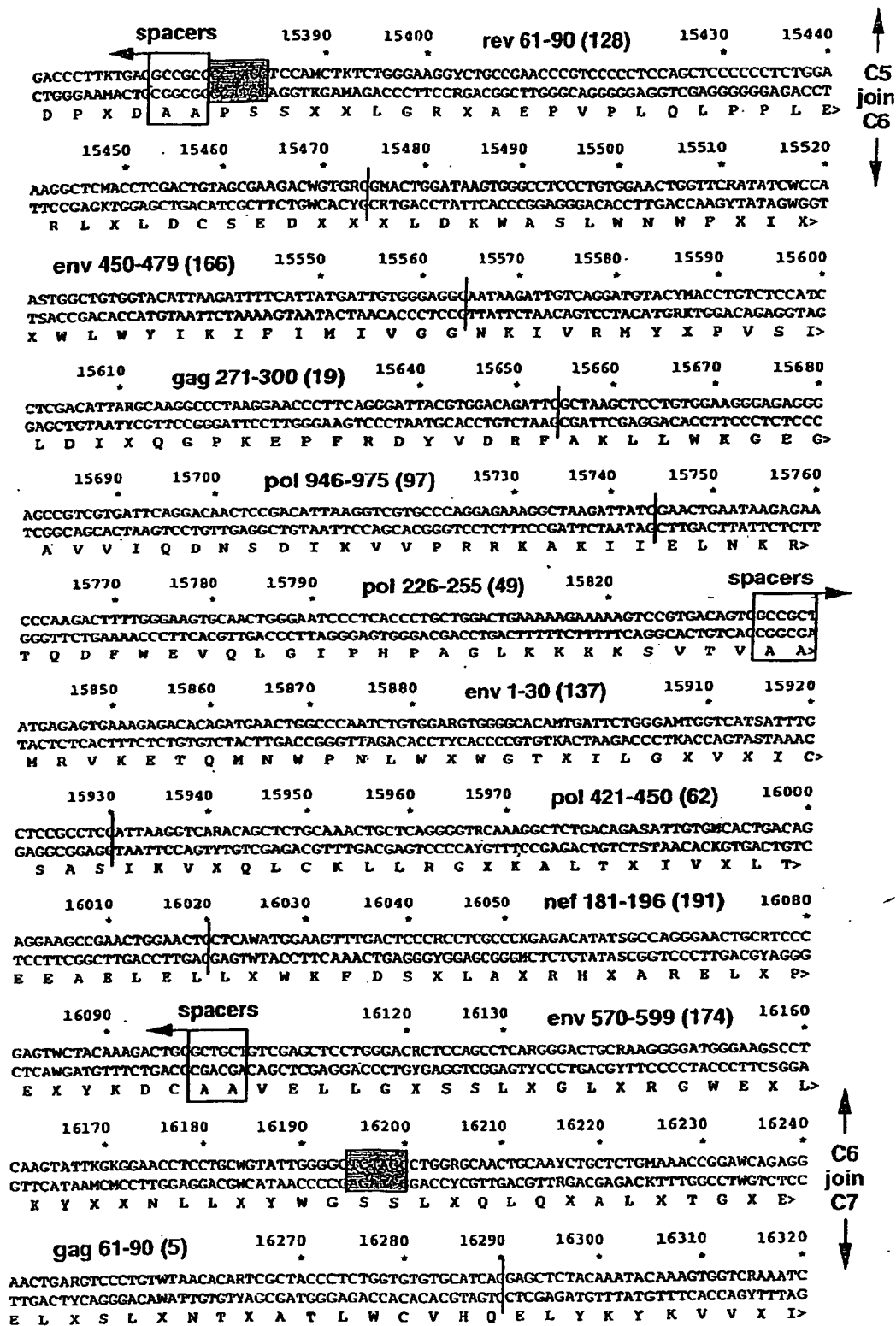


FIGURE 15 (Cont)

80/216

16330 env 270-299 (154) 16360 16370 16380 16390 16400
RAACCCCTCGGCRITGGCCCTACCARAGCCAAAAGGAGAGTGGTCSAGAGAGAGAAAAGCTCACCGANATCGTCMCACT
YTTGGGGAGCCGYAACGGGGATGGTYTCGGTTTCTCTCACCAGSTCTCTCTTTTCGAGTGGCTWTAGCAGKGTGA
X P L G X A P T X A K R R V V X R E K R L T X I V X L>

16410 16420 pol 436-465 (63) 16450 16460 16470 16480
CACCCAGAGGGCTGAGCTGGAGCTGGMGGAAAAACAGAGAGATTCTGARGGAACCCGTCCACGGAGTGTATAGAGTGGCTCG
GTGGCTTCTCCGACTCGACCTCGACCKCCTTTGTCTCTCTAAGACTYCTTGGGCAGGTGCCTCACATATCTCACGAGC
T E E A E L E L X E N R E I L X E P V H G V Y R V L>

16490 16500 16510 gag 361-390 (25) 16540 16550 16560
CCGAAGCCATGAGCCAAGYCAMCMATGCCAACATCATGATGCAGAGAGGCAATTTTCARAGGCCMAAGAGAATCRTCAAA
GGCTTCGGTACTCGGTTTCRGTACGKTACGGTTGTAGTACTACTCTCTCCGTTAAAGTYTCCGGKTTTCTCTAGYAGTTT
A E A M S Q X X X A N I M M Q R G N P X G X K R I X X>

16570 16580 16590 16600 nef 61-90 (183) 16630 16640
CAAGAGGAAGAGGRGGTCCGCTTCCCGCTCAGGCTCCAGTCCACTGAGACCTATGACCTACAAAGSAGCCRTCGATCT
GTTCTCTCTCTCCYCCAGCCGAAGGGGAGTCCGGAGTCCAGGGTACTCTGGATACTGGATGTTCTCSTCGGYAGCTAGA
Q E E E X V G P P V R P Q V P L R P M T Y K X A X D L>

16650 16660 16670 16680 16690 gag 286-315 (20) 16720
GTCCYTCTTTCARACAGGACCCAAAGAGCTTTTCAGAGACTATGTGGATAGGTTTTCWAAAACCCCTCAGGGCTGAGCAAG
CAGGRAGAATTTGTCTCCCTGGGTTTCTCGGAAAGTCTCTGATACACCTATCCAAAAGTTTGGGAGTCCCGACTCGTTC
S X P X Q G P K E P F R D Y V D R F X K T L R A E Q>

16730 16740 16750 16760 16770 gag 16-45 (2) 16800
CCWCACAGGAGGTGAAAAACTGGGAGAAAATCAGACTGAGACCTCGTGGCAAAAAGAAATACARAMTGAAACACMTGTG
GGWGTGCTCTWCACTTTTTCACCTCTTTTACTCTGACTCTGGACACCGTTTTCCTTATGTCTKACTTTGTGKAACAC
A X Q X V K N W E K I R L R P G G K K K Y X X K H X V>

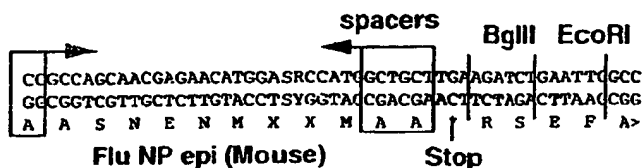
16810 16820 16830 16840 16850 pol 646-675 (77) 16880
TGGGCTCCAGGGAAGTGGAAAGGTTTGGCTTCCCACTATGCGCTCGGCATCATCCWAGCCCAACCCGATARGTCCGAGTC
ACCCGGAGGTCCCTTGACCTTTCCAAACGAGGGTATACGGGAGCCGTAGTAGGWTCCGGTTGGGCTATYCAAGCTCAG
W A S R E L E R F A S Q Y A L G I I X A Q P D X S E S>

16890 16900 16910 16920 16930 16940 16950 16960
CGAGSTCGTGARTCAGATTATCGAAGCTCATCAAGAAGATTGCGGTGCGCGRAGGACAGACAGARTCATTGAGGTCG
GCTCSAGCACTYACTCTAATAGCTTBTGAGTAGTTCTTCTAACGGCAGCGGCTTMCCTGCTCTYAGTAACTCCAGC
E X V X Q I I E X L I K K I A V A X X T D R X I E V>

env 615-644 (177) 16990 17000 17010 17020 17030 17040
YCCAAAGGGCTKGGAGAGCCATTCTGATATCCCCASGAGAATCAGACAGCTCTCGCCGGAAGGTGGCCCGTCARG
RGGTTTCCCGAMCCTCTCGGTAAAGACTATAGGGGTSCTCTTACTCTGTTCTGAGCGGCTTCCACCGGCAGTYC
X Q R A X R A I L X I P X R I R Q T R L A G R W P V X>

17050 pol 811-840 (88) 17080 17090 17100 17110 17120
RYAATCCATACCGATAACGGAAGCAATTTACAAAGCRCTTCCGTCAAGGCTGCCCTGCTGGTGGGCTGATGTGARACAGCT
YRTTAGGTATGGCTATTGCTTTCGTAAAGTGTTCGYGAYGGCAGTTCCGACCGACGACCCACCGACTACACTYTGTCGA
X I H T D N G S N P T S X X V K A A C W W A D V X Q L>

17130 17140 pol 511-540 (68) 17170 17180 17190 spacers
CACCGMAGYCGTCCAGAAARTCGCTACCGAAAGCATTTGTATATGGGGAAGACACCCAAAGTTCARACTGCCATATGCTG
GTGGCKTRCGCAGGTCTTTTACGATGGCTTTCTGAACACTATACCCCTTCTGTGGGTTCAAGTYTGACGGATACCGAC
T X X V Q K X A T E S I V I W G K T P K F X L P I A>



↑ C7
Join
C8 ↓

FIGURE 15 (Cont)

SUBSTITUTE SHEET (RULE 26)

81/216

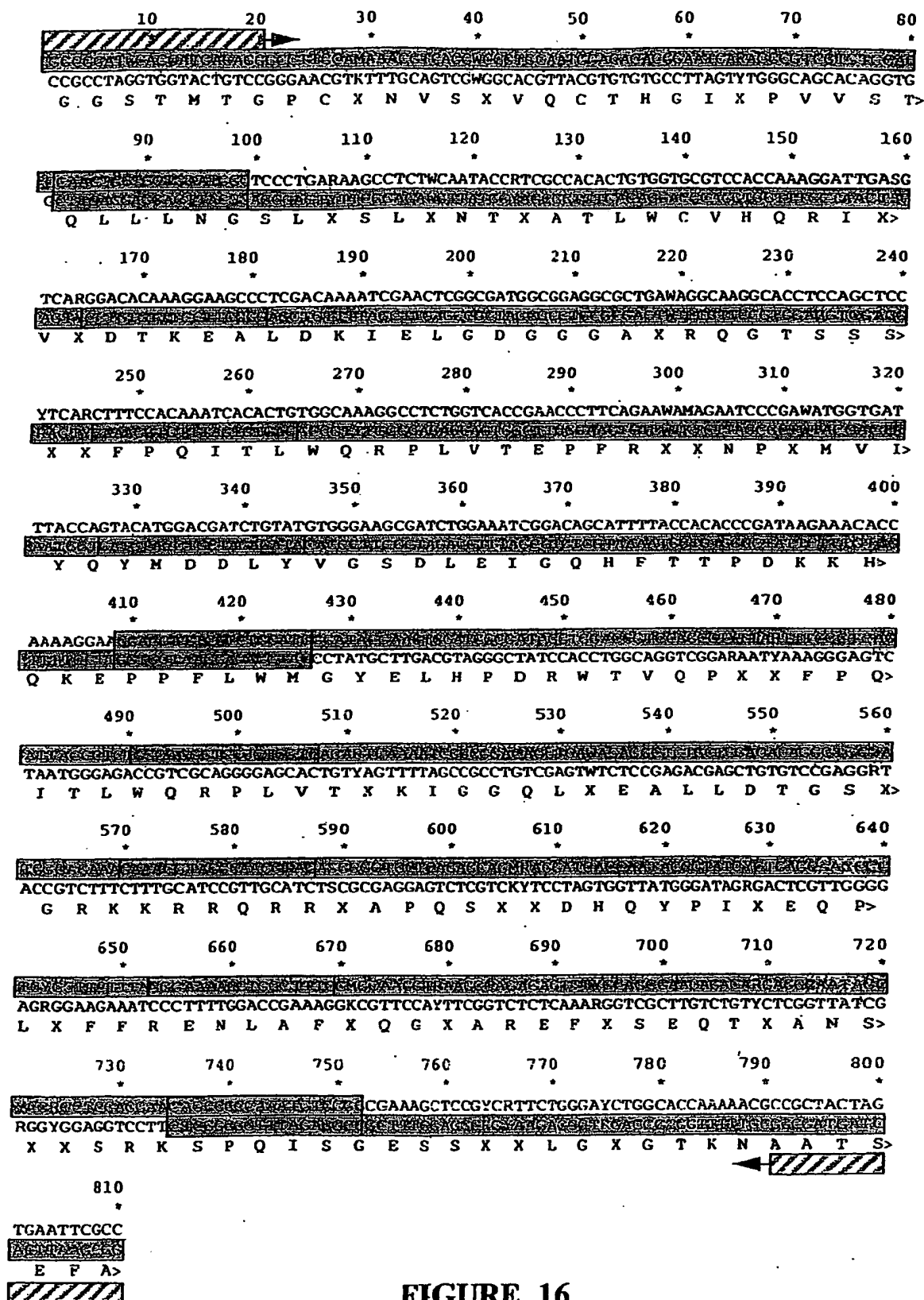
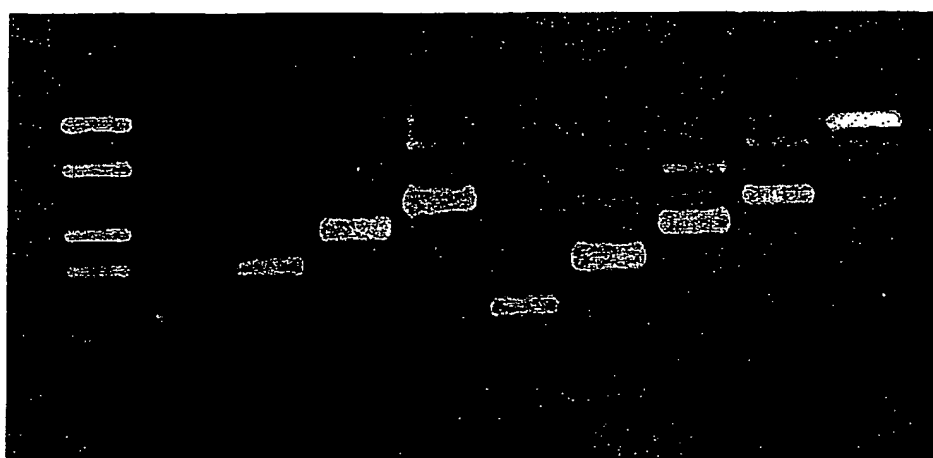


FIGURE 16

SUBSTITUTE SHEET (RULE 26)

82/216

A 1 2 3 4 5 6 7 8 9 10



B — A —||— B —||— C —|



FIGURE 17

83/216

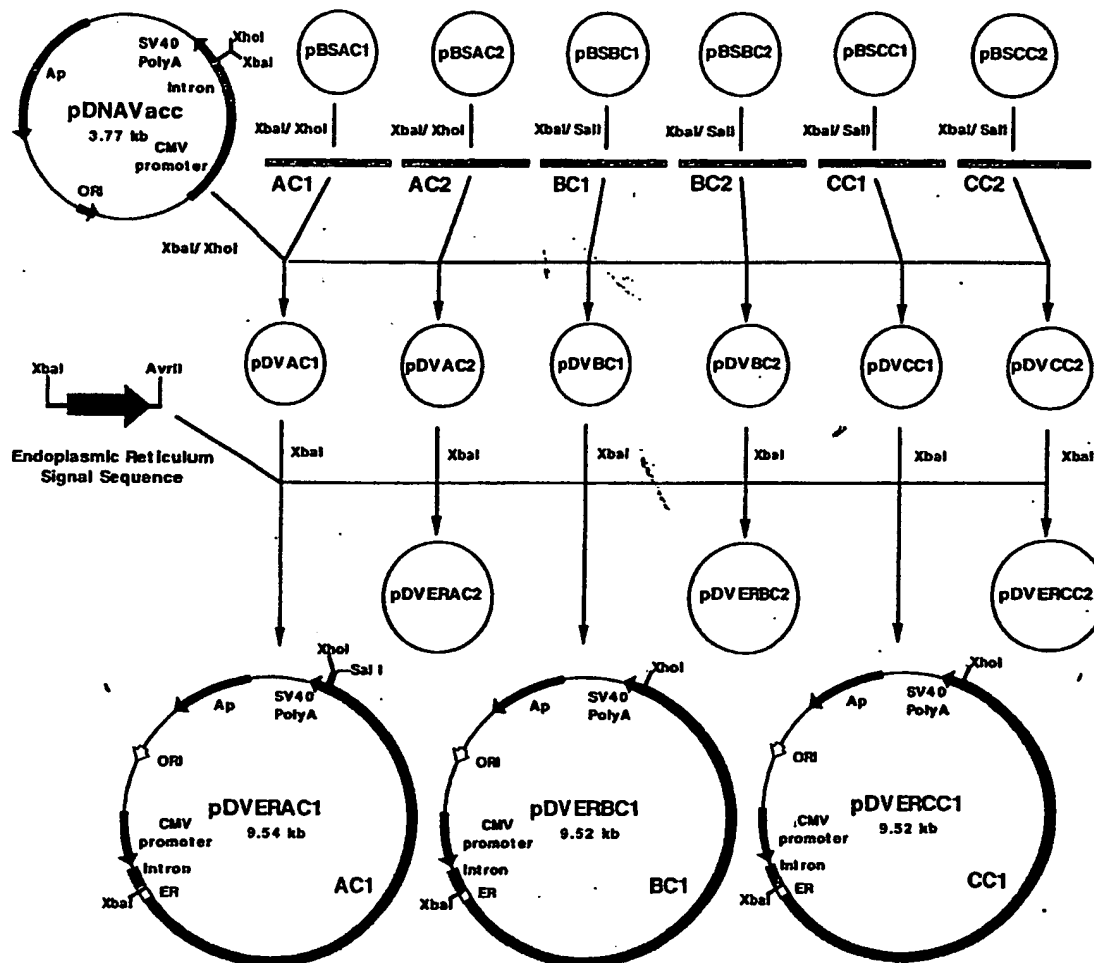


FIGURE 18A

84/216

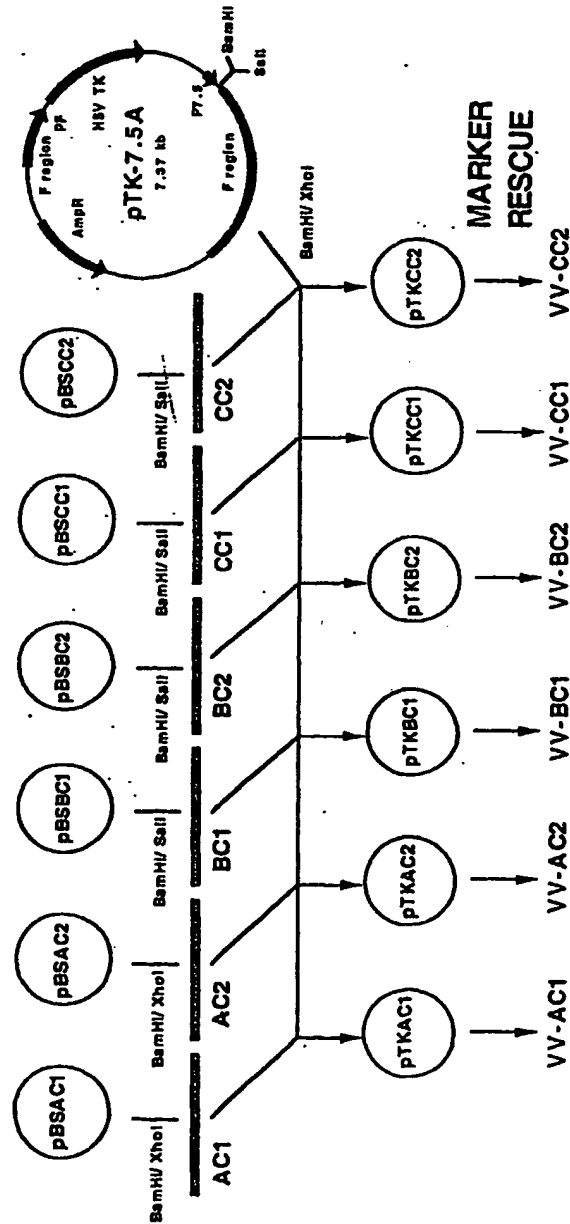


FIGURE 18B

85/216

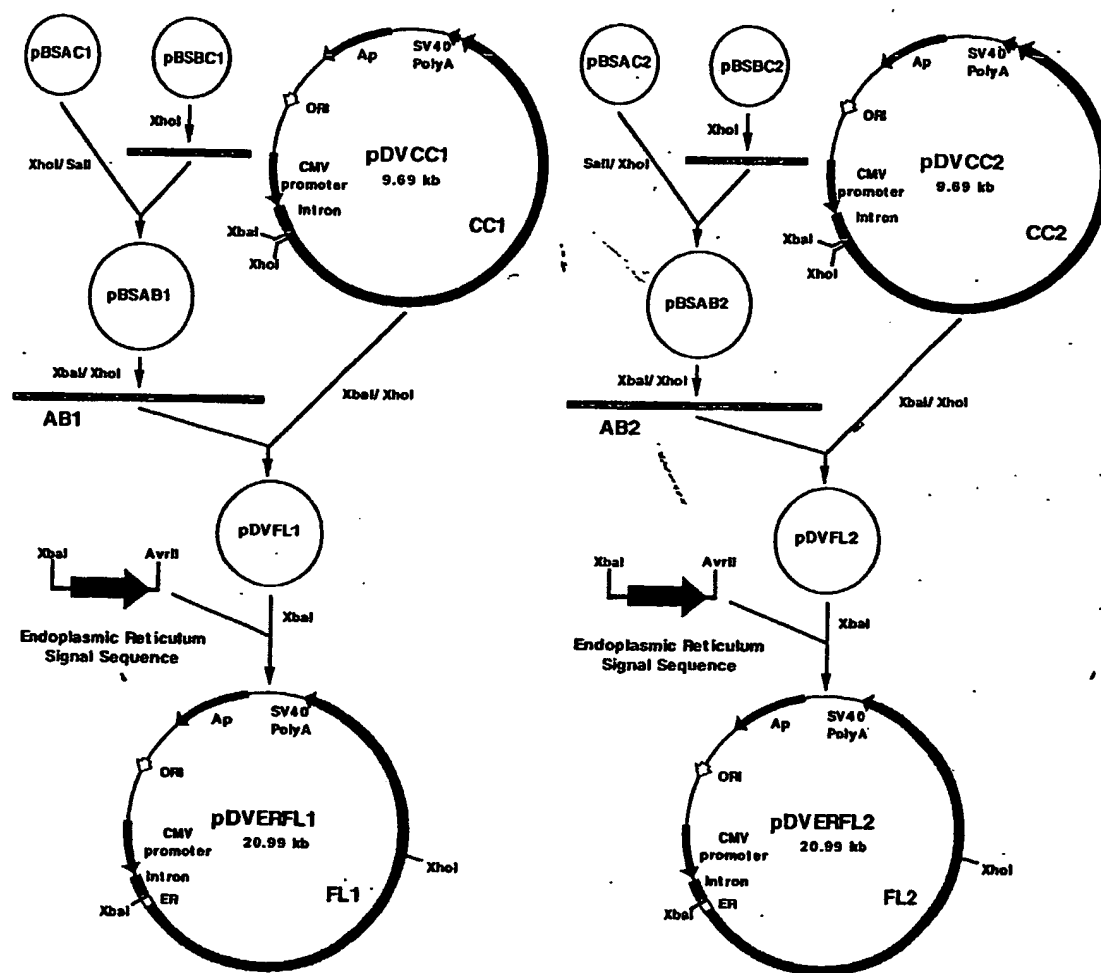
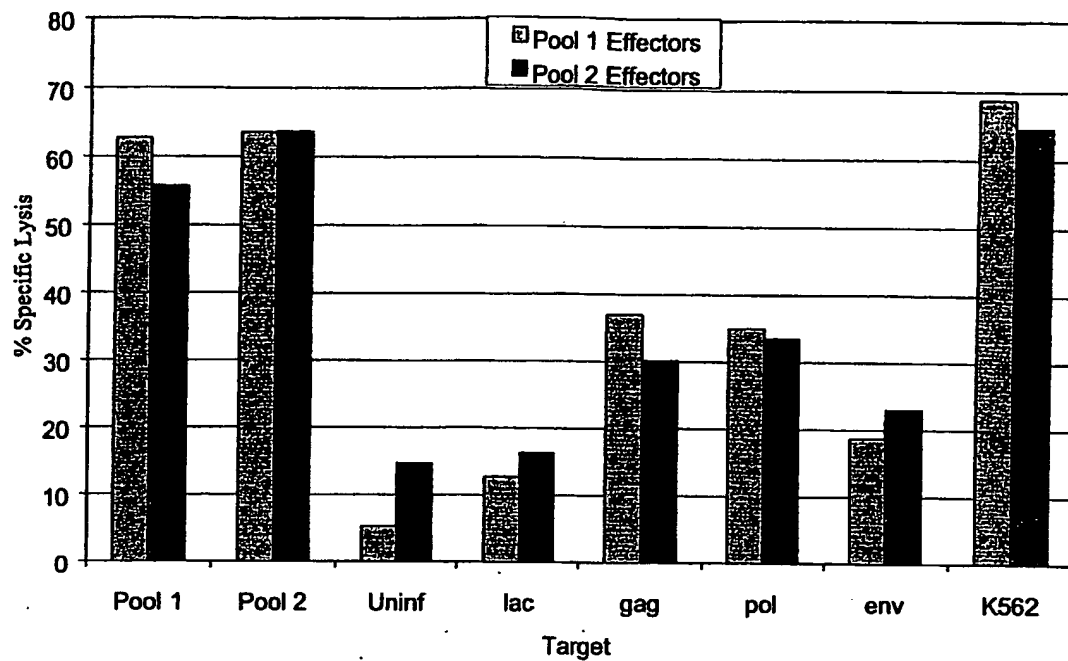


FIGURE 18C

86/216

Subject1



Subject2

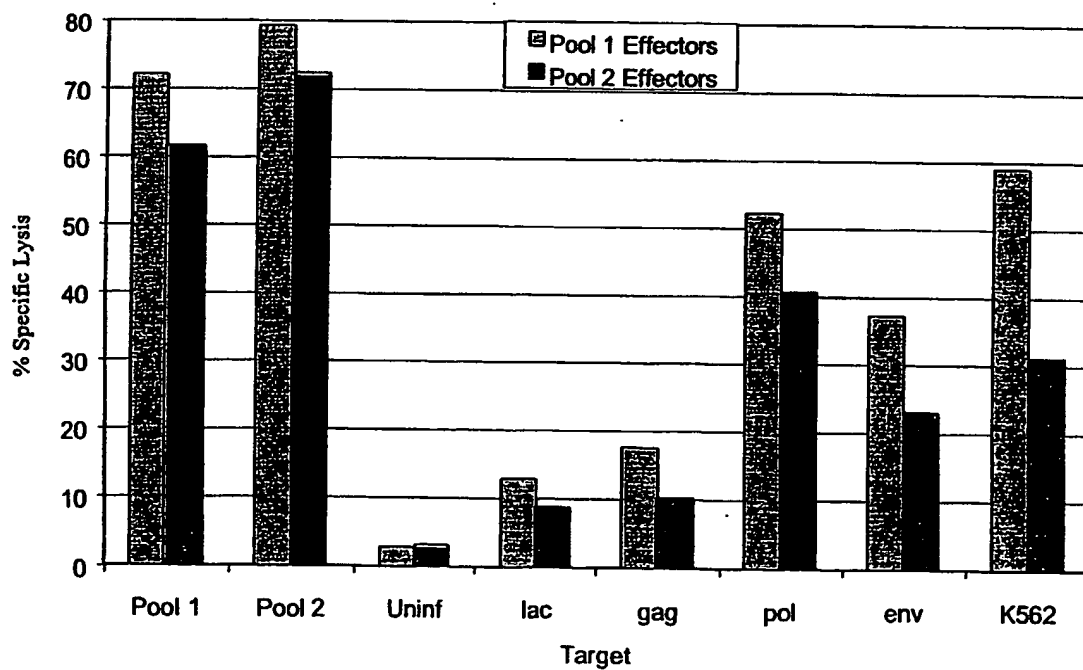


FIGURE 19

87/216

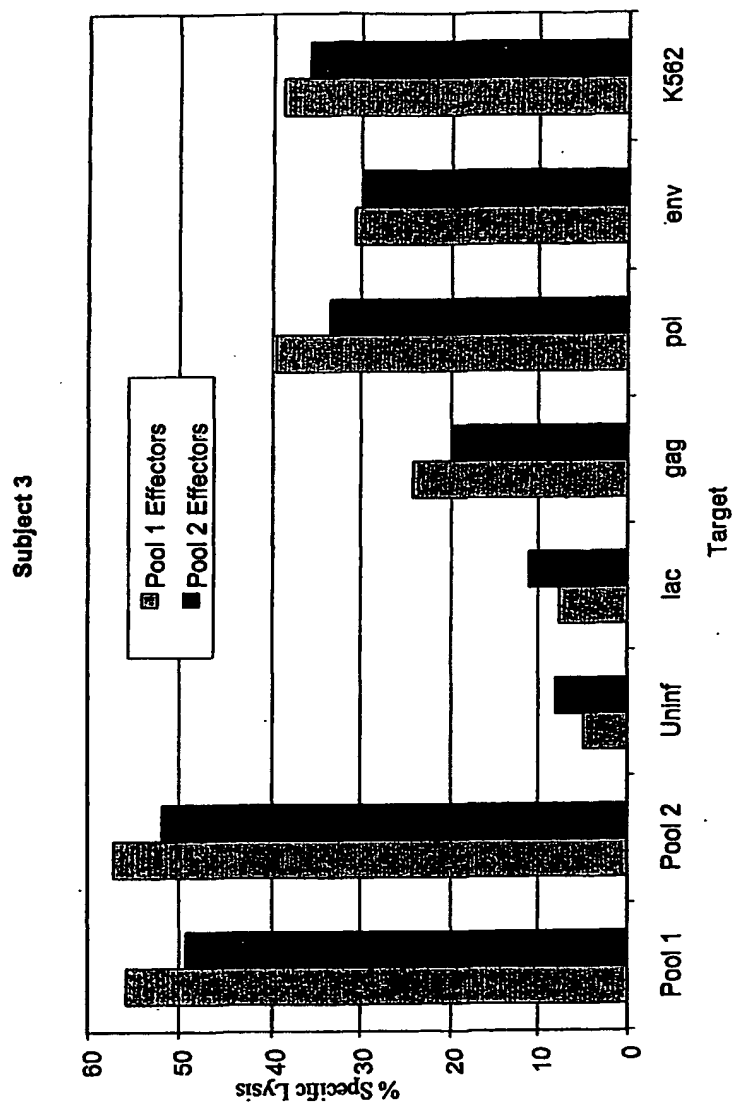


FIGURE 19 (Cont)

88/216

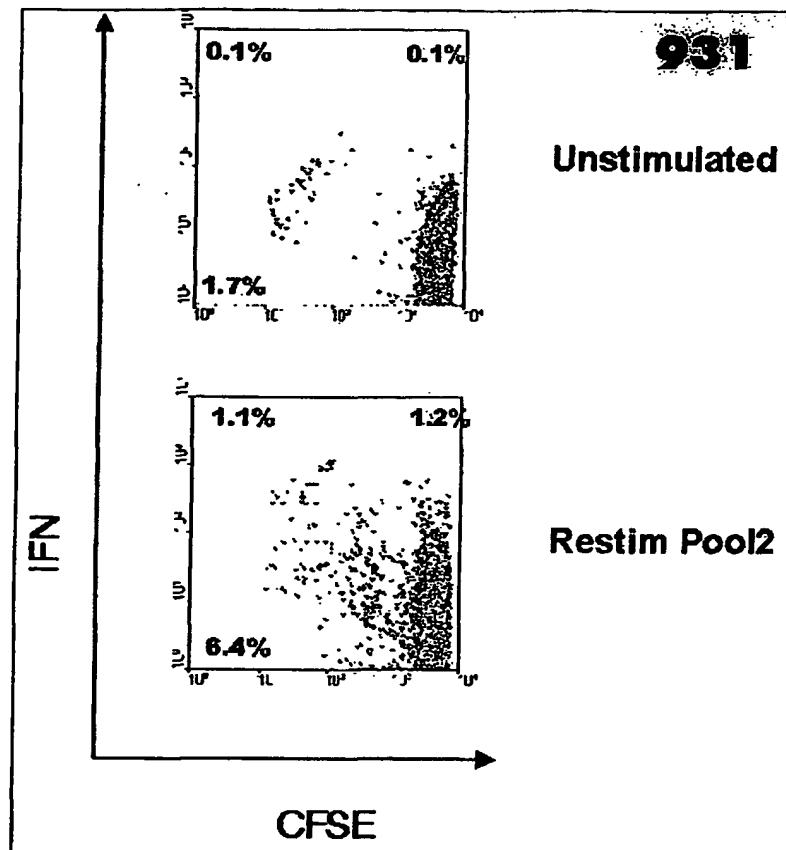


Figure 20

89/216

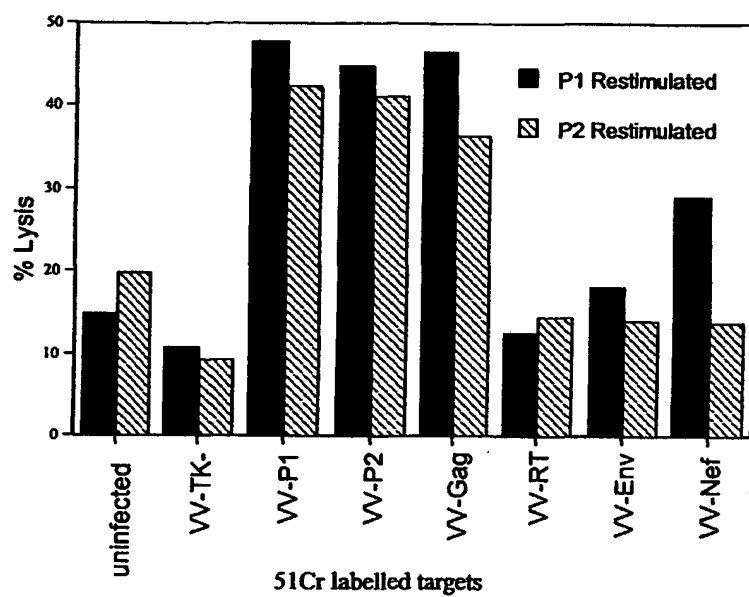


Figure 21

90/216

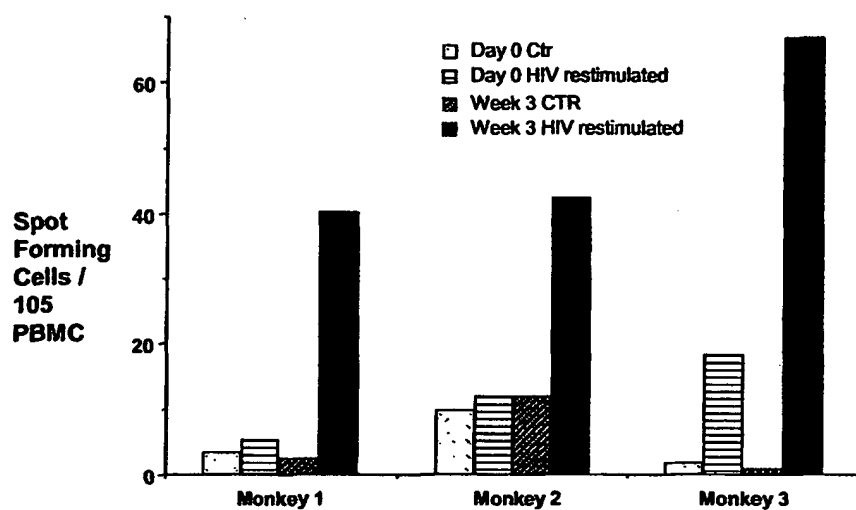


Figure 22A

91/216

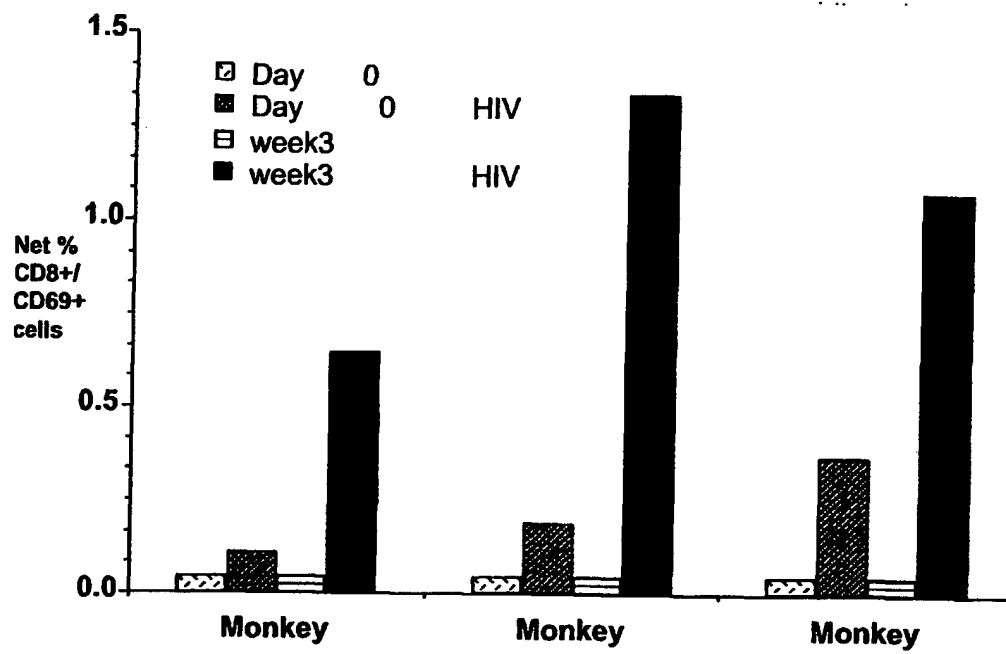


Figure 22B

92/216

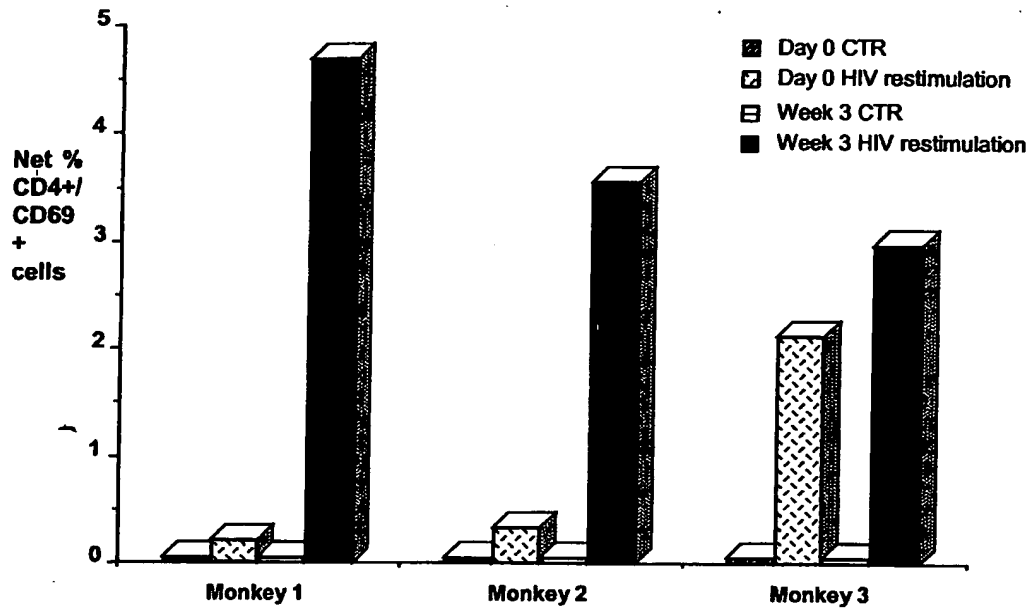


Figure 22C

93/216

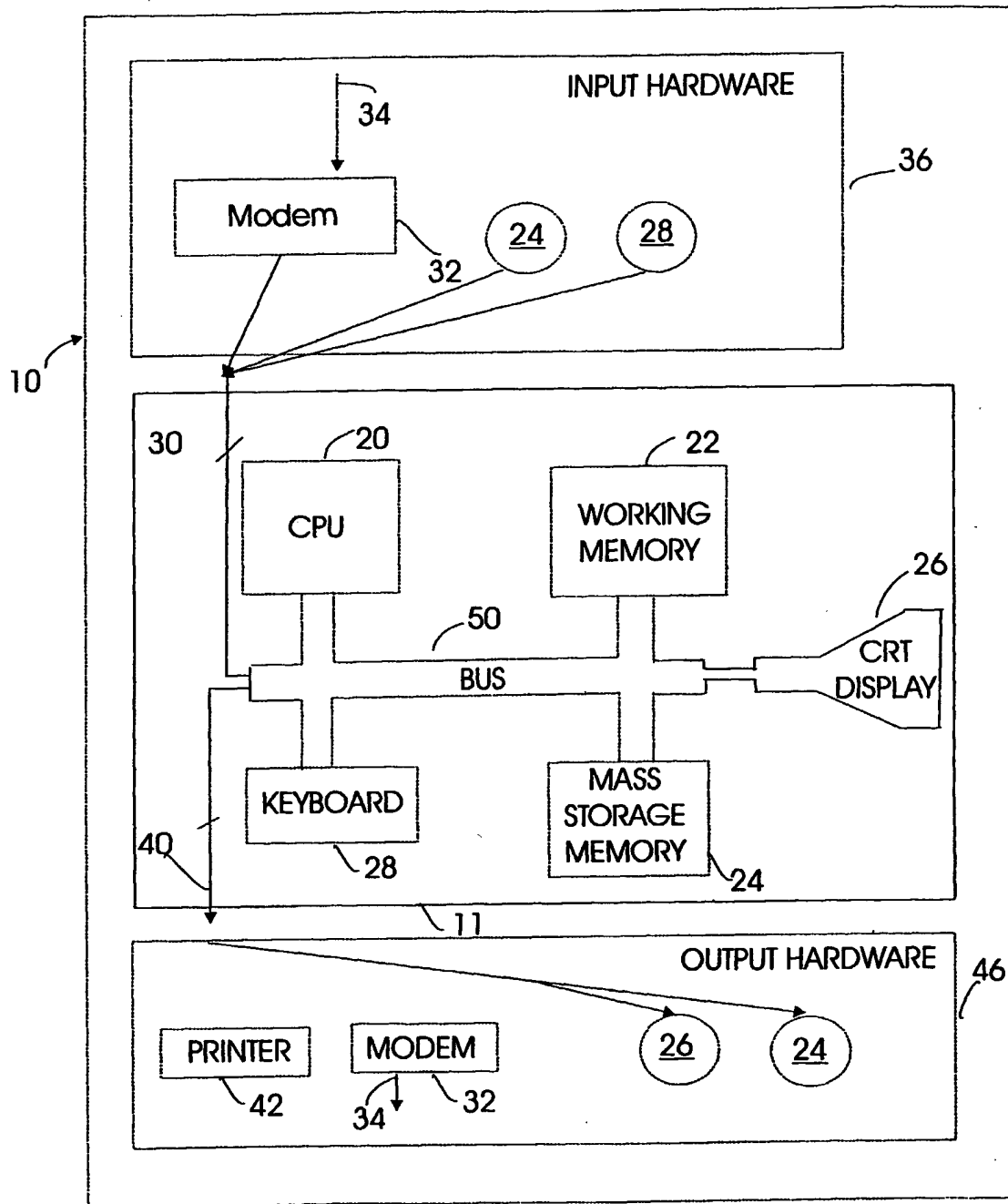


FIGURE 23

94/216

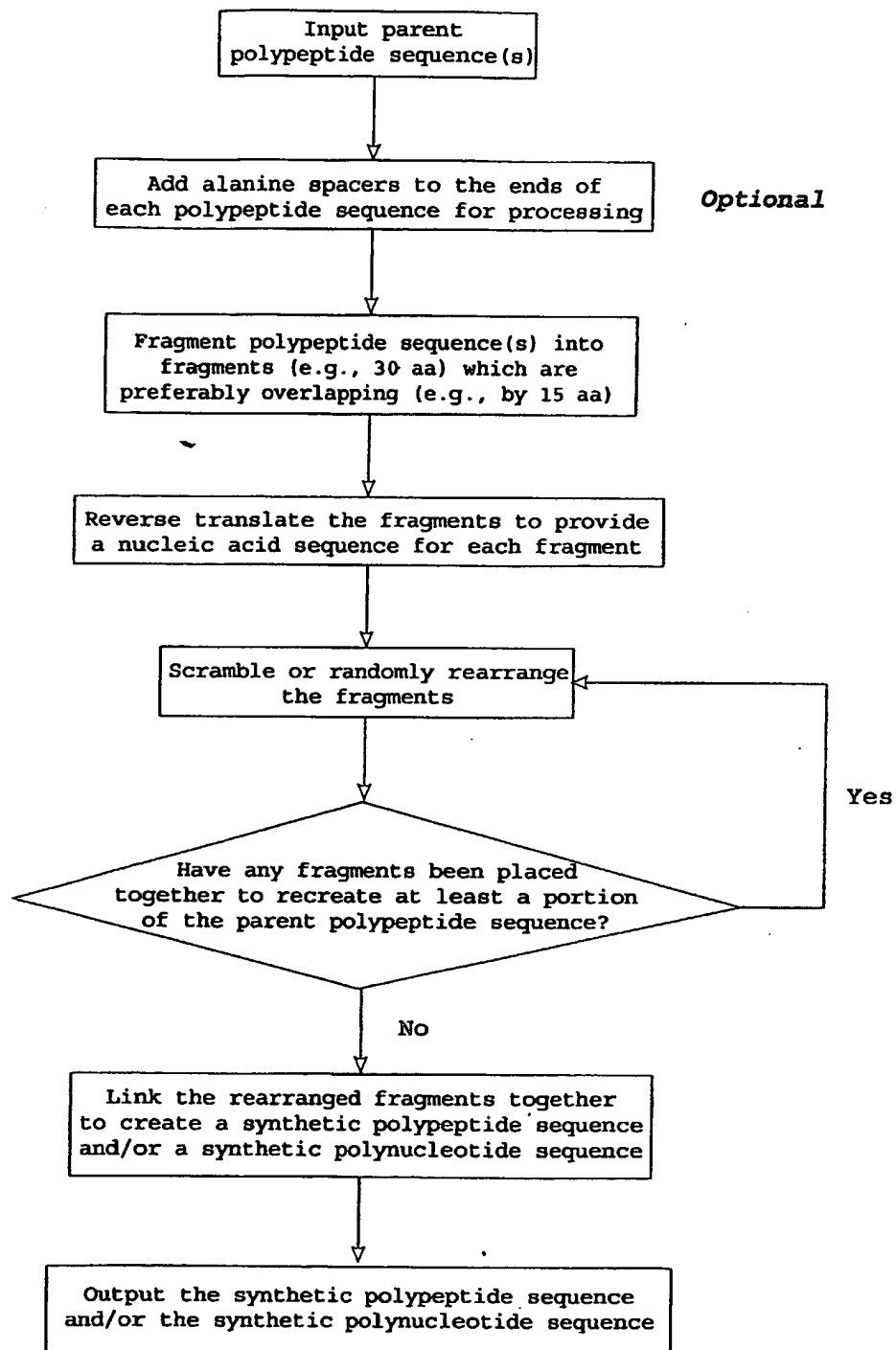


Figure 24

```

/* Scramble */
95/216

/* Includes */

#include <stdio.h>
#include <stdlib.h>
#include <string.h>
#include <time.h>

/* Constant definitions */

/* Version Information */
#define VERSION_NO "0.2"
#define VERSION_DATE "04/03/1999"

/* Misc */
#define KEYBOARD_BUFFER_SIZE 256 /*size of keyboard read buffer */
#define LEN_CODON 4 /*length of codon (including null) */
#define BUFFER_SIZE 10000 /*size of file read buffer */
#define TRUE 1 /*boolean true */
#define FALSE 0 /*boolean false */

/* Error codes */
#define E_NOERROR 0 /*no error */
#define E_NOINFILE 1 /*genes file not found */
#define E_MALLOC 2 /*memory allocation error */
#define E_FILEREAD 3 /*file read error */
#define E_CREATE_OUTPUT_FILE 4 /*error creating output file */
#define E_OVERLAP 5 /*segment overlap >= length */

/* Structure definitions */

typedef struct gene GENE;
typedef GENE * P_GENE;
typedef struct gene_segment GENE_SEGMENT;
typedef GENE_SEGMENT * P_GENE_SEGMENT;
struct gene {
    char * name;
    char * data;
    P_GENE next_gene;
};

struct gene_segment {
    P_GENE p_gene;
    int number;
    int offset;
    int first_codon_choice;
    char * amino_data;
    char * dna_data;
    P_GENE_SEGMENT next_seg;
};

```

Figure 25

/* Function prototypes */

96/216

```

int prolog();
int get_parameters();
int read_int(char * prompt);
int load_genes();
int add_gene(char * gene_name,char * gene_data);
void insert_gene(P_GENE * head,P_GENE new_gene);
int add_aa();
int split_genes();
int split_gene(P_GENE g);
int insert_segment(P_GENE_SEGMENT * head_seg,P_GENE_SEGMENT new_seg);
int convert_segments_aa_to_dna();
int convert_aa_to_dna(char * aa_ptr,char * dna_ptr,int first_choice);
char * codon(char acid_char,int preferred);
int perform_scramble();
int scramble_segments();
int adjacent_segments();
int display_genes();
int write_output_file();
void strip_newline(char * strip_str);
void pad_amino_string(char * amino_ptr, char * padded_ptr);
int even(int test_num);
void read_str(char * prompt,char * string);
char * read_nonblank_line(char * buf,int buf_size,FILE * in_file);
int user_confirmation();
void test();

```

/* Global variables */

```

char * codon_table[26][2] = {
/* A 00 */ {"GCC","GCT"},
/* - 01 */ {"???","???"},
/* C 02 */ {"TGC","TGT"},
/* D 03 */ {"GAC","GAT"},
/* E 04 */ {"GAG","GAA"},
/* F 05 */ {"TTC","TTT"},
/* G 06 */ {"GGC","GGA"},
/* H 07 */ {"CAC","CAT"},
/* I 08 */ {"ATC","ATT"},
/* - 09 */ {"???","???"},
/* K 10 */ {"AAG","AAA"},
/* L 11 */ {"CTG","CTC"},
/* M 12 */ {"ATG","ATG"},
/* N 13 */ {"AAC","AAT"},
/* - 14 */ {"???","???"},
/* P 15 */ {"CCC","CCT"},
/* Q 16 */ {"CAG","CAA"},
/* R 17 */ {"AGG","AGA"},
/* S 18 */ {"AGC","TCC"},
/* T 19 */ {"ACC","ACA"},
/* - 20 */ {"???","???"},
/* V 21 */ {"GTG","GTC"},
/* W 22 */ {"TGG","TGG"},

```

Figure 25 (Cont)

```

/* - 23 */ {"???", "???"},
/* Y 24 */ {"TAC", "TAT"},
/* - 25 */ {"???", "???"},
};

```

97/216

```

char * error_text[] = {
/* 00 */ ""
/* 01 */ "ERROR: Input file not found!"
/* 02 */ "ERROR: Memory allocation error"
/* 03 */ "ERROR: File read error"
/* 04 */ "ERROR: Could not create output file"
/* 05 */ "ERROR: Segment overlap must be less than segment length"
};

```

```

char disease_name[KEYBOARD_BUFFER_SIZE];
char input_file_name[KEYBOARD_BUFFER_SIZE];
char output_file_name[KEYBOARD_BUFFER_SIZE];
int num_genes = 0;
int num_segments = 0;
int len_segment;
int segment_overlap;
P_GENE first_gene = NULL;
P_GENE_SEGMENT first_segment = NULL;
P_GENE_SEGMENT * scrambled_segments = NULL;

```

```

/* Mainline */

```

```

void main() {
    int error = E_NOERROR;

    printf("Scramble - Version %s, %s\n\n", VERSION_NO, VERSION_DATE);

    /* Initial processing */
    if (!error)
        error = prolog();

    /* Get various program parameters from user */
    if (!error)
        error = get_parameters();

    /* Load genes from genes file */
    if (!error)
        error = load_genes();

    /* Add 'AA' to start and end of all genes */
    if (!error)
        error = add_aa();

    /* Split genes into overlapping chunks */
    if (!error)
        error = split_genes();

    /* Convert segment amino acid to dna */
    if (!error)
        error = convert_segments_aa_to_dna();
}

```

Figure 25 (Cont)

```

/* Scramble the segments */
if (!error)
    error = perform_scramble();

/* Write output file */
if (!error)
    error = write_output_file();

/* Show error if there was one */
if (error)
    printf("%s\n", error_text[error]);
}

/* prolog() */
/* Perform any initial processing required */

int prolog() {

    /* Seed the random number generator, using the system clock */
    /* Don't run the program more than once in the same second! */
    /* Or we'll get the same randomisation!!!!!!!!!!!!!!!!!!!! */
    srand(time(NULL));

    return E_NOERROR;
}

/* get_parameters() */
/* Ask for various parameters from the user (stdin) */
/* Disease name */
/* Input file name */
/* Output file name */
/* Segment length */

int get_parameters() {
    int valid;

    read_str("Enter disease name : ", disease_name);
    read_str("Enter input file name : ", input_file_name);
    read_str("Enter output file name : ", output_file_name);

    valid = FALSE;
    while (!valid) {
        len_segment = read_int("Enter segment length : ");
        if (len_segment % 2)
            printf("Segment length must be even!\n");
        else
            valid = TRUE;
    }
    segment_overlap = len_segment / 2;

    return E_NOERROR;
}

/* load_genes() */

```

98/216

Figure 25 (Cont)

/* Load the genes from the input file */

99/216

```

int load_genes() {
    FILE *input_file;
    char name_buf[BUFFER_SIZE];
    char data_buf[BUFFER_SIZE];
    int rc;

    /* Open genes file for reading */
    if (NULL == (input_file = fopen(input_file_name, "r")))
        return E_NOINFILE;

    printf("Loading genes from: %s\n", input_file_name);
    num_genes = 0;
    /* Read gene name */
    while (NULL != read_nonblank_line(name_buf, BUFFER_SIZE, input_file)) {
        /* Read the gene data */
        if (NULL != read_nonblank_line(data_buf, BUFFER_SIZE, input_file)) {
            /* Allocate memory for new gene and add to list */
            if (rc = add_gene(name_buf, data_buf))
                break;
        }
    }
    /* Close genes file */
    fclose(input_file);

    return rc;
}

```

/* add_gene() */

/* Allocate memory for new gene, then insert in list */

```

int add_gene(char *gene_name, char *gene_data) {
    P_GENE new_gene;

    /* Allocate storage for new gene */
    if (NULL == (new_gene = malloc(sizeof(GENE))))
        return E_MALLOCC;
    /* Initialise new gene */
    new_gene->next_gene = NULL;
    /* Allocate storage for gene name (+1 for null) */
    if (NULL == (new_gene->name = malloc(strlen(gene_name)+1)))
        return E_MALLOCC;
    /* Store gene name */
    strcpy(new_gene->name, gene_name);
    /* Allocate storage for gene data (+1 for null) */
    if (NULL == (new_gene->data = malloc(strlen(gene_data)+1)))
        return E_MALLOCC;
    /* Store gene data */
    strcpy(new_gene->data, gene_data);
    /* Insert the new gene into linked list */
    insert_gene(&first_gene, new_gene);
    /* Increment num_genes */
    num_genes++;
}

```

Figure 25 (Cont)

```

        return E_NOERROR;
    }

    /* insert_gene() */
    /* Insert gene into linked list */

    void insert_gene(P_GENE * head_gene, P_GENE new_gene) {
        P_GENE * cur_ptr = head_gene;

        while (NULL != (*cur_ptr))
            cur_ptr = &((*cur_ptr)->next_gene);

        *cur_ptr = new_gene;
    }

    /* add_aa() */
    /* Add 'AA' to the start and end of every gene */

    int add_aa() {
        P_GENE cur_gene = first_gene;
        char * new_data;

        while (NULL != cur_gene) {
            /* Allocate storage to fit the gene plus four characters */
            new_data = malloc(strlen(cur_gene->data)+5);
            /* Shift gene data to new storage, add "AA" */
            strcpy(new_data, "AA");
            strcat(new_data, cur_gene->data);
            strcat(new_data, "AA");
            /* Free previous gene data storage */
            free(cur_gene->data);
            /* Set gene data pointer to new storage */
            cur_gene->data = new_data;
            /* Advance to next gene */
            cur_gene = cur_gene->next_gene;
        }

        return E_NOERROR;
    }

    /* split_genes() */
    /* Split the genes into overlapping segments */

    int split_genes() {
        P_GENE cur_gene = first_gene;
        P_GENE_SEGMENT cur_seg = first_segment;

        printf("Splitting genes into segments...\n");

        /* Split the genes into segments */
        while (NULL != cur_gene) {
            /* Split the gene */
            split_gene(cur_gene);
            /* Advance to next gene */
        }
    }

```

Figure 25 (Cont)

101/216

```

        cur_gene = cur_gene->next_gene;
    }

    /* Count the number of segments */
    num_segments = 0;
    cur_seg = first_segment;
    while (NULL != cur_seg) {
        num_segments++;
        cur_seg = cur_seg->next_seg;
    }

    return E_NOERROR;
}

/* split_gene() */
/* Split a gene into overlapping segments */

int split_gene(P_GENE g) {
    char * seg_ptr;
    char * seg_buf;
    P_GENE_SEGMENT new_segment = NULL;
    int done;
    int seg_ctr = 0;

    /* Allocate memory for segment buffer */
    if (NULL == (seg_buf = malloc(len_segment+1)))
        return E_MALLOC;

    /* Insert a null at the end of the segment buffer, */
    /* so we can use it as a string */
    seg_buf[len_segment] = '\0';

    /* Set segment pointer to start of gene data */
    seg_ptr = g->data;

    done = FALSE;
    while (!done) {
        /* So we know if we copied data */
        seg_buf[0] = '\0';

        /* Copy a segment of gene data to the segment buffer */
        memcpy(seg_buf, seg_ptr, len_segment);

        /* If there was some gene data copied to the buffer */
        if (NULL != seg_buf[0]) {
            /* Allocate storage for a new segment */
            if (NULL == (new_segment = malloc(sizeof(GENE_SEGMENT))))
                return E_MALLOC;
            /* Increment segment counter */
            seg_ctr++;
            /* Setup the new segment */
            new_segment->p_gene = g;
            new_segment->number = seg_ctr;
            new_segment->offset = seg_ptr - g->data + 1;
            new_segment->next_seg = NULL;
        }
    }
}

```

Figure 25 (Cont)

102/216

```

        if (NULL == (new_segment->amino_data = malloc(len_segment+1)))
            return E_MALLOCC;
        if (NULL == (new_segment->dna_data = malloc(len_segment*3+1)))
            return E_MALLOCC;
        new_segment->amino_data[0] = '\0';
        new_segment->dna_data[0] = '\0';
        /* Copy segment data from buffer to new segment */
        strcpy(new_segment->amino_data, seg_buf);
        /* Insert new segment into chain from gene */
        insert_segment(&first_segment, new_segment);
    }

    /* If we didn't read a full segment, we are finished! */
    if (strlen(seg_buf) < len_segment)
        done = TRUE;
    /* Otherwise, advance segment pointer to next segment in buffer */
    else
        seg_ptr = seg_ptr + len_segment - segment_overlap;
}

/* insert_segment() */
/* Insert a segment node at the end of the list */

int insert_segment(P_GENE_SEGMENT * head_seg, P_GENE_SEGMENT new_seg) {
    P_GENE_SEGMENT * cur_ptr = head_seg;

    while (NULL != (*cur_ptr))
        cur_ptr = &((*cur_ptr)->next_seg);

    *cur_ptr = new_seg;
}

/* convert_segments_aa_to_dna */
/* Go thru segments, and for each, convert amino acids to dna */

int convert_segments_aa_to_dna() {
    P_GENE_SEGMENT cur_seg = first_segment;
    int first_choice = 1;
    int alternate;

    printf("Converting to DNA...\n");

    /* Work out if we need to alternate the first codon choice or not */
    /* Don't need to do this anymore, since the segment length is */
    /* forced to be even, and the overlap is half the length (odd). */
    /* alternate = ((even(len_segment) && even(segment_overlap))
        || (!even(len_segment) && !even(segment_overlap))); */
    alternate = FALSE;

    while (NULL != cur_seg) {
        cur_seg->first_codon_choice = first_choice;
        convert_aa_to_dna(cur_seg->amino_data, cur_seg->dna_data,
            cur_seg->first_codon_choice);
    }
}

```

Figure 25 (Cont)

103/216

```

        /* Address next segment */
        cur_seg = cur_seg->next_seg;

        /* If we are alternating, alternate the first codon choice */
        /*if (alternate)
            if (1 == first_choice)
                first_choice = 2;
            else
                first_choice = 1;*/
    }

    return E_NOERROR;
}

/* convert_aa_to_dna */
/* Converts a string of amino acid to dna */
/* NOTE: assumes that buffer at dna_ptr is large enough to hold dna!!! */
int convert_aa_to_dna(char * aa_ptr, char * dna_ptr, int first_choice) {
    char * p_codon;
    int cur_preferred = first_choice;

    while (*aa_ptr != '\0') {
        p_codon = codon(*aa_ptr, cur_preferred);
        strcat(dna_ptr, p_codon);
        /* If we didn't find a codon, log a warning */
        if (0 == strcmp(p_codon, "???\0"))
            printf("WARNING: no codon found for amino acid!\n");

        /* Alternate current preferred codon */
        if (1 == cur_preferred)
            cur_preferred = 2;
        else
            cur_preferred = 1;

        aa_ptr++;
    }

    return E_NOERROR;
}

/* codon */
/* Returns a pointer to a codon corresponding to the amino acid passed */
/* The codon pointer is to 3 characters, plus a terminating null */
char * codon(char acid_char, int preferred) {
    int codon_table_index;
    char * codon_ptr;

    /* Determine index into codon_table (table starts at 'A') */
    codon_table_index = acid_char - 'A';

    /* Set pointer to appropriate codon */
    codon_ptr = codon_table[codon_table_index][preferred-1];

```

Figure 25 (Cont)

104/216

```

        return codon_ptr;
    }

/* display_genes() */
/* Display the name and data for all genes */

int display_genes() {
    P_GENE cur_gene = first_gene;

    while (NULL != cur_gene) {
        printf("%s\n", cur_gene->name);
        printf("%s\n", cur_gene->data);
        cur_gene = cur_gene->next_gene;
    }

    return E_NOERROR;
}

/* perform_scramble() */
/* Scramble the segments */
/* Check for adjacent segments. If there are, rescramble */

int perform_scramble() {
    int done = FALSE;
    int rc = E_NOERROR;

    while (TRUE) {
        rc = scramble_segments();
        if (E_NOERROR == rc)
            if (adjacent_segments()) {
                printf("Adjacent segments detected! Rescramble? (y/n) ");
                if (!user_confirmation()) {
                    printf("WARNING: Adjacent segments in output
file.\n");
                    break;
                }
            }
            else
                break;
        else
            break;
    }

    return rc;
}

/* scramble_segments() */
/* Randomly scramble the segments, putting pointers in scrambled_segments[] */

int scramble_segments() {
    P_GENE_SEGMENT cur_seg = first_segment;
    int i, j;
    P_GENE_SEGMENT temp;

    printf("Scrambling segments...\n");

```

Figure 25 (Cont)

105/216

```

/* Allocate storage for array of segment pointers */
if (NULL == (scrambled_segments = malloc(sizeof(P_GENE_SEGMENT)*num_segments)))
    return E_MALLOC;

/* First, initialise scrambled_segments in same order as linked list */
i = 0;
while (cur_seg != NULL) {
    scrambled_segments[i] = cur_seg;
    cur_seg = cur_seg->next_seg;
    i++;
}

/* Now, randomly scramble the segments */
for (i=0;i<num_segments;i++) {
    j = rand() % num_segments;
    temp = scrambled_segments[i];
    scrambled_segments[i] = scrambled_segments[j];
    scrambled_segments[j] = temp;
}

return E_NOERROR;
}

/* adjacent_segments() */
/* Determine if the scrambled segment order has resulted in */
/* two segments which were adjacent originally (ie every */
/* second one) have ended up adjacent. */

int adjacent_segments() {
    int i;
    int rc = 0;
    P_GENE_SEGMENT cur_seg;
    P_GENE_SEGMENT next_seg;

    for (i=0;i<num_segments-1;i++) {
        /* Address current and next segments */
        cur_seg = scrambled_segments[i];
        next_seg = scrambled_segments[i+1];
        /* Do segments come from same gene, and are two apart? */
        if (((cur_seg->p_gene == next_seg->p_gene)
            && ((cur_seg->number == (next_seg->number)+2)
            || (cur_seg->number == (next_seg->number)-2))))
            return 1;
    }
    return 0;
}

/* write_output_file() */
/* Write out segments (in initial non-scrambled order) */
/* Write out synthetic protein (in scrambled order) */
/* Write out synthetic dna (in scrambled order) */

int write_output_file() {
    FILE * output_file;

```

Figure 25 (Cont)

106/216

```

char * amino_buffer;
P_GENE_SEGMENT cur_seg;
int i;

/* Open output file for writing (erase any contents) */
if (NULL == (output_file = fopen(output_file_name, "w")))
    return E_CREATE_OUTPUT_FILE;

/* Allocate memory for padded amino string buffer */
if (NULL == (amino_buffer = malloc(len_segment*3+1)))
    return E_MALLOC;

printf("Writing output file: %s\n", output_file_name);

/* Write output file header information */
fprintf(output_file, "Scramble %s - Output File\n", VERSION_NO);
fprintf(output_file, "\n");
fprintf(output_file, "Disease name   : %s\n", disease_name);
fprintf(output_file, "Input filename  : %s\n", input_file_name);
fprintf(output_file, "Output filename : %s\n", output_file_name);
fprintf(output_file, "Number genes    : %d\n", num_genes);
fprintf(output_file, "Number segments : %d\n", num_segments);
fprintf(output_file, "Segment length  : %d\n", len_segment);
fprintf(output_file, "Segment overlap : %d\n", segment_overlap);

/* Write out segments in initial non-scrambled order */
fprintf(output_file, "\n");
fprintf(output_file, "Segments in original order:\n");
fprintf(output_file, "-----\n");
cur_seg = first_segment;
while (NULL != cur_seg) {
    /* Format amino data to line up with codons */
    pad_amino_string(cur_seg->amino_data, amino_buffer);
    fprintf(output_file, "Gene      : %s\n", cur_seg->p_gene->name);
    fprintf(output_file, "Segment#  : %d\n", cur_seg->number);
    fprintf(output_file, "Offset    : %d\n", cur_seg->offset);
    fprintf(output_file, "1st Codon : %d\n", cur_seg->first_codon_choice);
    fprintf(output_file, "%s\n", amino_buffer);
    fprintf(output_file, "%s\n", cur_seg->dna_data);
    fprintf(output_file, "\n");
    cur_seg = cur_seg->next_seg;
}

/* Write out segment names in scrambled order */
fprintf(output_file, "Segments in scrambled order:\n");
fprintf(output_file, "-----\n");
for (i=0; i<num_segments; i++) {
    /* Format amino data to line up with codons */
    pad_amino_string(scrambled_segments[i]->amino_data, amino_buffer);
    /* Write segment details */
    fprintf(output_file, "%s # %d\n", scrambled_segments[i]->p_gene->name,
            scrambled_segments[i]->number);
    fprintf(output_file, "%s\n", amino_buffer);
    fprintf(output_file, "%s\n", scrambled_segments[i]->dna_data);
    fprintf(output_file, "\n");
}

```

Figure 25 (Cont)

107/216

```

    }

    /* Write synthetic protein in one long string */
    fprintf(output_file,"Synthetic Protein:\n");
    fprintf(output_file,"-----\n");
    for (i=0;i<num_segments;i++)
        fprintf(output_file,"%s",scrambled_segments[i]->amino_data);

    fprintf(output_file,"\n\n");

    /* Write synthetic dna in one long string */
    fprintf(output_file,"Synthetic DNA:\n");
    fprintf(output_file,"-----\n");
    for (i=0;i<num_segments;i++)
        fprintf(output_file,"%s",scrambled_segments[i]->dna_data);

    return E_NOERROR;
}

/* strip_newline() */
/* Replace the first newline character with a null */

void strip_newline(char * strip_str) {
    char * newline_pos;

    /* Find the newline char */
    newline_pos = strchr(strip_str,'\n');

    /* If we found one, replace it with a null */
    if (NULL != newline_pos)
        newline_pos[0] = '\0';
}

/* pad_amino_string */
/* Copy amino chars from amino_ptr to padded_ptr, padding each */
/* side with a space. */

void pad_amino_string(char * amino_ptr, char * padded_ptr) {
    while ('\0' != *amino_ptr) {
        *padded_ptr = ' ';
        padded_ptr++;
        *padded_ptr = *amino_ptr;
        padded_ptr++;
        *padded_ptr = ' ';
        padded_ptr++;
        amino_ptr++;
    }

    /* Stick a null at the end of the padded string */
    *padded_ptr = '\0';
}

/* even() */
/* True if test_num is even, otherwise false */

```

Figure 25 (Cont)

108/216

```

int even(int test_num) {
    return !(test_num % 2);
}

/* read_int() */
/* Read an integer from stdin. Keep trying until valid int > 0 entered. */
/* Return the integer read, or 0 if error reading from stdin. */

int read_int(char * prompt) {
    char buffer[KEYBOARD_BUFFER_SIZE];
    int value_read;
    int valid = FALSE;

    while (!valid) {
        printf("%s",prompt);
        valid = TRUE;
        fgets(buffer,KEYBOARD_BUFFER_SIZE,stdin);
        if (1 != sscanf(buffer,"%d",&value_read))
            valid = FALSE;
        if (valid && (value_read < 1))
            valid = FALSE;
        if (!valid)
            printf("Positive integer value please!\n");
    }

    return value_read;
}

/* read_str() */
/* Read a string from the user (stdin) */
/* Strip the newline from it */

void read_str(char * prompt,char * string) {
    char buffer[KEYBOARD_BUFFER_SIZE];

    printf(prompt);
    fgets(buffer,KEYBOARD_BUFFER_SIZE,stdin);
    sscanf(buffer,"%s",string);
}

/* read_nonblank_line() */
/* Read a line from file until we get a non-blank one */

char * read_nonblank_line(char * buf,int buf_size,FILE * in_file) {
    char * return_ptr;

    /* Read lines until we get a non-black one, or EOF */
    do
        return_ptr = fgets(buf,buf_size,in_file);
    while ((NULL != return_ptr) && ((' ' == buf[0]) || ('\n' == buf[0])));

    /* If we got a line, change the newline char to a null */
    if (NULL != return_ptr)
        strip_newline(buf);
}

```

Figure 25 (Cont)

109/216

```
        return return_ptr;
    }

    /* user_confirmation() */
    /* Read input from user. If user types 'y', return 1, otherwise 0 */
    int user_confirmation() {
        char buffer[KEYBOARD_BUFFER_SIZE];

        fgets(buffer, KEYBOARD_BUFFER_SIZE, stdin);
        if (('y' == buffer[0]) || ('Y' == buffer[0]))
            return 1;
        else
            return 0;
    }

    /* test() */
    /* For debugging/development */
    void test() {
        char str[100];
        printf("Enter something: ");
        fgets(str, 100, stdin);
        printf("line1\n");
        printf("%s", str);
        printf("line2\n");
        fgets(str, 100, stdin);
    }
}
```

Figure 25 (Cont)

110/216

HepC Savine design

HepC 1a consensus polyprotein sequence used for scramble program

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGRRQPIPKARRPEGRTWAO
 PGYPWPLYGNEGCGWAGWLLSPRGSRPSWGPTDPRRSRNLGKVIDTLTCGFADLMGYIPLVGAPLGGAAARALAHGVR
 VLEDGVNYATGNLPGCSFSIFLLALLSCLTVPASAYQVRNSTGLYHVTNDCPNSSIVYEAADAILHTPGCVPCVREGN
 ASRCWVAMTPTVATRDGKLPATQLRRHIDLLVGSATLCSALYVGDLCGSVFLVGQLFTFSPRRHWTTQGCNCSIYPGH
 ITGHRMAWDMMNWSPTAALVMAQLLRIPQAILDMIAGAHWGLAGIAYFSMVGNWAKVLVLLLLFAGVDAETHVTGG
 NAGRTTSGLVSLTTPGAKQNIQLINTNGSWHINSTALNCNESLNTGWLGLFYQHKNSSGCPERLASCRRLTDFDQG
 WGPISYANGSGPDQRPYCWHPKPCGIVPAKSVCGPVYCFPTSPVVVGTTDRSGAPTYSWGANDTVFVLNNTRPPL
 GNWFGCTWMNSTGFTKVCGAPPCVIGGAGNNTLHCPTDCFRKHPEATYSRCGSGPWITPRCLVDYYPRLWHYPCTINY
 TIFKVRMYVGGVEHRLEAACNWRGERCDLEDRDRSELSPLLLSTTQWQVLPSCPTTLPALSTGLIHLHQNIVDVQYL
 YGVGSSIASWAIKWEYVVLFLLLADARVCSCLWMLLLISQAEAALENLVILNAASLAGTHGLVSFLVFFCFAWYLKG
 RWVPGAVYALYGMWPLLLLLLALPQRAYALDTEVAASCGGVVLVGLMALTLSPYKRYISWCLWWLQYFLTRVEAQLH
 VWVPPNLNVRGGRDAVILLMCVVHPTLVFDITKLLAVFGPLWILQASLLKVPYFVRVQGLLRICALARKMIGGHYVQM
 AI IKLGALTGTYYVNHLPRLDWAHNGLRDLAVAVEPVVFSQMETKLI TWGADTAACGDIINGLPVSARRGREILLGP
 ADGMVSKGWRLLAPITAYAQQTGRLLGCIITSLTGRADKNQPPSVDQMWKCLIRLKPTLHGPTLLYRLGAVQNEVTLT
 PKGPVIQMYTNDQDLVGWPAPQGSRLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPI SYLKGSSGGPLL
 CPAGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMRSPVFTDNSSPPAVPQSFQVAHLHAPTGSKGSTKVPAAAYAAQ
 YKVLVLNPSVAATLGFAYMSKAHGIDPNIRGTGVRTITTGSPITYSTYKGLADGGCSGGAYDIIICDECHSTDATSI
 LGIGTVLDQAGTAGARLVVLTATPPGSVTVPHPNIEEVALSTTGEIPFYGKAI PLEVIKGGRHILIFCHSKKKCDELA
 AKLVALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDSVIDCNTCVTQTVD FSLDPTFTIETTTLPQDAV
 SRTQRRGRTGRGKPGIYRFVAPGERPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPLPVCQDHLFEWEG
 VFTGLTHIDAHFLSQTKQSGENFPYLVAQATVCARAQAPPSPWDQMWKCLIRLKPTLHGPTLLYRLGAVQNEVTLT
 HPVTKYIMTMSADLEVVTSTWVLVGGVLAALAAAYCLSTGCVVIVGRIVLSGKPAIIPDREVLVREFDEMEECSSQHL
 YIEQGMMLAEQFKQKALGLLQTASRQAEVIAPAVQTNWQKLEVFVWAKHMWNFISGIQYLAGLSTLPGNPAIASLMAFT
 AAVTSPLTTSQTLLFNILGGWVAAQLAAPGAATAFVGAGLAGAAIGSVGLKVLVDILAGYAGVAGALVAFKIMSGE
 VPSTEDLVNLLPAILSPGALVVGVCACILRRHVGPGEVAVQWMNRLIAFASRGNHVSPTHYVPESDAAARVTAILSS
 LTVTQLLRLLHQWISSECTTPCSGSLRDIWDWICEVLSDFKTWLAKALMPQLPGIPFVSCQRGYKGVWRGDGIMHTR
 CHCGAEITGHVKNGTMRIVGPRTCRNMWSGTFPINAYTTGFPCTPLPAPNYTFALWRVSAEYVEIRRVGDFHYVTGMT
 TDNLKCPQVPSPEFFTEL DGVRLHRFAPPCKPLLRREEVSFRVGLHEYPVGSQLPCEPEPDVAVLTSMLTDP SHITAE
 AAGRRLARGSPPSMASSASQLSAPSLKATCTANHDSFDAELIEANLLWRQEMGNITRVESENKVILDSFDPLVAE
 EDEREISVPABILRKSRRFAQALPVWARPDYNPPLVETWKKPDYEPPVHGCPLPPPRSPVPPPRKKRTVVLTSTL
 STALAEATKSFSGSSSTGITGDNSTTSSEPAPSGCPPDSDAESYSSMPLEGEPEGDPDLSDGSWSTVSSEAGTEDVV
 CCSMSYSWTGALVTPCAAEEQKL PINALSNSLLRHNLVYSTTSRSACQRQKVTFDRLQVLD SHYQDVLKEVKAAAS
 KVKANLLSVEEACSLTPPHSAKSKFGYGAQDVRCARKAVAHINSVWKDLED SVTPI DTTIMAKNEVFCVQPEKGG
 KPARLIVFPDLGVVCEKMALYDVVSKLPLAVMGSSYGFQYSPGQRFVFLVQAWKSKKTPMGFSYDTRCFDSTVTESD
 IRTERAIYQCCDLDPQARVAIKSLTERLYVGGPLTNSRGYNGCYRRRCRAGSVLTTSCGNLTTCYIKARAACRAAGLQD
 CTMLVCGDDL VVICESAGVQEDAASLRAFTEAMTRYSAAPPDPPQPEYDLELITSCSSNVSAHDGAGKRVYLLTRDP
 TTPLARAAWETARHTPVNSWLGNIIMFAPTLWARMILMTHFFSVLIARDQLEQALDCEIYGACYSIEPLDLPPIIQRL
 HGLSAFSLHSYSPGEINRVAACLRLKLGVPPLRAWHRARSVRARLLARGGAAICGKYLFWAVRTKLKLTPIAAAGR
 LDLSGWFTAGYSGGDIYHSVSHARPRWFVFCLLLLAAGVGIYLLPNR

Scramble - Output File

Scramble version : 0.1 beta, 08/02/1999

Num. genes : 1
 Num. segments : 201
 Segment length : 30
 Segment overlap : 15

Segments in original order:

 Gene : HepC1a
 Segment# : 1
 Offset : 1
 1st Codon : 1

A A M S T N P K P Q R K T K R N T N R R P Q D V K F P G G G
 GCCGCTATGTCCACCAATCCCAACCCAAAGGAAAACCAAAAGGAATACCAATAGGAGACCCCAAGACGTCAAGTTTCCCGAGGCGGA

Figure 26

111/216

Gene : HepC1a
Segment# : 2
Offset : 16
1st Codon : 1
N T N R R P Q D V K F P G G G Q I V G G V Y L L P R R G P R
AACACAAACAGAAGGCCTCAGGATGTGAAATTCCTGGCGGAGGCCAAATCGTCGGCGGAGTGTATCTGCTCCCAGAGGGGACCCAGA

Gene : HepC1a
Segment# : 3
Offset : 31
1st Codon : 1
Q I V G G V Y L L P R R G P R L G V R A T R K T S E R S Q P
CAGATTGTGGGAGGCGTCTACCTCTGCCTAGGAGAGGCCCTAGGCTCGGCGTCAGGGCTACCAGAAAGACAAGCGAAAGGTCCCAGCCT

Gene : HepC1a
Segment# : 4
Offset : 46
1st Codon : 1
L G V R A T R K T S E R S Q P R G R R Q P I P K A R R P E G
CTGGGAGTGAGAGCCACAAGGAAAACCTCCGAGAGAAGCCAACCCAGAGGCAGAAGGCAACCCATTCCCAAAGCCAGAAGGCCTGAGGGA

Gene : HepC1a
Segment# : 5
Offset : 61
1st Codon : 1
R G R R Q P I P K A R R P E G R T W A Q P G Y P W P L Y G N
AGGGGAAGGAGACAGCCTATCCCTAAGGCTAGGAGACCCGAAGGCAGAACCTGGGCCCAACCCGATACCCCTTGGCCTCTGTATGGCAAT

Gene : HepC1a
Segment# : 6
Offset : 76
1st Codon : 1
R T W A Q P G Y P W P L Y G N E G C G W A G W L L S P R G S
AGGACATGGGCTCAGCCTGGCTATCCCTGGCCCTCTACGGAACGAAGGCTGTGGCTGGGCGGATGGCTCCTGTCCCCCAGAGGCTCC

Gene : HepC1a
Segment# : 7
Offset : 91
1st Codon : 1
E G C G W A G W L L S P R G S R P S W G P T D P R R R S R N
GAGGATGCGGATGGCTGGCTGGCTGCTCAGCCCTAGGGGAAGCAGACCCTCCTGGGGACCCACAGACCCTAGGAGAAGGTCCAGGAAT

Gene : HepC1a
Segment# : 8
Offset : 106
1st Codon : 1
R P S W G P T D P R R R S R N L G K V I D T L T C G F A D L
AGGCCCTAGCTGGGGCCTACCGATCCAGAAGGAGAAGCAGAAACCTCGGCAAGTGATTGACACACTGACATGCGGATTCTGCTGACCTC

Gene : HepC1a
Segment# : 9
Offset : 121
1st Codon : 1
L G K V I D T L T C G F A D L M G Y I P L V G A P L G G A A
CTGGGAAAGGTATCGATACCCCTCACCTGTGGCTTTGCGGATCTGATGGGCTATATCCCTCTGGTCGGCGCTCCCTCGGCGGAGCCGCT

Gene : HepC1a
Segment# : 10
Offset : 136
1st Codon : 1
M G Y I P L V G A P L G G A A R A L A H G V R V L E D G V N
ATGGGATACATTCCCTCTGTGGGAGCCCTCTGGGAGGCGCTGCCAGAGCCCTCGCCCATGGCGTCAGGGTCTGGAAGACGGAGTGAAT

Gene : HepC1a
Segment# : 11
Offset : 151
1st Codon : 1
R A L A H G V R V L E D G V N Y A T G N L P G C S F S I F L
AGGGCTCTGGCTCACGGAGTGAGAGTCTCGAGGATGGCGTCAACTATGCCACAGGCAATCTGCCTGGCTGTAGCTTTAGCATTTTCCTC

Gene : HepC1a
Segment# : 12
Offset : 166

Figure 26 (cont)

112/216

1st Codon : 1
Y A T G N L P G C S F S I F L L A L L S C L T V P A S A Y Q
TACGCTACCGGAAACCTCCCGGATGCTCCTTCTCCATCTTTCTGCTCGCCCTCCTGCTCCTCACCCTCCCGCTAGCGCTTACCAA

Gene : HepC1a
Segment# : 13
Offset : 181
1st Codon : 1
L A L L S C L T V P A S A Y Q V R N S T G L Y H V T N D C P
CTGGCTCTGCTCAGCTGTCTGACAGTGCCTGCCTCCGCCTATCAGGTGAGGAATAGCACAGGCCTCTACCATGTGACAAACGATTGCCCT

Gene : HepC1a
Segment# : 14
Offset : 196
1st Codon : 1
V R N S T G L Y H V T N D C P N S S I V Y E A A D A I L H T
GTGAGAACTCCACCGACTGTATCAGTCCCAATGACTGTCCCAATAGCTCCATCGTCTACGAAGCCGCTGACGCTATCCTCCACACA

Gene : HepC1a
Segment# : 15
Offset : 211
1st Codon : 1
N S S I V Y E A A D A I L H T P G C V P C V R E G N A S R C
AACTCCAGCATGTGTATGAGGCTGCCGATGCCATTCTGCATACCCCTGGCTGTGTGCTTGCCTCAGGAAGGCAATGCCCTCCAGGTGT

Gene : HepC1a
Segment# : 16
Offset : 226
1st Codon : 1
P G C V P C V R E G N A S R C W V A M T P T V A T R D G K L
CCCGGATCGCTCCCTGTGTGAGAGAGGAAACGCTAGCAGATGCTGGTGGCTATGACACCCACAGTGGCTACAGAGACGGAAAGCTC

Gene : HepC1a
Segment# : 17
Offset : 241
1st Codon : 1
W V A M T P T V A T R D G K L P A T Q L R R H I D L L V G S
TGGGTGCGCATGACCCCTACCGTCGCCACAAGGGATGGCAAAGTGCCTGCCACACAGCTCAGGAGACACATTGACCTCCTGGTGGCTCC

Gene : HepC1a
Segment# : 18
Offset : 256
1st Codon : 1
P A T Q L R R H I D L L V G S A T L C S A L Y V G D L C G S
CCCGCTACCCAACTGAGAAGGCATATCGATCTGCTCGTGGGAAGCGCTACCCCTCTGCTCCGCCCTCTACGTGGGCGATCTGTGTGGCTCC

Gene : HepC1a
Segment# : 19
Offset : 271
1st Codon : 1
A T L C S A L Y V G D L C G S V P L V G Q L F T F S P R R H
GCCACATGTGTAGCGCTCTGTATGTGGAGACCTCTGCGGAAGCGTCTTCTCGTGGGACAGCTCTTCACATTCTCCCCAGAAGGCAT

Gene : HepC1a
Segment# : 20
Offset : 286
1st Codon : 1
V F L V G Q L F T F S P R R H W T T Q G C N C S I Y P G H I
GTGTTCTGGTGGGCAACTGTTTACCTTTAGCCCTAGGAGACACTGGACCACACAGGGATGCAATTGCTCCATCTATCCCGGACACATT

Gene : HepC1a
Segment# : 21
Offset : 301
1st Codon : 1
W T T Q G C N C S I Y P G H I T G H R M A W D M M M N W S P
TGGACAACCCAGGCTGTAACGTAGCATTTACCTTGCCATATCACAGGCCATAGGATGGCTGGGACATGATGATGAACCTGGAGCCCT

Gene : HepC1a
Segment# : 22
Offset : 316
1st Codon : 1
T G H R M A W D M M M N W S P T A A L V M A Q L L R I P Q A
ACCGGACACAGAATGGCTTGGGATATGATGATGAATTGGTCCCCACAGCCGCTCTGGTCATGGCTCAGCTCCTGAGAATCCCTCAGGCT

Figure 26 (Cont)

113/216

Gene : HepCla
Segment# : 23
Offset : 331
1st Codon : 1
T A A L V M A Q L L R I P Q A I L D M I A G A H W G V L A G
ACCGCTGCCCTCGTGATGGCCCAATGCTCAGGATTCCTCCCAAGCCATTCTGGATATGATTGCCGGAGCCCATTTGGGGAGTGCTCGCCGGA

Gene : HepCla
Segment# : 24
Offset : 346
1st Codon : 1
I L D M I A G A H W G V L A G I A Y F S M V G N W A K V L V
ATCCTCGACATGATCGCTGGCGCTCACTGGGGCGTCTGGCTGGCATTGCCTATTCTCCATGGTCGGCAATTGGGCTAAGGTCCTGGTC

Gene : HepCla
Segment# : 25
Offset : 361
1st Codon : 1
I A Y F S M V G N W A K V L V V L L L F A G V D A E T H V T
ATCGCTTACTTTAGCATGTGGGAACTGGGCCAAAGTGCTCGTGGTCTGCTCTGTTTGCCGGAGTGGATGCCGAAACCCATGTGACA

Gene : HepCla
Segment# : 26
Offset : 376
1st Codon : 1
V L L L F A G V D A E T H V T G G N A G R T T S G L V S L L
GTGCTCCTGCTCTTCGCTGGCGTCGACGCTGAGACACAGTCACCGGAGGCAATGCCGGAAGGACAACCTCCGGCCTCGTGTCCCTGCTC

Gene : HepCla
Segment# : 27
Offset : 391
1st Codon : 1
G G N A G R T T S G L V S L L T P G A K Q N I Q L I N T N G
GGCGAAACGCTGGCAGAACCAAGCGGACTGGTCAGCCTCCTGACACCCGGAGCCAAACAGAATATCCAACCTGATTAACACAAACGGA

Gene : HepCla
Segment# : 28
Offset : 406
1st Codon : 1
T P G A K Q N I Q L I N T N G S W H I N S T A L N C N E S L
ACCCCTGGCGCTAAGCAAAACATTGAGCTCATCAATACCAATGGCTCCTGGCATATCAATAGCACAGCCCTCAACTGTAAACGAAGCCTC

Gene : HepCla
Segment# : 29
Offset : 421
1st Codon : 1
S W H I N S T A L N C N E S L N T G W L A G L F Y Q H K F N
AGCTGGCACATTAACCTCACCGCTCTGAATTGCAATGAGTCCCTGAATACCGGATGGCTCGCCGGACTGTTTTACCAACACAAATTCAT

Gene : HepCla
Segment# : 30
Offset : 436
1st Codon : 1
N T G W L A G L F Y Q H K F N S S G C P E R L A S C R R L T
AACACAGGCTGGCTGGCTCTTCTATCAGCATAAGTTTAACTCCAGCGGATGCCCTGAGAGACTGGCTAGCTGTAGGAGACTGACA

Gene : HepCla
Segment# : 31
Offset : 451
1st Codon : 1
S S G C P E R L A S C R R L T D F D Q G W G P I S Y A N G S
AGCTCGGGCTGTCCGAAAGCTCGCCTCCTGCAGAAGGCTCACCGATTTCGATCAGGGATGGGACCCATTAGCTATGCCAATGGCTCC

Gene : HepCla
Segment# : 32
Offset : 466
1st Codon : 1
D F D Q G W G P I S Y A N G S G P D Q R P Y C W H Y P P K P
GACTTTGACCAAGGCTGGGCCCCATCTCTACGCTAACGGAAGCGGACCCGATCAGAGACCCATTGCTGGCACTATCCCCCTAAGCCT

Gene : HepCla
Segment# : 33

Figure 26 (Cont)

114/216

Offset : 481
1st Codon : 1
G P D Q R P Y C W H Y P P K P C G I V P A K S V C G P V Y C
GGCCCTGACCAAAGCCCTTACTGTGTGGCATTACCCCTCCCAAACCTGTGGCATTGTGCCTGCCAAAAGCGTCTGCGGACCCGCTCTACTGT

Gene : HepC1a
Segment# : 34
Offset : 496
1st Codon : 1
C G I V P A K S V C G P V Y C F T P S P V V V G T T D R S G
TGCGGAATCGTCCCGCTAAGTCGGTGTGTGGCCCTGTGTATTGCTTTACCCCTAGCCCTGTGGTCTGTTGGGAACACAGACAGAAGCGGA

Gene : HepC1a
Segment# : 35
Offset : 511
1st Codon : 1
F T P S P V V V G T T D R S G A P T Y S W G A N D T D V F V
TTCACACCCCTCCCGCTGTGGTCTGGCACAACCGATAGGTCTCGGCGCTCCACATACTCTGGGGAGCCAATGACACAGACGTCTTCGTC

Gene : HepC1a
Segment# : 36
Offset : 526
1st Codon : 1
A P T Y S W G A N D T D V F V L N N T R P P L G N W F G C T
GCCCTACCTATAGCTGGGGCGCTAACGATACCGATGTGTTTGTGCTCAACAATACCAGACCCCTCTGGGAAACTGTTGGATGCACA

Gene : HepC1a
Segment# : 37
Offset : 541
1st Codon : 1
L N N T R P P L G N W F G C T W M N S T G F T K V C G A P P
CTGAATAACACAAGGCTCCCTCGGCAATTGGTTGGCTGTACCTGGATGAATAGCACAGGCTTTACCAAAGTGTGTGGCGCTCCCGCT

Gene : HepC1a
Segment# : 38
Offset : 556
1st Codon : 1
W M N S T G F T K V C G A P P C V I G G A G N N T L H C P T
TGGATGAATCCACCGGATTCAAAAGGTCTGCGGAGCCCTCCCTGTGTGATTGGCGGAGCCGGAACAATACCTCCACTGTCCACACA

Gene : HepC1a
Segment# : 39
Offset : 571
1st Codon : 1
C V I G G A G N N T L H C P T D C F R K H P E A T Y S R C G
TGCCTCATCGGAGGCGCTGGCAATAACACACTGCATTGCCCTACCGATTGCTTTAGGAAACACCCCTGAGGCTACCTATAGCAGATGCGGA

Gene : HepC1a
Segment# : 40
Offset : 586
1st Codon : 1
D C F R K H P E A T Y S R C G S G P W I T P R C L V D Y P Y
GACTGTTTCAGAAAGCATCCCGAAGCCACATACTCCAGGTGTGGCTCCGGCCCTTGATTACCCCTAGGTGTCTGGTCTGACTATCCCTAT

Gene : HepC1a
Segment# : 41
Offset : 601
1st Codon : 1
S G P W I T P R C L V D Y P Y R L W H Y P C T I N Y T I F K
AGCGGACCCCTGGATCACACCCAGATGCCCTCGTGGATTACCCCTACAGACTGTGGCACTATCCCTGTACCATTAACCTATACCATTTTCAAA

Gene : HepC1a
Segment# : 42
Offset : 616
1st Codon : 1
R L W H Y P C T I N Y T I F K V R M Y V G G V E H R L E A A
AGGCTCTGGCATTACCCCTGCACAATCAATTACACAATCTTTAAGGTGAGGATGTACGTGCGCGGAGTGAACACAGACTGGAAGCCGCT

Gene : HepC1a
Segment# : 43
Offset : 631
1st Codon : 1
V R M Y V G G V E H R L E A A C N W T R G E R C D L E D R D

Figure 26 (Cont)

115/216

GTGAGAATGTATGTGGGAGGCGTCGAGCATAGGCTCGAGGCTGCCTGTAACCTGGACCAGAGGGGAAAGGTGTGACCTCGAGGATAGGGAT

Gene : HepC1a

Segment# : 44

Offset : 646

1st Codon : 1

C N W T R G E R C D L E D R D R S E L S P L L L S T T Q W Q
TGCAATTGGACAAGGGGAGAGAGATGCGATCTGGAAGACAGAGACAGAAGCGAACTGTCCCCCTCCTGCTCAGCACAACCCAATGGCAA

Gene : HepC1a

Segment# : 45

Offset : 661

1st Codon : 1

R S E L S P L L L S T T Q W Q V L P C S F T T L P A L S T G
AGGTCCGAGCTCAGCCCTCTGCTCCTGTCCACCACACAGTGGCAGGTCTGCCTTGCTCCTTCACAACCCCTCCCGCTCTGTCCACCGGA

Gene : HepC1a

Segment# : 46

Offset : 676

1st Codon : 1

V L P C S F T T L P A L S T G L I H L H Q N I V D V Q Y L Y
GTGCTCCCCGTAGCTTTACCACACTGCCTGCCCTCAGCACAGGCCTCATCCATCTGCATCAGAATATCGTCGACGTCAGTATCTGTAT

Gene : HepC1a

Segment# : 47

Offset : 691

1st Codon : 1

L I H L H Q N I V D V Q Y L Y G V G S S I A S W A I K W E Y
CTGATTCACCTCCACCAAAACATTGTGGATGTGCAATACCTCTACGGAGTGGGAAGCTCCATCGCTAGCTGGGCCATTAAAGTGGGAGTAT

Gene : HepC1a

Segment# : 48

Offset : 706

1st Codon : 1

G V G S S I A S W A I K W E Y V V L L F L L L A D A R V C S
GGCGTCGGCTCCAGCATTGCCTCCTGGGCTATCAATGGGAATACGTGCTGCTCCTGTTTCTGCTCCTGGCTGACGCTAGGGTCTGCTCC

Gene : HepC1a

Segment# : 49

Offset : 721

1st Codon : 1

V V L L F L L L A D A R V C S C L W M M L L I S Q A E A A L
GTGGTCTGCTCTTCTCCTGCTCGCCGATGCCAGATGTGTAGCTGTCTGTGGATGATGCTGCTCATCTCCAGGCTGAGGCTGCCCTC

Gene : HepC1a

Segment# : 50

Offset : 736

1st Codon : 1

C L W M M L L I S Q A E A A L E N L V I L N A A S L A G T H
TGCCTCTGGATGATGCTCCTGATTAGCCAAGCCGAAGCCGCTCTGGAACCTCGTGATTCTGAATGCCGCTAGCCTCGCCGGAACCCAT

Gene : HepC1a

Segment# : 51

Offset : 751

1st Codon : 1

E N L V I L N A A S L A G T H G L V S F L V F F C F A W Y L
GAGAATCTGGTCATCTCAACGCTGCCTCCCTGGCTGGCACACAGGACTGGTCAGCTTCTGGTCTTCTTTGCTTTGCCTGGTACCTC

Gene : HepC1a

Segment# : 52

Offset : 766

1st Codon : 1

G L V S F L V F F C F A W Y L K G R W V P G A V Y A L Y G M
GGCCTCGTGTCTTCTCCTGCTGTTTCTGTTTCTGCTTGGTATCTGAAAGGCAGATGGGTCCCGGAGCCGCTACGCTCTGTATGGCATG

Gene : HepC1a

Segment# : 53

Offset : 781

1st Codon : 1

K G R W V P G A V Y A L Y G M W P L L L L L L A L P Q R A Y
AAGGGAAGTGGGTGCTGGCGCTGTGTATGCCCTCTACGGAATGTGGCCCTCCTGCTCCTGCTCCTGGCTCTGCCTCAGAGAGCCTAT

Gene : HepC1a

Figure 26 (Cont)

116/216

Segment# : 54
Offset : 796
1st Codon : 1
W P L L L L L A L P Q R A Y A L D T E V A A S C G G V V L
TGGCCTCTGCTCTGCTCTGCTCGCCCTCCCCAAAGGGCTTACGCTCTGGATACCGAAGTGGCTGCCTCTGCGGAGGCGTCTGCTCTC

Gene : HepC1a
Segment# : 55
Offset : 811
1st Codon : 1
A L D T E V A A S C G G V V L V G L M A L T L S P Y Y K R Y
GCCCTCGACACAGAGGTGCGCGCTAGCTGTGGCGGAGTGGTCTGGTCGGCCTCATGGCTCTGACACTGTCCCCCTATTACAAAAGGTAT

Gene : HepC1a
Segment# : 56
Offset : 826
1st Codon : 1
V G L M A L T L S P Y Y K R Y I S W C L W W L Q Y F L T R V
GTGGGACTGATGGCCCTCACCTCAGCCCTTACTATAAGAGATACATTAGCTGGTGCCTCTGGTGGCTGCAATACTTTCTGACAAGGGTC

Gene : HepC1a
Segment# : 57
Offset : 841
1st Codon : 1
I S W C L W W L Q Y F L T R V E A Q L H V W V P P L N V R G
ATCTCTGGTGTCTGTGGTGGCTCCAGTATTTCTCACCAGAGTGAAGCCCAACTGCATGTGTGGGTGCCTCCCTCAACGTACAGGGGA

Gene : HepC1a
Segment# : 58
Offset : 856
1st Codon : 1
E A Q L H V W V P P L N V R G G R D A V I L L M C V V H P T
GAGGCTCAGTCCACGTCTGGGTCCCCCTCTGAATGTGAGAGGCGGAAGGGATGCCGTCTCTCTGATGTGCGTCTGTCATCCCCACA

Gene : HepC1a
Segment# : 59
Offset : 871
1st Codon : 1
G R D A V I L L M C V V H P T L V F D I T K L L L A V F G P
GGCAGAGACGCTGTGATTCTGCTCATGTGTGTGGTCCACCCTACCTCGTGTGACATTACCAAACGTCTCTGGCTGTGTTTGGCCCT

Gene : HepC1a
Segment# : 60
Offset : 886
1st Codon : 1
L V F D I T K L L L A V F G P L W I L Q A S L L K V P Y F V
CTGGTCTTCGATATCACAAAGCTCTGCTCGCGTCTTCGGACCCCTCTGGATTCTGCAAGCCTCCCTGCTCAAGGTCCCTATTTCGTC

Gene : HepC1a
Segment# : 61
Offset : 901
1st Codon : 1
L W I L Q A S L L K V P Y F V R V Q G L L R I C A L A R K M
CTGTGGATCCTCCAGGCTAGCCTCCTGAAAGTGCCTTACTTTGTGAGAGTGCAGGGCTCTGAGAATCTGTGCCCTCGCCAGAAAGATG

Gene : HepC1a
Segment# : 62
Offset : 916
1st Codon : 1
R V Q G L L R I C A L A R K M I G G H Y V Q M A I I K L G A
AGGGTCCAGGGACTGCTCAGGATTTCGCTCTGGCTAGGAAAATGATTGGCGGACACTATGTGCAAATGGCTATCATTAGCTCGGCGCT

Gene : HepC1a
Segment# : 63
Offset : 931
1st Codon : 1
I G G H Y V Q M A I I K L G A L T G T Y V Y N H L T P L R D
ATCGGAGGCCATTACGTCCAGATGGCCATTATCAAACCTGGGAGCCCTCACCAGAACCTATGTGTATAACCATCTGACACCCCTCAGGGAT

Gene : HepC1a
Segment# : 64
Offset : 946
1st Codon : 1

Figure 26 (Cont)

117/216

L T G T Y V Y N H L T P L R D W A H N G L R D L A V A V E P
CTGACAGGCACATACGTCTACAATCACCTCACCCCTCTGAGAGACTGGGCCCATACGGACTGAGAGACCTCGCCGTCGCCGTCGAGCCT

Gene : HepC1a
Segment# : 65
Offset : 961
1st Codon : 1
W A H N G L R D L A V A V E P V V F S Q M E T K L I T W G A
TGGGCTCACAATGGCCTCAGGATCTGGCTGTGGCTGTGGAAACCCGTCGTGTTAGCCAAATGGAAACCAAACCTGATTACCTGGGGCGCT

Gene : HepC1a
Segment# : 66
Offset : 976
1st Codon : 1
V V F S Q M E T K L I T W G A D T A A C G D I I N G L P V S
GTGGTCTTCTCCAGATGGAGACAAAGCTCATCACATGGGGAGCCGATACCGCTGCCTGTGGCGATATCATTACGGACTGCCTGTGTCC

Gene : HepC1a
Segment# : 67
Offset : 991
1st Codon : 1
D T A A C G D I I N G L P V S A R R G R E I L L G P A D G M
GACACAGCCGCTTGGGAGACATTATCAATGGCCTCCCGTCAGCGCTAGGAGAGGCAGAGAGATTCTGCTCGGCCCTGCCGATGGCAGT

Gene : HepC1a
Segment# : 68
Offset : 1006
1st Codon : 1
A R R G R E I L L G P A D G M V S K G W R L L A P I T A Y A
GCCAGAAGGGGAAGGAAATCCTCCTGGGACCCGCTGACGGAATGGTCAGCAAAGGCTGGAGGCTCCTGGCTCCCATACCGCTTACGCT

Gene : HepC1a
Segment# : 69
Offset : 1021
1st Codon : 1
V S K G W R L L A P I T A Y A Q Q T R G L L G C I I T S L T
TGTCGAAGGGATGGAGACTGCTCGCCCTATCACAGCCTATGCCAACAGACAAGGGGACTGCTCGGCTGTATCATTACCTCCCTGACA

Gene : HepC1a
Segment# : 70
Offset : 1036
1st Codon : 1
Q Q T R G L L G C I I T S L T G R D K N Q V E G E V Q I V S
CAGCAAACAGAGGCTCCTGGGATGCATTATCACAAGCCTCACCGGAAGGGATAAGAATCAGGTCGAGGGAGAGGTCCAGATTGTGTCC

Gene : HepC1a
Segment# : 71
Offset : 1051
1st Codon : 1
G R D K N Q V E G E V Q I V S T A A Q T F L A T C I N G V C
GGCAGAGACAAAACCAAGTGAAGGCGAAGTGCAATCGTCAGCACAGCCGCTCAGACATTCTCGCCACATGCATTACGGAGTGTGT

Gene : HepC1a
Segment# : 72
Offset : 1066
1st Codon : 1
T A A Q T F L A T C I N G V C W T V Y H G A G T R T I A S P
ACCGTGCCTCAAACCTTTCTGGCTACCTGTATCAATGGCGTCTGCTGGACCGTCTACCATGGCGCTGGCACAAGGACAATCGCTAGCCCT

Gene : HepC1a
Segment# : 73
Offset : 1081
1st Codon : 1
W T V Y H G A G T R T I A S P K G P V I Q M Y T N V D Q D L
TGGACAGTGTATCAGGAGCCGGAACCAACCATTCCTCCCAAGGCCCTGTGATTGATGATGACACAAACGTCGACCAAGACCTC

Gene : HepC1a
Segment# : 74
Offset : 1096
1st Codon : 1
K G P V I Q M Y T N V D Q D L V G W P A P Q G S R S L T P C
AAGGGACCCCTCATCCAAATGTATACCAATGTGGATCAGGATCTGGTGGCGCCGCTCCCAAGGCTCCAGGTCCCTGACACCCCTGT

Figure 26 (Cont)

118/216

Gene : HepCla
Segment# : 75
Offset : 1111
1st Codon : 1
V G W P A P Q G S R S L T P C T C G S S D L Y L V T R H A D
GTGGGATGGCCTGCCCCCTCAGGGAAGCAGAAGCCTCACCCCTTGACATGCGGAAGCTCCGACCTCTACCTCGTGACAAGGCATGCCGAT

Gene : HepCla
Segment# : 76
Offset : 1126
1st Codon : 1
T C G S S D L Y L V T R H A D V I P V R R R G D S R G S L L
ACCTGTGGCTCCAGCGATCTGTATCTGGTCACCAGACACGCTGACGTCATCCCTGTGAGAAGGAGAGGCGATAGCAGAGGCTCCCTGCTC

Gene : HepCla
Segment# : 77
Offset : 1141
1st Codon : 1
V I P V R R R G D S R G S L L S P R P I S Y L K G S S G G P
GTGATTCCTCGTCAGGAGAAGGGGAGACTCCAGGGGAAGCCTCCTGTCCCCCAGACCCATTAGCTATCTGAAAGGCTCCAGCGGAGGCCCT

Gene : HepCla
Segment# : 78
Offset : 1156
1st Codon : 1
S P R P I S Y L K G S S G G P L L C P A G H A V G I F R A A
AGCCCTAGGCCTATCTCTCACTCAAGGGAAGCTCCGGCGGACCCCTCCTGTGTCCCGCTGGCCATGCCGTCCGTCATTTTCAGAGCCGCT

Gene : HepCla
Segment# : 79
Offset : 1171
1st Codon : 1
L L C P A G H A V G I F R A A V C T R G V A K A V D F I P V
CTGCTCTGCCCTGCCGACACGCTGTGGGAATCTTTAGGGCTGCCGTCTGCACAAGGGGAGTGGCTAAGGCTGTGGATTTTCATTCCCGCT

Gene : HepCla
Segment# : 80
Offset : 1186
1st Codon : 1
V C T R G V A K A V D F I P V E N L E T T M R S P V F T D N
GTGTGTACCAGAGGCGTCGCCAAAGCCGTCGACTTTATCCCTGTGGAAAACCTCGAGACAACCATGAGGTCCCCCGTCTTCACAGACAAT

Gene : HepCla
Segment# : 81
Offset : 1201
1st Codon : 1
E N L E T T M R S P V F T D N S S P P A V P Q S F Q V A H L
GAGAATCTGGAACCAATGAGAAGCCCTGTGTTACCGATAACTCCAGCCCTCCCGCTGTGCCTCAGTCCTTCCAAGTGGCTCACCTC

Gene : HepCla
Segment# : 82
Offset : 1216
1st Codon : 1
S S P P A V P Q S F Q V A H L H A P T G S G K S T K V P A A
AGCTCCCCCTGCCGTCCCCCAAAGCTTTCAGGTGCCCCATCTGCATGCCCTACCGGAAGCGGAAAGTCCACCAAAGTGCCTGCCGCT

Gene : HepCla
Segment# : 83
Offset : 1231
1st Codon : 1
H A P T G S G K S T K V P A A Y A A Q G Y K V L V L N P S V
CACGCTCCACAGGCTCCGGCAAAGCACAAAGGTCCCCGCTGCCTATGCCGCTCAGGGATACAAAGTGCTCGTGCTCAACCCTAGCGTC

Gene : HepCla
Segment# : 84
Offset : 1246
1st Codon : 1
Y A A Q G Y K V L V L N P S V A A T L G F G A Y M S K A H G
TAGCTGCCCAAGGCTATAAGGTCTGTGCTGAATCCCTCCGTGGCTGCCACACTGGGATTCCGAGCCTATATGTCCAAGGCTCACGGT

Gene : HepCla
Segment# : 85
Offset : 1261

Figure 26 (Cont)

119/216

1st Codon : 1
A A T L G F G A Y M S K A H G I D P N I R T G V R T I T T G
GCCGCTACCCCTCGGCTTTGGCGCTTACATGAGCAAAGCCCATGGCATTGACCCTAACATTAGGACAGGCGTCAGGACAATCACAAACCGGA

Gene : HepC1a
Segment# : 86
Offset : 1276
1st Codon : 1
I D P N I R T G V R T I T T G S P I T Y S T Y G K F L A D G
ATCGATCCCAATATCAGAACCGGAGTGAGAACCATTACCAAGGCTCCCCATTACCTATAGCACATACGGAAAGTTTCTGGCTGACGGA

Gene : HepC1a
Segment# : 87
Offset : 1291
1st Codon : 1
S P I T Y S T Y G K F L A D G G C S G G A Y D I I I C D E C
AGCCCTATCACATATCCACCTATGGCAAATTCCTCGCCGATGGCGGATGCTCCGGCGGAGCCTATGACATTATCATTTGCGATGAGTGT

Gene : HepC1a
Segment# : 88
Offset : 1306
1st Codon : 1
G C S G G A Y D I I I C D E C H S T D A T S I L G I G T V L
GGCTGTAGCGGAGGCGCTTACGATATCATTATCTGTGACGAATGCCATAGCACAGACGCTACCTCCATCCTCGGCATTGGCACAGTGCTC

Gene : HepC1a
Segment# : 89
Offset : 1321
1st Codon : 1
H S T D A T S I L G I G T V L D Q A E T A G A R L V V L A T
CACTCCACCGATGCCACAAGCATTCGGGAATCGGAACCGTCTGGATCAGGCTGAGACAGCCGGAGCCAGACTGGTCTGCTCGCCACA

Gene : HepC1a
Segment# : 90
Offset : 1336
1st Codon : 1
D Q A E T A G A R L V V L A T A T P P G S V T V P H P N I E
GACCAAGCCGAACCGCTGGCGTAGGCTCGTGGTCTGGCTACCGCTACCCCTCCCGAAGCGTCACCGTCCCCATCCCAATATCGAA

Gene : HepC1a
Segment# : 91
Offset : 1351
1st Codon : 1
A T P P G S V T V P H P N I E E V A L S T T G E I P F Y G K
GCCACACCCCTGGCTCCGTGACAGTGCCCTACCCCTAACATTGAGGAAGTGGCTCTGTCCACCACAGGCGAAATCCCTTTCTATGGCAA

Gene : HepC1a
Segment# : 92
Offset : 1366
1st Codon : 1
E V A L S T T G E I P F Y G K A I P L E V I K G G R H L I F
GAGTGGCCCTCAGCACAAACCGAGAGATTCCTTTTACGGAAGGCTATCCCTCTGGAAGTGATTAAGGGAGGCAGACCTCATCTTT

Gene : HepC1a
Segment# : 93
Offset : 1381
1st Codon : 1
A I P L E V I K G G R H L I F C H S K K K C D E L A A K L V
GCCATTCCCCTCGAGGTCAACAAAGCGGAAGGCATCTGATTTTCTGTCACTCCAAGAAAAAGTGTGACGAACTGGCTGCCAAACTGGTC

Gene : HepC1a
Segment# : 94
Offset : 1396
1st Codon : 1
C H S K K K C D E L A A K L V A L G I N A V A Y Y R G L D V
TGCCATAGCAAAAAGAAATGCGATGAGCTGCGCGCTAAGCTCGTGGCTCTGGGAATCAATGCCGTGCGCTATTACAGAGGCCTCGACGTC

Gene : HepC1a
Segment# : 95
Offset : 1411
1st Codon : 1
A L G I N A V A Y Y R G L D V S V I P T S G D V V V V A T D
GCCCTCGGCATTAAACGCTGTGGCTTACTATAGGGGACTGGATGTGTCCGTGATCCCAAGCGGAGACGTCGTGGTCTGGCTACCGAT

Figure 26 (Cont)

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Gene       : HepC1a
Segment#   : 96
Offset     : 1426
1st Codon  : 1
S V I P T S G D V V V V A T D A L M T G Y T G D F D S V I D
AGCGTCATCCCTACCTCGGCGGATGTGGTCGTGGTCCACAGACGCTCTGATGACCGGATACACAGCGGATTTTCGATAGCGTCATCGAT

Gene       : HepC1a
Segment#   : 97
Offset     : 1441
1st Codon  : 1
A L M T G Y T G D F D S V I D C N T C V T Q T V D F S L D P
GCCTCATGCAGGCTATACCGGAGACTTGACTCCGTGATTGACTGTAACACATGCGTCACCCAAACCGTCGACTTTAGCCTCGACCTT

Gene       : HepC1a
Segment#   : 98
Offset     : 1456
1st Codon  : 1
C N T C V T Q T V D F S L D P T F T I E T T T L P Q D A V S
TGCAATACCTGTGTGACACAGACAGTGGATTCTCCCTGGATCCACATTACAATCGAAACCACAACCCTCCCCAAGACGCTGTGTCC

Gene       : HepC1a
Segment#   : 99
Offset     : 1471
1st Codon  : 1
T F T I E T T T L P Q D A V S R T Q R R G R T G R G K P G I
ACCTTTACCACTGAGACAACCACTGCCTCAGGATGCCGTGACAGAAACCAAGGAGAGGAGAAACCGGAAGGGGAAGCCTGGCATT

Gene       : HepC1a
Segment#   : 100
Offset     : 1486
1st Codon  : 1
R T Q R R G R T G R G K P G I Y R F V A P G E R P S G M F D
AGGACACAGAGAAGGGGAAGGACAGGCAGAGGCAAAACCCGGAATCTATAGGTTTGTGGCTCCCGGAGAGAGACCTCCGGCATGTTTCGAT

Gene       : HepC1a
Segment#   : 101
Offset     : 1501
1st Codon  : 1
Y R F V A P G E R P S G M F D S S V L C E C Y D A G C A W Y
TACAGATTGTCGCCCTCGCGAAAGGCCTAGCGGAATGTTTGACTCCAGCGTCTGTGTGAGTGTACGATGCCGGATGCGCTTGGTAT

Gene       : HepC1a
Segment#   : 102
Offset     : 1516
1st Codon  : 1
S S V L C E C Y D A G C A W Y E L T P A E T T V R L R A Y M
AGCTCCGTGCTCTGCGAATGCTATGACGCTGGCTGTGCCTGGTACGAACCTGACACCGCTGAGACAACCGTCAGGCTCAGGGCTTACATG

Gene       : HepC1a
Segment#   : 103
Offset     : 1531
1st Codon  : 1
E L T P A E T T V R L R A Y M N T P G L P V C Q D H L E F W
GAGCTCACCCCTGCGGAACCAAGTGGAGACTGAGAGCCTATATGAATACCCCTGGCCCTCCCGCTGCGCAAGACCATCTGGAATTCTGG

Gene       : HepC1a
Segment#   : 104
Offset     : 1546
1st Codon  : 1
N T P G L P V C Q D H L E F W E G V F T G L T H I D A H F L
ACACACCCGGATGCGCTGTGTGTGAGGATCACTTCGAGTTTGTGGGAAGGCGTCTTTCACAGGCTCACCCATATCGATGCCCATTTCCCTT

Gene       : HepC1a
Segment#   : 105
Offset     : 1561
1st Codon  : 1
E G V F T G L T H I D A H F L S Q T K Q S G E N F P Y L V A
GAGGAGTGTTTACCGGACTGACACACATTGACGCTCACTTCTGTGCCAGACAAGCAAAGCGGAGAGAATTTCCCTTACCTCGTGGCT

Gene       : HepC1a
Segment#   : 106

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Figure 26 (Cont)

121/216

Offset : 1576
1st Codon : 1
S Q T K Q S G E N F P Y L V A Y Q A T V C A R A Q A P P P S
AGCCAAACCAACAGTCCGGCGAAAACCTTCCCTATCTGGTCGCCCTATCAGGCTACCGCTCTGGCTAGGGCTCAGGCTCCCCCTCCCTCC

Gene : HepC1a
Segment# : 107
Offset : 1591
1st Codon : 1
Y Q A T V C A R A Q A P P P S W D Q M W K C L I R L K P T L
TACCAAGCCACAGTGTGTGCCAGAGCCCAAGCCCCTCCCCCTAGCTGGGACCAATGTGGAAGTGTCTGATTAGGCTCAAGCCTACCCCTC

Gene : HepC1a
Segment# : 108
Offset : 1606
1st Codon : 1
W D Q M W K C L I R L K P T L H G P T P L L Y R L G A V Q N
TGGGATCAGATGTGGAATGCTCATCAGACTGAAACCCCACTGCATGGCCCTACCCCTCTGCTCTACAGACTGGGAGCCGCTCCAGAAT

Gene : HepC1a
Segment# : 109
Offset : 1621
1st Codon : 1
H G P T P L L Y R L G A V Q N E V T L T H P V T K Y I M T C
CACGGACCCACACCCCTCCTGTATAGGCTCGGCGCTGTGCAAAACGAAGTACACTGACACACCCCTGTGACAAAGTATATCATGACCTGT

Gene : HepC1a
Segment# : 110
Offset : 1636
1st Codon : 1
E V T L T H P V T K Y I M T C M S A D L E V V T S T W V L V
GAGGTCACCCCTACCCATCCCGTCACCAATACATTATGACATGCATGAGCGCTGACCTCGAGGTCGTGACAAGCACATGGGTCTGGTCTC

Gene : HepC1a
Segment# : 111
Offset : 1651
1st Codon : 1
M S A D L E V V T S T W V L V G G V L A A L A A Y C L S T G
ATGTCCGCGATCTGGAAGTGGTCACCTCCACCTGGGTGCTCGTGGGAGGCGTCTGGCTGCCCTCGCGCTTACTGTCTGTCCACCGGA

Gene : HepC1a
Segment# : 112
Offset : 1666
1st Codon : 1
G G V L A A L A A Y C L S T G C V V I V G R I V L S G K P A
GGCGAGTGCTCGCGCTCTGGCTGCCTATTGCCCTCAGCACAGGCTGTGTGGTCATCGTCCGCGAGAATCGTCTGTCCGGCAAACCCGTC

Gene : HepC1a
Segment# : 113
Offset : 1681
1st Codon : 1
C V V I V G R I V L S G K P A I I P D R E V L Y R E F D E M
TCCGTCGTGATTGTGGAAGGATTGTGCTCAGCGGAAAGCCTGCCATTATCCCTGACAGAGAGGTCTGTATAGGGAATTCGATGAGATG

Gene : HepC1a
Segment# : 114
Offset : 1696
1st Codon : 1
I I P D R E V L Y R E F D E M E E C S Q H L P Y I E Q G M M
ATCATTCCCGATAGGGAAGTGTCTACAGAGAGTTTGACGAAATGGAAGAGTGTAGCCAACACCTCCCTATATCGAACAGGGAATGATG

Gene : HepC1a
Segment# : 115
Offset : 1711
1st Codon : 1
E E C S Q H L P Y I E Q G M M L A E Q F K Q K A L G L L Q T
GAGGAATGCTCCAGCATCTGCCTTACATTGAGCAAGGCATGATGCTCGCCGAACAGTTTAAGCAAAGGCTCTGGGACTGCTCCAGACA

Gene : HepC1a
Segment# : 116
Offset : 1726
1st Codon : 1
L A E Q F K Q K A L G L L Q T A S R Q A E V I A P A V Q T N

Figure 26 (Cont)

122/216

CTGGCTGAGCAATTCAAACAGAAAGCCCTCGGCTCCTGCAAAACGCTAGCAGACAGGCTGAGGTCAATCGCTCCCGCTGTGCAAAACCAAT

Gene : HepC1a
Segment# : 117
Offset : 1741
1st Codon : 1

A S R Q A E V I A P A V Q T N W Q K L E V F W A K H M W N F
GCCTCCAGGCAAGCCGAAGTGATTGCCCTGCCGTCCAGACAACTGGCAGAACTGGAAGTGTTTGGGCTAAGCATATGTGGAACCTT

Gene : HepC1a
Segment# : 118
Offset : 1756
1st Codon : 1

W Q K L E V F W A K H M W N F I S G I Q Y L A G L S T L P G
TGGCAAAGCTCGAGGTCTTCTGGGCCAAACACATGTGGAATTTCTATTAGCGGAATCCAATACCTCGCGGACTGTCCACCTCCCGGGA

Gene : HepC1a
Segment# : 119
Offset : 1771
1st Codon : 1

I S G I Q Y L A G L S T L P G N P A I A S L M A F T A A V T
ATCTCGGCATTGAGTATCTGGCTGGCCTCAGCACACTGCTGGCAATCCCGCTATCGCTAGCCTCATGGCTTTCACAGCCGCTGTGACA

Gene : HepC1a
Segment# : 120
Offset : 1786
1st Codon : 1

N P A I A S L M A F T A A V T S P L T T S Q T L L F N I L G
AACCCTGCCATTGCCCTCCCTGATGGCCTTTACCGCTGCCGTACCTCCCCCTCACCACAAGCCAAACCTCCTGTTTAACTTCTGGGA

Gene : HepC1a
Segment# : 121
Offset : 1801
1st Codon : 1

S P L T T S Q T L L F N I L G G W V A A Q L A A P G A A T A
AGCCCTCTGACAACCTCCAGACACTGCTCTCAATATCCTCGGCGGATGGGTGCGCGCTCAGCTCGCGCTCCCGGAGCCGCTACCGCT

Gene : HepC1a
Segment# : 122
Offset : 1816
1st Codon : 1

G W V A A Q L A A P G A A T A F V G A G L A G A A I G S V G
GGTGGGTGGCTGCCCACTGGCTGCCCTGGCGCTGCCACAGCCTTTGTGGAGCCGGACTGGCTGGCGCTGCCATTGGCTCCGTGGGA

Gene : HepC1a
Segment# : 123
Offset : 1831
1st Codon : 1

F V G A G L A G A A I G S V G L G K V L V D I L A G Y G A G
TTCGTGGCGCTGGCCTCGCCGGAGCCGCTATCGGAAGCGTGGCCTCGGCAAAGTGCTCGTGGATATCCTCGCCGGATACGGAGCCGGA

Gene : HepC1a
Segment# : 124
Offset : 1846
1st Codon : 1

L G K V L V D I L A G Y G A G V A G A L V A F K I M S G E V
CTGGAAAGGTCCTGGTCGACATTCTGGCTGGCTATGGCGCTGGCGTCCCGGAGCCCTCGTGGCTTTCAAAATCATGAGCGGAGAGGTC

Gene : HepC1a
Segment# : 125
Offset : 1861
1st Codon : 1

V A G A L V A F K I M S G E V P S T E D L V N L L P A I L S
GTGGCTGGCGCTCGGTCCCTTTAAGATTATGTCCGGCGAAGTGCTAGCACAGAGGATCTGGTCAACCTCCTGCCCTGCCATTCTGTCT

Gene : HepC1a
Segment# : 126
Offset : 1876
1st Codon : 1

P S T E D L V N L L P A I L S P G A L V V G V V C A A I L R
CCCTCCACCGAAGACCTCGTGAATCTGCTCCCGCTATCCTCAGCCCTGGCGCTCGGTCTGGGAGTGGTCTGCCGTGCCATTCTGAGA

Gene : HepC1a

Figure 26 (Cont)

123/216

Segment# : 127
Offset : 1891
1st Codon : 1
P G A L V V G V V C A A I L R R H V G P G E G A V Q W M N R
CCCGAGCCCTCGTGGTCGGCGTCGTGTGTGCCGTATCCTCAGGAGACACGTCGGCCCTGGCGAAGGCGCTGTGCAATGGATGAACAGA

Gene : HepC1a
Segment# : 128
Offset : 1906
1st Codon : 1
R H V G P G E G A V Q W M N R L I A F A S R G N H V S P T H
AGGCATGTGGGACCCGGAGAGGAGCCGTCCAGTGGATGAATAGGCTCATCGCTTCGCTAGCAGAGGCAATCACGTCAGCCCTACCCAT

Gene : HepC1a
Segment# : 129
Offset : 1921
1st Codon : 1
L I A F A S R G N H V S P T H Y V P E S D A A A R V T A I L
CTGATTGCCTTTGCCTCCAGGGAAACCATGTGTCCCCACACACTATGTGCCTGAGTCCGACGCTGCCGCTAGGGTCACCGCTATCCTC

Gene : HepC1a
Segment# : 130
Offset : 1936
1st Codon : 1
Y V P E S D A A A R V T A I L S S L T V T Q L L R R L H Q W
TAGCTCCCCGAAGCGATGCCGCTGCCAGAGTGACAGCCATTCTGTCCAGCCTCACCGTCACCCAACTGCTCAGGAGACTGCATCAGTGG

Gene : HepC1a
Segment# : 131
Offset : 1951
1st Codon : 1
S S L T V T Q L L R R L H Q W I S S E C T T P C S G S W L R
AGCTCCCTGACAGTGACACAGCTCCTGAGAAGGCTCCACCAATGGATTAGCTCCGAGTGTACCACCCCTGTAGCGGAAGCTGGCTGAGA

Gene : HepC1a
Segment# : 132
Offset : 1966
1st Codon : 1
I S S E C T T P C S G S W L R D I W D W I C E V L S D F K T
ATCTCCAGCGAATGCACAACCCCTTGCTCCGGCTCCTGGCTCAGGATATCTGGGACTGGATCTGTGAGGTCTGTCCGACTTTAAGACA

Gene : HepC1a
Segment# : 133
Offset : 1981
1st Codon : 1
D I W D W I C E V L S D F K T W L K A K L M P Q L P G I P F
GACATTTGGGATTGGATTTCGGAAGTGTCTAGCGATTTCAAAACCTGGCTGAAAGCCAACTGATGCCCCAACTGCCTGGCATTCCCTTT

Gene : HepC1a
Segment# : 134
Offset : 1996
1st Codon : 1
W L K A K L M P Q L P G I P F V S C Q R G Y K G V W R G D G
TGGCTCAAGGCTAAGCTCATGCCTCAGCTCCCCGGAATCCCTTTGCTCAGCTGTCTAGAGAGGCTATAAGGGAGTGTGGAGGGGAGACGGA

Gene : HepC1a
Segment# : 135
Offset : 2011
1st Codon : 1
V S C Q R G Y K G V W R G D G I M H T R C H C G A E I T G H
GTGTCCTGCCAAGGGGATACAAAGGCGTCTGGAGAGGCGATGGCATTATGCATACCAGATGCCATTGCCGAGCCGAAATCACAGGCCAT

Gene : HepC1a
Segment# : 136
Offset : 2026
1st Codon : 1
I M H T R C H C G A E I T G H V K N G T M R I V G P R T C R
ATCATGCACACAAGGTGTCACTGTGGCGCTGAGATTACCGGACACGTCAGAAATGGCACAATGAGAATCGTGGGCCCTAGGACATGCAGA

Gene : HepC1a
Segment# : 137
Offset : 2041
1st Codon : 1

Figure 26 (Cont)

124/216

V K N G T M R I V G P R T C R N M W S G T F P I N A Y T T G
GTGAAAAACGGAAACCATGAGGATTGTGGGACCCAGAACCTGTAGGAATATGTGGAGCGGAACCTTTCCCATTAACGCTTACACAAACCGGA

Gene : HepC1a
Segment# : 138
Offset : 2056
1st Codon : 1

N M W S G T F P I N A Y T T G P C T P L P A P N Y T F A L W
AACATGTGGTCCGGCACATTCCCTATCAATGCCTATACACAGGCCCTTGACACCCCTCCCGCTCCCAATTACACATTGCTCTGTGG

Gene : HepC1a
Segment# : 139
Offset : 2071
1st Codon : 1

P C T P L P A P N Y T F A L W R V S A E E Y V E I R R V G D
CCCTGTACCCCTCTGCCCTGCCCTAACTATACCTTTGCCCTCTGGAGAGTGTCCGCCGAAGAGTATGTGGAATCAGAAGGGTCCGCCGAT

Gene : HepC1a
Segment# : 140
Offset : 2086
1st Codon : 1

R V S A E E Y V E I R R V G D F H Y V T G M T T D N L K C P
AGGGTCAGCCCTGAGGAATACGTCGAGATTAGGAGAGTGGGAGACTTTCATATGTGACAGGCATGACCAAGACAATCTGAAATGCCCT

Gene : HepC1a
Segment# : 141
Offset : 2101
1st Codon : 1

F H Y V T G M T T D N L K C P C Q V P S P E F F T E L D G V
TTCCATTACGTCCCGAATGACAAACGATAACCTCAAGTGTCCCTGTGAGGTCCCTCCCGCAATCTTTACCGAACTGGATGGCGTC

Gene : HepC1a
Segment# : 142
Offset : 2116
1st Codon : 1

C Q V P S P E F F T E L D G V R L H R F A P P C K P L L R E
TGCCAGTGCCTAGCCCTGAGTTTTCACAGAGCTCGACGGAGTGAGACTGCATAGTTTGGCCCTCCCTGTAAGCCTCTGCTCAGGGAA

Gene : HepC1a
Segment# : 143
Offset : 2131
1st Codon : 1

R L H R F A P P C K P L L R E E V S F R V G L H E Y P V G S
AGGCTCCACAGATTCCCTCCCGCTTGCAAAACCCCTCCTGAGAGAGGAAGTGTCTTCAGAGTGGGACTGCATGAGTATCCCGTCCGCTCC

Gene : HepC1a
Segment# : 144
Offset : 2146
1st Codon : 1

E V S F R V G L H E Y P V G S Q L P C E P E P D V A V L T S
GAGGTCAAGTTAGGGTCCGCCCTCCAGGAATACCTGTGGGAAGCCAAGTGCCTTGCGAACCCGAACCCGATGTGGCTGTGCTACCTCC

Gene : HepC1a
Segment# : 145
Offset : 2161
1st Codon : 1

Q L P C E P E P D V A V L T S M L T D P S H I T A E A A G R
CAGCTCCCTGTGAGCCTGAGCCTGACGTGCCGTCTGACAAGCATGCTGACAGACCTAGCCATATCACAGCCGAAGCCGCTGGCAGA

Gene : HepC1a
Segment# : 146
Offset : 2176
1st Codon : 1

M L T D P S H I T A E A A G R R L A R G S P P S M A S S S A
ATGCTCACCGATCCCTCCACATTACCGCTGAGGCTGCCGGAAGGAGACTGGCTAGGGGAAGCCCTCCCTCCATGGCTAGCTCCAGCGTC

Gene : HepC1a
Segment# : 147
Offset : 2191
1st Codon : 1

R L A R G S P P S M A S S S A S Q L S A P S L K A T C T A N
AGGCTGCCAGAGGCTCCCGCCCTAGCATGGCTCCAGCTCCGCTCCAGCTCAGCGCTCCCTCCCTGAAAGCCACATGCACAGCCAAAT

Figure 26 (Cont)

125/216

Gene : HepC1a
Segment# : 148
Offset : 2206
1st Codon : 1
S Q L S A P S L K A T C T A N H D S P D A E L I E A N L L W
AGCCAAC TGT CGC C C C T A G C C T C A A G G C T A C C T G T A E C G C T A A C C A T G A C T C C C C G A T G C C G A A C T G A T T G A G G C T A A C C T C C T G T G G

Gene : HepC1a
Segment# : 149
Offset : 2221
1st Codon : 1
H D S P D A E L I E A N L L W R Q E M G G N I T R V E S E N
C A C G A T A G C C C T G A C G T G A G C T C A T C G A A G C C A A T C T G C T C T G G A G A C A G G A A T G G G A G G C A A T A T C A C A A G G G T C G A G T C C G A G A A T

Gene : HepC1a
Segment# : 150
Offset : 2236
1st Codon : 1
R Q E M G G N I T R V E S E N K V V I L D S F D P L V A E E
A G G C A A G A G A T G G G C G G A A A C A T T A C C A G A G T G G A A A G C G A A A C A A A G T G G T C A T C C T C G A C T C C T T C G A T C C C C T G T G G C T G A G G A A

Gene : HepC1a
Segment# : 151
Offset : 2251
1st Codon : 1
K V V I L D S F D P L V A E E D E R E I S V P A E I L R K S
A A G T C G T G A T T C T G G A T A G C T T T G A C C C T C T G G T C G C G A A G A G A G A T A G A G A G A G A T T A G C G T C C C G C T G A G A T T C T G A G A A A G T C C

Gene : HepC1a
Segment# : 152
Offset : 2266
1st Codon : 1
D E R E I S V P A E I L R K S R R F A Q A L P V W A R P D Y
G A C G A A A G G G A A A T C C C G T G C C T G C C G A A A T C C T C A G G A A A G C A G A A G G T T T G C C C A A G C C C T C C C C G T C T G G G C T A G G C C T G A C T A T

Gene : HepC1a
Segment# : 153
Offset : 2281
1st Codon : 1
R R F A Q A L P V W A R P D Y N P P L V E T W K K P D Y E P
A G G A G A T T C G C T C A G G C T C T G C C T G T G T G G G C C A G A C C C G A T T A C A A T C C C C C T C T G G T C G A G A C A T G G A A A A G C C T G A C T A T G A G C C T

Gene : HepC1a
Segment# : 154
Offset : 2296
1st Codon : 1
N P P L V E T W K K P D Y E P P V V H G C P L P P P R S P P
A A C C C T C C C C T G T G G A A C C T G G A A G A A C C C G A T T A C G A A C C C C T G T G G T C C A C G G A T G C C C T C T G C C T C C C C C T A G G T C C C C C C C T

Gene : HepC1a
Segment# : 155
Offset : 2311
1st Codon : 1
P V V H G C P L P P P R S P P V P P P R K K R T V V L T E S
C C G T C G T G C A T G G C T G T C C C C T C C C C C C T C C C A G A G C C C T C C G T C C C C C C T C C C A G A A G A A A G G A C A G T G G T C C T G A C A G A G T C C

Gene : HepC1a
Segment# : 156
Offset : 2326
1st Codon : 1
V P P P R K K R T V V L T E S T L S T A L A E L A T K S F G
G T G C C T C C C C T A G G A A A A G A G A A C C G T C G T G C T C A C G A A A G C A C A C T G T C C A C C G C T C T G G C T G A G C T C G C C A C A A A G T C C T C G G A

Gene : HepC1a
Segment# : 157
Offset : 2341
1st Codon : 1
T L S T A L A E L A T K S F G S S S T S G I T G D N T T T S
A C C C T C A G C A C A G C C C T G C C G A A C T G G C T A C C A A A G C T T T G G C T C C A G T C C A C C T C C G G C A T T A C C G G A G A C A A T A C C A C A A C C T C C

Gene : HepC1a
Segment# : 158
Offset : 2356

Figure 26 (Cont)

126/216

1st Codon : 1
S S S T S G I T G D N T T T S S E P A P S G C P P D S D A E
AGCTCCAGCACAGCGGAATCACAGGCGATAACACAACCACAAGCTCCGAGCCTGCCCCCTAGCGGATGCCCTCCCGATAGCGATGCCGAA

Gene : HepC1a
Segment# : 159
Offset : 2371
1st Codon : 1
S E P A P S G C P P D S D A E S Y S S M P P L E G E P G D P
AGCGAACCCTCCCTCCGGCTGTCCCCCTGACTCCGACGCTGAGTCTACTCCAGCATGCCCTCTGGAAGGCGAACCCTGAGACCCCT

Gene : HepC1a
Segment# : 160
Offset : 2386
1st Codon : 1
S Y S S M P P L E G E P G D P D L S D G S W S T V S S E A G
AGCTATAGCTCCATGCCCTCCCTCGAGGAGAGCCTGGCGATCCCGATCTGTCCGACGGAAGCTGGAGCACAGTGTCCAGCGAAGCCGGA

Gene : HepC1a
Segment# : 161
Offset : 2401
1st Codon : 1
D L S D G S W S T V S S E A G T E D V V C C S M S Y S W T G
GACCTCAGCGATGGCTCCTGGTCCACCGTCAGCTCCGAGGCTGGCACAGAGGATGTGGTCTGCTGTAGCATGAGCTATAGCTGGACCGGA

Gene : HepC1a
Segment# : 162
Offset : 2416
1st Codon : 1
T E D V V C C S M S Y S W T G A L V T P C A A E E Q K L P I
ACCGAAGACGTGCTGTGCTCCATGTCTACTCTGGACAGGCGCTCTGGTCACCCCTTGCGCTGCCGAAGAGCAAAGCTCCCCATT

Gene : HepC1a
Segment# : 163
Offset : 2431
1st Codon : 1
A L V T P C A A E E Q K L P I N A L S N S L L R H H N L V Y
GCCCTCGTGACACCTGTGCGCTGAGGAACAGAAAAGCTGCTATCAATGCCCTCAGCAATAGCCTCCTGAGACACCATAACCTCGTGTAT

Gene : HepC1a
Segment# : 164
Offset : 2446
1st Codon : 1
N A L S N S L L R H H N L V Y S T T S R S A C Q R Q K K V T
AACGCTCTGTCCAATCCCTGCTCAGGCATCACAATCTGGTCTACTCCACCACAAGCAGAACGCTTGCCAAAGGCAAAGAAAGTGACA

Gene : HepC1a
Segment# : 165
Offset : 2461
1st Codon : 1
S T T S R S A C Q R Q K K V T F D R L Q V L D S H Y Q D V L
AGCAACACCTCCAGGTCCGCTGTGAGAGACAGAAAAGGTCACTTTGACAGACTGCAAGTGTCTGACTCCCACTATCAGGATGTGCTC

Gene : HepC1a
Segment# : 166
Offset : 2476
1st Codon : 1
F D R L Q V L D S H Y Q D V L K E V K A A A S K V K A N L L
TTCGATAGGCTCCAGGTCCCTGGATAGCCATTACCAAGACGCTCTGAAAGAGGTCAAGGCTGCCGCTAGCAAAGTGAAAGCCAATCTGCTC

Gene : HepC1a
Segment# : 167
Offset : 2491
1st Codon : 1
K E V K A A A S K V K A N L L S V E E A C S L T P P H S A K
AAGGAAGTGAAAGCGCTGCCCTCCAGGTCAAGGCTAACCTCTGTCCGTGGAAGAGGCTTGCTCCCTGACACCCCTCACTCCGCCAAA

Gene : HepC1a
Segment# : 168
Offset : 2506
1st Codon : 1
S V E E A C S L T P P H S A K S K F G Y G A K D V R C H A R
AGCGTCGAGGAAGCCTGTAGCCTCACCCCTCCCCATAGCGCTAAGTCCAAGTTTGGCTATGGCGCTAAGGATGTGAGATGCCATGCCAGA

Figure 26 (Cont)

127/216

Gene : HepC1a
Segment# : 169
Offset : 2521
1st Codon : 1
S K F G Y G A K D V R C H A R K A V A H I N S V W K D L L E
AGCAAATTCGGATACGGAGCCAAAGACGTCAGGTGTACGCTAGGAAAGCCGTCGCCCATATCAATAGCGTCTGGAAAGACCTCTCGGAA

Gene : HepC1a
Segment# : 170
Offset : 2536
1st Codon : 1
K A V A H I N S V W K D L L E D S V T P I D T T I M A K N E
AAGGCTGTGGCTCACATTAACCTCGTGTGGAAGGATCTGCTCGAGGATAGCGTCACCCCTATCGATACCACAATCATGGCCAAAAACGAA

Gene : HepC1a
Segment# : 171
Offset : 2551
1st Codon : 1
D S V T P I D T T I M A K N E V F C V Q P E K G G R K P A R
GACTCCGTGACACCCATTGACACAACCATTATGGCTAAGAAATGAGGTCTTCTGTGTGCAACCCGAAAAGGGAGGCAGAAAGCCTGCCAGA

Gene : HepC1a
Segment# : 172
Offset : 2566
1st Codon : 1
V F C V Q P E K G G R K P A R L I V F P D L G V R V C E K M
GTGTTTTCGGCTCCAGCCTGAGAAAGGCGGAAGGAAACCGCTAGGCTCATCGTCTTCCCTGACCTCGGCGTCAGGGTCTGCGAAAAGATG

Gene : HepC1a
Segment# : 173
Offset : 2581
1st Codon : 1
L I V F P D L G V R V C E K M A L Y D V V S K L P L A V M G
CTGATTGTGTTTCCCGATCTGGGAGTGAGAGTGTGTGAGAAAATGGCTCTGTATGACGTGCTGTCCAAAGCTCCCCCTCGCGTCATGGGA

Gene : HepC1a
Segment# : 174
Offset : 2596
1st Codon : 1
A L Y D V V S K L P L A V M G S S Y G F Q Y S P G Q R V E F
GCCCTCTACGATGTGGTCAGCAAACCTGCTCTGGCTGTGATGGGCTCCAGCTATGGCTTTCAGTATAGCCCTGGCCAAAGGGTCGAGTTT

Gene : HepC1a
Segment# : 175
Offset : 2611
1st Codon : 1
S S Y G F Q Y S P G Q R V E F L V Q A W K S K K T P M G F S
AGCTCTACGATTCCCACTACTCCCCGGACAGAGAGTGAATTCCTGTGCAAGCCTGGAAGTCCAAGAAAACCCCTATGGGATTCTCC

Gene : HepC1a
Segment# : 176
Offset : 2626
1st Codon : 1
L V Q A W K S K K T P M G F S Y D T R C F D S T V T E S D I
CTGGTCCAGGCTTGGAAGCAAAAAGACACCCATGGGCTTTAGCTATGACACAAGGTGTTTCGATAGCACAGTGACAGAGTCCGACATT

Gene : HepC1a
Segment# : 177
Offset : 2641
1st Codon : 1
Y D T R C F D S T V T E S D I R T E E A I Y Q C C D L D P Q
TACGATACCAGATGCTTTGACTCCACCGTCACCGAAAGCGATATCAGAACCGAAGAGGCTATCTATCAGTGTTCGGATCTGGATCCCCAA

Gene : HepC1a
Segment# : 178
Offset : 2656
1st Codon : 1
R T E E A I Y Q C C D L D P Q A R V A I K S L T E R L Y V G
AGGACAGAGGAAGCCATTACCAATGCTGTGACCTCGACCTCAGGCTAGGGTCGCCATTAAGTCCCTGACAGAGAGACTGTATGTGGGA

Gene : HepC1a
Segment# : 179

Figure 26 (Cont)

128/216

Offset : 2671
1st Codon : 1
A R V A I K S L T E R L Y V G G P L T N S R G E N C G Y R R
GCCAGAGTGGCTATCAAAAGCCTCACCGAAAGGCTCTAGTCGGCGGACCCCTCACCAATAGCAGAGGCGAAACTGTGGCTATAGGAGA

Gene : HepC1a
Segment# : 180
Offset : 2686
1st Codon : 1
G P L T N S R G E N C G Y R R C R A S G V L T T S C G N T L
GGCCCTCTGACAAACTCCAGGGGAGAGAATTGCGGATACAGAAGGTGTAGGGCTAGCGGAGTGCTCACCACAAGCTGTGGCAATACCCCTC

Gene : HepC1a
Segment# : 181
Offset : 2701
1st Codon : 1
C R A S G V L T T S C G N T L T C Y I K A R A A C R A A G L
TGCAGAGCCTCCGGCGTCTGACAACTCTGCGGAAACACACTGACATGCTATATCAAAGCCAGAGCCGCTTGAGAGCCGCTGGCCCTC

Gene : HepC1a
Segment# : 182
Offset : 2716
1st Codon : 1
T C Y I K A R A A C R A A G L Q D C T M L V C G D D L V V I
ACCTGTACATTAAGGCTAGGGCTGCTGTAGGGCTGCCGAGTGCAGAGCTGTACCATGCTGGTCTGCGGAGACGATCTGGTCTGTGATT

Gene : HepC1a
Segment# : 183
Offset : 2731
1st Codon : 1
Q D C T M L V C G D D L V V I C E S A G V Q E D A A S L R A
CAGATTGCACATGCTCGTGTGTGGCGATGACCTCGTGGTCATCTGTGAGTCCGCGGAGTGCAAGAGGATGCGCTAGCCTCAGGGCT

Gene : HepC1a
Segment# : 184
Offset : 2746
1st Codon : 1
C E S A G V Q E D A A S L R A F T E A M T R Y S A P P G D P
TGCGAAAGCGCTGGCGTCCAGGAAGACGCTGCCCTCCCTGAGAGCCTTTACCGAAGCCATGACCAGATACTCCGCCCCCTCCCGGAGACCTC

Gene : HepC1a
Segment# : 185
Offset : 2761
1st Codon : 1
F T E A M T R Y S A P P G D P P Q P E Y D L E L I T S C S S
TTACAGAGGCTAGACAAAGGTATAGCGCTCCCCCTGGCGATCCCCCTCAGCCTGAGTATGACCTCGAGCTCATCACAAAGCTGTAGCTCC

Gene : HepC1a
Segment# : 186
Offset : 2776
1st Codon : 1
P Q P E Y D L E L I T S C S S N V S V A H D G A G K R V Y Y
CCCCAACCGAATACGATCTGGAAGTATTACCTCCTGCTCCAGCAATGTGTCCGTGGCTCAGATGGCGCTGGCAAAAGGCTACTAT

Gene : HepC1a
Segment# : 187
Offset : 2791
1st Codon : 1
N V S V A H D G A G K R V Y Y L T R D P T T P L A R A A W E
AACGTACGCTGCCCCATGACGGAGCCGGAAGAGAGTGTATTACCTCACCAGAGACCTACCAACCCCTCGCCAGAGCCGCTTGGGAA

Gene : HepC1a
Segment# : 188
Offset : 2806
1st Codon : 1
L T R D P T T P L A R A A W E T A R H T P V N S W L G N I I
CTGACAAAGGATCCCAACCCCTCTGGCTAGGGCTGCTGGGAGACAGCCAGACACACCCGCTCAACTCCTGGCTCGGCAATATCATT

Gene : HepC1a
Segment# : 189
Offset : 2821
1st Codon : 1
T A R H T P V N S W L G N I I M F A P T L W A R M I L M T H

Figure 26 (Cont)

129/216

ACCGCTAGGCATACCCCTGTGAATAGCTGGCTGGGAAACATTATCATGTTGCTCCACACTGTGGGCCAGAATGATTCTGATGACCCAT

Gene : HepC1a
Segment# : 190
Offset : 2836
1st Codon : 1

M F A P T L W A R M I L M T H F F S V L I A R D Q L E Q A L
ATGTTTGCCCTACCCCTCTGGGCTAGGATGATCCTCATGACACACTTTTCTCCGTGCTCATCGCTAGGGATCAGCTCGAGCAAGCCCTC

Gene : HepC1a
Segment# : 191
Offset : 2851
1st Codon : 1

F F S V L I A R D Q L E Q A L D C E I Y G A C Y S I E P L D
TTCTTTAGCGTCTGATTGCCAGAGACCACTGGAAACAGGCTCTGGATTGCGAAATCTATGGCGCTTGCTATAGCATTGAGCCTCTGGAT

Gene : HepC1a
Segment# : 192
Offset : 2866
1st Codon : 1

D C E I Y G A C Y S I E P L D L P P I I Q R L H G L S A F S
GACTGTGAGATTACGGAGCCTGTACTCCATCGAACCCCTCGACCTCCCCCTATCATTAGAGACTGCATGGCCTCAGCGCTTTCTCC

Gene : HepC1a
Segment# : 193
Offset : 2881
1st Codon : 1

L P P I I Q R L H G L S A F S L H S Y S P G E I N R V A A C
CTGCCCTCCATTATCCAAAGGCTCCACGGACTGTCCGCTTTAGCTCCACTCTACTCCCCGGAGAGATTAAACAGAGTGGCTGCGCTGT

Gene : HepC1a
Segment# : 194
Offset : 2896
1st Codon : 1

L H S Y S P G E I N R V A A C L R K L G V P P L R A W R H R
CTGCATAGCTATAGCCCTGGCGAAATCAATAGGGTCGCCGCTTGCTCAGGAACTGGGAGTGCCTCCCCCTCAGGGCTTGGAGACACAGA

Gene : HepC1a
Segment# : 195
Offset : 2911
1st Codon : 1

L R K L G V P P L R A W R H R A R S V R A R L L A R G G R A
CTGAGAAAGCTCGGCGTCCCCCTCTGAGAGCCTGGAGGCATAGGGCTAGGTCCGTGAGAGCCAGACTGCTCGCCAGAGGCGGAAGGGCT

Gene : HepC1a
Segment# : 196
Offset : 2926
1st Codon : 1

A R S V R A R L L A R G G R A A I C G K Y L F N W A V R T K
GCCAGAAGCCTCAGGCTAGGCTCTGGCTAGGGGAGGCAGAGCCGCTATCTGTGGCAAATACCTCTTCAATTGGGCTGTGAGAACCAAA

Gene : HepC1a
Segment# : 197
Offset : 2941
1st Codon : 1

A I C G K Y L F N W A V R T K L K L T P I A A A G R L D L S
GCCATTTGCGGAAAGTATCTGTTAACTGGGCGCTCAGGACAAAGCTCAAGCTCACCCCTATCGCTGCCGCTGGCAGACTGGATCTGTCC

Gene : HepC1a
Segment# : 198
Offset : 2956
1st Codon : 1

L K L T P I A A A G R L D L S G W F T A G Y S G G D I Y H S
CTGAAACTGACACCCATTGCCGCTGCCGGAAGGCTCGACCTCAGCGGATGGTTTACCGCTGGCTATAGCGGAGGCGATATCTATCACTCC

Gene : HepC1a
Segment# : 199
Offset : 2971
1st Codon : 1

G W F T A G Y S G G D I Y H S V S H A R P R W F W F C L L L
GGCTGGTTACAGCCGATACTCCGGCGGAGACATTTACCATAGCGTCAGCCATGCCAGACCAGATGGTTTTGGTTTTGCTCCTGCTC

Gene : HepC1a

Figure 26 (Cont)

130/216

Segment# : 200
Offset : 2986
1st Codon : 1
V S H A R P R W F W F C L L L L A A G V G I Y L L P N R A A
GTGTCACGCTAGGCCTAGGTGGTTCGTCTGCTCGCTCGCCGCTGGCGCTGGCATTACCTCCTGCCTAACAGAGCCGCT

Gene : HepC1a
Segment# : 201
Offset : 3001
1st Codon : 1
L A A G V G I Y L L P N R A A
CTGGCTGCCGAGTGGGAATCTATCTGCTCCCAATAGGGCTGCC

Segments in scrambled order:

HepC1a #77
V I P V R R R G D S R G S L L S P R P I S Y L K G S S G G P
GTGATTCCTCAGGAGAAGGGGAGACTCCAGGGGAAGCCTCCTGTCCCCCAGACCCATTAGCTATCTGAAAGGCTCCAGCGGAGGCCCT

HepC1a #68
A R R G R E I L L G P A D G M V S K G W R L L A P I T A Y A
GCCAGAAGGGGAAGGAAATCCTCCTGGGACCCGCTGACGGAATGGTCAGCAAAGGCTGGAGGCTCCTGGCTCCATTACCGCTACGCT

HepC1a #143
R L H R F A P P C K P L L R E E V S F R V G L H E Y P V G S
AGGCTCCACAGATTCCCTCCCCCTGCAAACCCCTCCTGAGAGAGGAAGTGTCTTCAGAGTGGGACTGCATGAGTATCCCGTGGGCTCC

HepC1a #66
V V F S Q M E T K L I T W G A D T A A C G D I I N G L P V S
GTGGTCTTCTCCAGATGGAGACAAAGCTCATCACATGGGGAGCCGATACCGCTGCCTGTGGCGATATCATTAAACGGACTGCCTGTGTCTC

HepC1a #79
L L C P A G H A V G I F R A A V C T R G V A K A V D F I P V
CTGCTCTGCCCTGCCGACACGCTGTGGGAATCTTAGGGCTGCCCTCTGCACAAGGGGAGTGGCTAAGGCTGTGGATTTCATTCCCGTC

HepC1a #113
C V V I V G R I V L S G K P A I I P D R E V L Y R E F D E M
TGCGTCGTGATGTGGGAAGGATTGTGCTCAGCGGAAAGCCTGCCATTATCCCTGACAGAGAGGCTCCTGTATAGGAATTTCGATGAGATG

HepC1a #139
P C T P L P A P N Y T F A L W R V S A E E Y V E I R R V G D
CCCTGTACCCCTCTGCCTGCCCTAACTATACCTTTGCCCTCTGGAGAGTGTCCGCCGAAGAGTATGTGGAAATCAGAAGGGTCCGGCGAT

HepC1a #174
A L Y D V V S K L P L A V M G S S Y G F Q Y S P G Q R V E F
GCCCTCTACGATGTGGTCAGAACTGCCTCTGGCTGTGATGGGCTCCAGCTATGGCTTTCAGTATAGCCCTGGCCAAAGGGTCGAGTTT

HepC1a #57
I S W C L W W L Q Y F L T R V E A Q L H V W V P P L N V R G
ATCTCCTGGTGTCTGTGGTGGCTCCAGTATTCTCTCACCAGAGTGGGAAGCCCACTGCATGTGTGGGTGCCTCCCCTCAACGTACGGGGA

HepC1a #51
E N L V I L N A A S L A G T H G L V S F L V F P C F A W Y L
GAGAATCTGGTCATCCTCAACGCTGCCCTCCCTGGCTGGCACACAGGACTGGTCAGCTTTCTGGTCTTCTTTTGTCTTGGCTGGTACCTC

HepC1a #193
L P P I I Q R L H G L S A F S L H S Y S P G E I N R V A A C
CTGCTCCCATATACCAAGGCTCCACGGACTGTCCGCCCTTAGCCTCCACTCCTACTCCCCCGGAGAGATTAAACAGAGTGGCTGCCTGT

HepC1a #154
N P P L V E T W K K P D Y E P P V V H G C P L P P P R S P P
AACCCTCCCCCTCGTGGAAACCTGGAAGAAACCCGATTACGAACCCCTGTGGTCCACGGATGCCCTCTGCCTCCCCCTAGGTCCCCCCT

HepC1a #48
G V G S S I A S W A I K W E Y V V L L F L L L A D A R V C S
GGCGTCGGCTCAGCATGCTCTCTGGGCTATCAAAATGGGAATACGTGCTGCTCTGTTCTGCTCCTGGCTGACGCTAGGGCTGCTCTC

HepC1a #37
L N N T R P P L G N W F G C T W M N S T G F T K V C G A P P
CTGAATAACACAAGGCCCTCCCTCGGCAATTGGTTTGGCTGTACCTGGATGAATAGCACAGGCTTTACCAAAGTGTGTGGCGCTCCCCCT

HepC1a #185
F T E A M T R Y S A P P G D P P Q P E Y D L E L I T S C S S

Figure 26 (Cont)

131/216

TTCACAGAGGCTATGACAAGGTATAGCGCTCCCCCTGGCGATCCCCCTCAGCCTGAGTATGACCTCGAGCTCATCACAAGCTGTAGCTCC

HepCla #54

W P L L L L L L A L P Q R A Y A L D T E V A A S C G G V V L
TGGCCTCTGCTCCTGCTCCTGCTCGCCCTCCCCAAAGGGCTTACGCTCTGGATACCGAAGTGGCTGCCTCTGCGGAGGCGTGTGCTC

HepCla #70

Q Q T R G L L G C I I T S L T G R D K N Q V E G E V Q I V S
CAGCAAACAGAGGCTCCTGGGATGCATTATCACAAGCCTACCGGAAGGGATAAGAATCAGGTCGAGGGAGAGGTCCAGATTGTGTCC

HepCla #82

S S P P A V P Q S F Q V A H L H A P T G S G K S T K V P A A
AGCTCCCCCCTGCCGTCCCCAAAGCTTTAGGTCGCCATCTGTCATGCCCTACCGGAAGCGGAAAGTCCACCAAAGTGCCTGCCGCT

HepCla #104

N T P G L P V C Q D H L E F W E G V F T G L T H I D A H F L
AACACACCGGACTGCCTGTGTGTCAGGATCACCCTGAGTTTGGGAAGGCGTCTTCACAGGCTCACCCATATCGATGCCATTTCCTC

HepCla #26

V L L L F A G V D A E T H V T G G N A G R T T S G L V S L L
GTGCTCCTGCTCTTCGTGGCGTCGACGCTGAGACACACGTCACCGGAGGCAATGCCGAAGGACAACCTCCGGCCTCGTGTCCCTGCTC

HepCla #110

E V T L T H P V T K Y I M T C M S A D L E V V T S T W V L V
GAGTCCACCTCACCCATCCCGTCACCAAATACATTATGACATGCATGAGCGCTGACCTCGAGGTCGTGACAAGCACATGGGTCTGGTC

HepCla #56

V G L M A L T L S P Y Y K R Y I S W C L W W L Q Y F L T R V
GTGGACTGATGGCCCTCACCCCTCAGCCCTTACTATAAGAGATACATTAGCTGTGCCTCTGGTGGCTGCAATCTTTCTGACAAGGGTC

HepCla #197

A I C G K Y L F N W A V R T K L K L T P I A A A G R L D L S
GCCATTTGCGGAAAGTATCTGTTAACTGGGCGCTCAGGACAAAGCTCAAGCTCACCCCTATCGCTGCCGCTGGCAGACTGGATCTGTCC

HepCla #25

I A Y F S M V G N W A K V L V V L L L F A G V D A E T H V T
ATCGCTTACTTTAGCATGGTGGGAACTGGGCCAAAGTGCTCGTGGTCTGTCTCTGTTTGCCGGAGTGGATGCCGAAACCCATGTGACA

HepCla #147

R L A R G S P P S M A S S S A S Q L S A P S L K A T C T A N
AGGCTCGCCAGAGCTCCCCCCTAGCATGGCTCCAGCTCCGCTCCAGCTCAGCGCTCCCTCCCTGAAAGCCACATGCACAGCCAAT

HepCla #52

G L V S F L V F F C F A W Y L K G R W V P G A V Y A L Y G M
GGCCTCGTGTCTCTCCTCGTGTCTTTCTGTTTCGCTTGGTATCTGAAAGGCAGATGGGTCCCCGGAGCCGTCTACGCTCTGTATGGCATG

HepCla #145

Q L P C B E P E P D V A V L T S M L T D P S H I T A E A A G R
CAGCTCCCCCTGTGAGCCTGAGCCTGACGTCGCGCTCCTGACAAGCATGCTGACAGACCCTAGCCATATCACAGCCGAAGCGCTGGCAGA

HepCla #171

D S V T P I D T T I M A K N E V F C V Q P E K G G R K P A R
GACTCCGTGACCCATTGACACAACCATTTATGGCTAAGAATGAGGTCTTCTGTGTGCAACCCGAAAGGGAGGCAGAAAGCCTGCCAGA

HepCla #84

Y A A Q G Y K V L V L N P S V A A T L G F G A Y M S K A H G
TACGTCGCCAAGGCTATAAGGTCTGTGCTGAATCCCTCCGTGGCTGCCACACTGGGATTGGAGCCTATATGTCCAAGGCTCACGGA

HepCla #14

V R N S T G L Y H V T N D C P N S S I V Y E A A D A I L H T
GTGAGAACTCCACCGACTGTATCACGTACCAATGACTGTCCCAATAGCTCCATCGTCTACGAAGCCGCTGACGCTATCTCCACACA

HepCla #175

S S Y G F Q Y S P G Q R V E F L V Q A W K S K K T P M G F S
AGCTCCTACGGATTCCAATACTCCCCGGACAGAGTGGAAATCTCTGTGCAAGCCTGGAAGTCCAAGAAAACCCCTATGGGATTCTCC

HepCla #67

D T A A C G D I I N G L P V S A R R G R E I L L G P A D G M
GACACAGCCGCTTGGCGAGACATTATCAATGGCCTCCCGCTCAGCGCTAGGAGAGGCAGAGAGATTCTGCTCGGCCCTGCCGATGGCATG

HepCla #148

S Q L S A P S L K A T C T A N H D S P D A E L I E A N L L W
AGCCAACTGTCCGCCCTAGCCTCAAGGCTACCTGTACCGCTAACCATGACTCCCCCGATGCCGAAGTGAATGAGGCTAACCTCCTGTGG

Figure 26 (Cont)

HepC1a #120
N P A I A S L M A F T A A V T S P L T T S Q T L L F N I L G.
A A C C C T G C C A T T G C C T C C C T G A T G G C C T T T A C C G C T G C C G T C A C C T C C C C C C T C A C C A G A G C C A A A C C C T C C T G T T T A A C A T T C T G G G A

HepC1a #176
L V Q A W K S K K T P M G F S Y D T R C F D S T V T E S D I
C T G G T C C A G G C T T G G A A A G C A A A A A G A C A C C C A T T G G G C T T T A G C T A T G A C A C A G G T G T T T C G A T A G C A C A G T G A C A G A G T C C G A C A T T

HepC1a #152
D E R E I S V P A R I L R K S R R F A Q A L P V W A R P D Y
G A C G A A A G G G A A A T C C G T G C C T G C C G A A A T C C T C A G G A A A G C A G A A G G T T T G C C A A G C C C T C C C G T C T G G G C T A G G C C T G A C T A T

HepC1a #190
M F A P T L W A R M I L M T H F F S V L I A R D Q L E Q A L
A T G T T T G C C C T A C C C T C T G G G C T A G G A T G A T C C T C A T G A C A C A T T T T C T C G T G C T C A T C G T A G G G A T C A G C T C G A G C A A G C C C T C

HepC1a #96
S V I P T S G D V V V V A T D A L M T G Y T G D F D S V I D
A G C G T C A T C C C T A C C T C C G G C G A T G T G G T C G T G G T C G C C A C A G A C G C T C T G A T G A C C G G A T A C A C A G G C G A T T T C G A T A G C G T C A T C G A T

HepC1a #94
C H S K K K C D E L A A K L V A L G I N A V A Y Y R G L D V
T G C C A T A G C A A A A G A A A T G C G A T G A G C T C G C C G T A A G C T C G T G G C T C T G G A A T C A A T G C C G T C G C C T A T T A C A G A G G C C T C G A C G T C

HepC1a #46
V L P C S F T T L P A L S T G L I H L H Q N I V D V Q Y L Y
G T G C T C C C C T G T A G C T T T A C C A C A C T G C C T G C C C T C A G C A C A G G C C T C A T C C A T C T G C A T C A G A A T A T C G T C G A C G T C C A G T A T C T G T A T

HepC1a #53
K G R W V P G A V Y A L Y G M W P L L L L L L A L P Q R A Y
A A G G G A A G G T G G G T G C T G G C G T G T G T A T G C C C T C T A C G G A A T G T G G C C C C T C C T G C T C C T G C T C T G G C T C T G C C T C A G A G A G C C T A T

HepC1a #87
S P I T Y S T Y G K F L A D G G C S G G A Y D I I I C D E C
A G C C C T A T C A C A T A C T C C A C C T A T G G C A A A T T C C T C G C C G A T G G C G G A T G C T C C G G C G G A G C C T A T G A C A T T A T C A T T T G C G A T G A G T G T

HepC1a #196
A R S V R A R L L A R G G R A A I C G K Y L F N W A V R T K
G C C A G A A G C T C A G G C T A G G C T C C T G G C T A G G G G A G G C A G A G C C G C T A T C T G T G C A A A T A C C T C T T C A A T T G G G C T G T G A G A C C A A

HepC1a #170
K A V A H I N S V W K D L L E D S V T P I D T T I M A K N E
A A G G C T G T G G C T C A C A T T A A C C G T G T G G A A G G A T C T G C T C A G A T A G C C T A C C C C T A T C G A T A C C A A T C A T G G C C A A A A C G A A

HepC1a #35
F T P S P V V V G T T D R S G A P T Y S W G A N D T D V F V
T T C A C A C C C T C C C C G T C G T G G T C G G C A C A A C G A T A G G T C G G G C G T C C C A C A T A C T C C T G G G G A G C C A A T G A C A C A G A C G T C T T C G T C

HepC1a #16
P G C V P C V R E G N A S R C W V A M T P T V A T R D G K L
C C C G G A T C G C T C C C C T G T G T G A G A G A G G A A C G C T A G C A G A T G C T G G G T G G C T A T G A C A C C C A C A G T G G C T A C C A G A G A C G G A A A G C T C

HepC1a #183
Q D C T M L V C G D D L V V I C E S A G V Q E D A A S L R A
C A G G A T T G C A C A A T G C T C G T G T G G C G A T G A C C T C G T G G T C A T C T G T G A G T C G C C G G A G T G C A A G A G G A T G C C G C T A G C C T C A G G C T

HepC1a #125
V A G A L V A F K I M S G E V P S T E D L V N L L P A I L S
F T G G C T G G C G C T C T G G T G C C T T T A A G A T A T G T C C G G C G A A G T G C C T A G C A C A G A G A T C T G G T C A A C C T C C T G C C T G C C A T T C T G T C C

HepC1a #177
Y D T R C F D S T V T E S D I R T E E A I Y Q C C D L D P Q
T A C G A T A C C A G A T G C T T T G A C T C C A C C G T C A C C G A A A G C G A T A T C A G A A C C G A A G A G G C T A T C T A T C A G T G T G C G A T C T G G A T C C C C A A

HepC1a #103
E L T P A E T T V R L R A Y M N T P G L P V C Q D H L E F W
S A G C T A C C C C T G C C G A A A C C A C A G T G A G A C T G A G A G C C T A T A T G A A T A C C C C T G G C C T C C C C G T C T G C C A A G A C C A T C T G G A A T T C T G G

HepC1a #186
P Q P E Y D L E L I T S C S S N V S V A H D G A G K R V Y Y
C C C A A C C G A A T A C G A T C T G G A A C T G A T T A C C T C C T G C T C C A G C A A T G T G T C G T G G C T C A C G A T G G C G T G G C A A A A G G G T C T A C T A T

Figure 26 (Cont)

133/216

HepC1a #9

L G K V I D T L T C G F A D L M G Y I P L V G A P L G G A A
CTGGGAAAGGTCATCGATACCCCTCACCTGTGGCTTTGCCGATCTGATGGGCTATATCCCTCTGGTCGGCGCTCCCTCGGCGGAGCCGCT

HepC1a #93

A I P L E V I K G G R H L I F C H S K K K C D E L A A K L V
GCCATTCCCTCGAGGTCATCAAAGGCGGAAGGCATCTGATTTTCTGTCTACTCCAAGAAAAGTGTGACGAACCTGGCTGCCAAACTGGTC

HepC1a #112

G G V L A A L A A Y C L S T G C V V I V G R I V L S G K P A
GGCGAGTGTCTCGCGCTCTGGCTGCCTATTGCCTCAGCACAGGCTGTGTGGTCATCGTCGGCAGAATCGTCCTGTCCGGCAAACCCGCT

HepC1a #184

C E S A G V Q E D A A S L R A F T E A M T R Y S A P P G D P
TGCGAAAGCGCTGGCGTCCAGGAAGACGCTGCCTCCCTGAGAGCCTTTACCGAAGCCATGACCAGATACTCCGCCCTCCCGGAGACCTC

HepC1a #199

G W F T A G Y S G G D I Y H S V S H A R P R W F W F C L L L
GGCTGGTTACAGCCGGATACTCCGGCGGAGACATTTACCATAGCGTCAGCCATGCCAGACCAGATGGTTTGGTTTGGCTCTCTGCTC

HepC1a #158

S S S T S G I T G D N T T T S S E P A P S G C P P D S D A E
AGCTCCAGCACAAGCGGAATCACAGGCGATAACACAACCAAGCTCCGAGCCCTGCCCTTAGCGGATGCCCTCCCGATAGCGATGCCGAA

HepC1a #100

R T Q R R G R T G R G K P G I Y R F V A P G E R P S G M F D
AGCACACAGAGAAGGGGAAGGACAGGCGAGGCAAAACCCGAATCTATAGGTTTGTGGCTCCCGGAGAGACCCCTCCGGCATGTTTCGAT

HepC1a #43

V R M Y V G G V E H R L E A A C N W T R G E R C D L E D R D
GTGAGAATGTATGTGGGAGGCGTCGAGCATAGGCTCGAGGCTGCCTGTAACTGGACCAGAGGCGAAAGGTGTGACCTCGAGGATAGGGAT

HepC1a #58

E A Q L H V W V P P L N V R G G R D A V I L L M C V V H P T
GAGGCTCAGCTCCACGTCCTGGGTCCCCCTCTGAATGTGAGAGGCGGAAGGATGCCGTCATCCTCCTGATGTGCGTCGTGCATCCACACA

HepC1a #4

L G V R A T R K T S E R S Q P R G R R Q P I P K A R R P E G
CTGGGAGTGAGAGCCACAAGGAAAACCTCCGAGAGAAGCCAAACCCAGAGGCGAGAAGGCAACCCATTCCCAAAGCCAGAAGGCTGAGGGGA

HepC1a #187

N V S V A H D G A G K R V Y Y L T R D P T T P L A R A A W E
AACGTCAGCGTCGCCCATGACGGAGCCGGAAGAGAGTGTATTACCTACCCAGAGACCCCTACCACACCCCTCGCCAGAGCCGCTTGGGAA

HepC1a #159

S E P A P S G C P P D S D A E S Y S S M P P L E G E P G D P
AGCGAACCCGCTCCCTCCGGCTGTCCCCCTGACTCCGACGCTGAGTCTTACTCCAGCATGCCCCCTCTGGAAGGCGAACCCTGGAGACCTC

HepC1a #63

I G G H Y V Q M A I I K L G A L T G T Y V Y N H L T P L R D
ATCGGAGGCCATTACGTCCAGATGGCCATTATCAAATGGGAGCCCTACCGGAACCTATGTGTATAACCATCTGACACCCCTCAGGGAT

HepC1a #126

P S T E D L V N L L P A I L S P G A L V V G V V C A A I L R
CCCTCCACCGAAGACCTCGTGAATCTGCTCCCCGCTATCCTCAGCCCTGGCGCTCTGGTCGTGGGAGTGGTCTGCGCTGCCATTCTGAGA

HepC1a #24

I L D M I A G A H W G V L A G I A Y F S M V G N W A K V L V
ATCCTCGACATGATCGCTGGCGCTCACTGGGGCGTCTGGCTGGCAATTGCCTATTCTCCATGGTCGGCAATTGGGCTAAGGTCTGGTC

HepC1a #7

E G C G W A G N L L S P R G S R P S W G P T D P R R R S R N
GAGGATGCGGATGGGCTGGCTGGCTGCTCAGCCCTAGGGGAAGCAGACCCCTCCTGGGGACCCACAGACCCCTAGGAGAAGGTCCAGGAAT

HepC1a #21

W T T Q G C N C S I Y P G H I T G H R M A W D M M M N W S P
TGGACAACCCAGGCTGTAACTGTAGCATTTACCTGGCCATATCACAGGCCATAGGATGGCCTGGGACATGATGATGAATGGAGCCCT

HepC1a #17

W V A M T P T V A T R D G K L P A T Q L R R H I D L L V G S
TGGGTGCGCATGACCCCTACCGTCCGCCACAAGGATGGCAAACTGCCACACAGCTCAGGAGACACATTGACCTCCTGGTCGGCTCC

HepC1a #42

Figure 26 (Cont)

134/216

R L W H Y P C T I N Y T I F K V R M Y V G G V E H R L E A A
AGGCTCTGGCATTACCTTGCAATCAATTACACAATCTTTAAGGTCAGGATGTACGTCGGCGGAGTGGAAACAGACTGGAAGCCGCT

HepC1a #172

V F C V Q P E K G G R K P A R L I V F P D L G V R V C E K M
GTGTTTTCGCTCCAGCCTGAGAAAGGCGGAAGGAAACCCGCTAGGCTCATCGTCTTCCCTGACCTCGGCGTCAGGGTCTGCGAAAGATG

HepC1a #10

M G Y I P L V G A P L G G A A R A L A H G V R V L E D G V N
ATGGGATACATTCCCTCGTGGGAGCCCTCTGGGAGGCGCTGCCAGAGCCCTCGCCCATGGCGTCAGGGTCTTGGGAAGACGGAGTGAAT

HepC1a #27

G G N A G R T T S G L V S L L T P G A K Q N I Q L I N T N G
GGCGGAAACGCTGGCAGAACCACAAGCGGACTGGTCAGCCTCTGACACCCGGAGCCAAACAGAATATCCAACCTGATTAAACACAAACCGGA

HepC1a #13

L A L L S C L T V P A S A Y Q V R N S T G L Y H V T N D C P
CTGGCTCTGCTCAGCTGTCTGACAGTGCCCTCGCCCTATCAGGTCAGGAATAGCACAGGCCCTTACCATGTGACAAACGATTGCCCT

HepC1a #71

G R D K N Q V E G E V Q I V S T A A Q T F L A T C I N G V C
GGCAGAGACAAAAACCAAGTGAAGGCGAAGTGCAATCGTCAGCACAGCCGCTCAGACATTCTCGCCACATGCATTAAACGGAGTGTGT

HepC1a #18

P A T Q L R R H I D L L V G S A T L C S A L Y V G D L C G S
CCCGCTACCCAACCTGAGAAGGCATATCGATCTGCTCGTGGGAAGCGCTACCCCTGCTCGGCCCTCTACGTCGGCGATCTGTGTGGCTCC

HepC1a #83

H A P T G S G K S T K V P A A Y A A Q G Y K V L V L N P S V
CACGCTCCACAGGCTCCGGCAAAAGCACAAAGGTCCCGCTGCCTATGCCGCTCAGGGATACAAAGTGCTGCTCAACCCCTAGCGTC

HepC1a #6

R T W A Q P G Y P W P L Y G N E G C G W A G W L L S P R G S
AGGACATGGCTCAGCCTGGCTATCCCTGGCCCTCTACGGAACGAAGGCTGTGGCTGGGCGGATGGCTCTGTCCTCCAGAGGCTCC

HepC1a #162

T E D V V C C S M S Y S W T G A L V T P C A A E E Q K L P I
ACCGAAGAGCTGTGTGTGCTCCATGTCTACTCTCTGGACAGGCGCTCTGGTCACCCCTTGGCTGCCGAAGAGCAAAAGCTCCCAT

HepC1a #55

A L D T E V A A S C G G V V L V G L M A L T L S P Y Y K R Y
GCCCTCGACACAGAGGTCCCGCTAGCTGTGGCGGAGTGGTCTGTGGCTCTGACACTGTCCCCCTATTACAAAAGGTAT

HepC1a #38

W M N S T G F T K V C G A P P C V I G G A G N N T L H C P T
TGGATGAACCTCACCGGATTACAAAAGTCTGCGGAGCCCTCCCTGTGTGATTGGCGGAGCGGAAACAATACCCTCCACTGTCCACAC

HepC1a #168

S V E B A C S L T P P H S A K S K F G Y G A K D V R C H A R
AGCGTCGAGGAAGCCTGTAGCCTCACCCCTCCCATAGCGCTAAGTCCAAGTTTGGCTATGGCGCTAAGGATGTGAGATGCCATGCCAGA

HepC1a #119

I S G I Q Y L A G L S T L P G N P A I A S L M A F T A A V T
ATCTCCGGCATTCAATATCTGGCTGCGCTCAGCACACTGCCTGGCAATCCCGCTATCGCTAGCCTCATGGCTTTACAGCCGCTGTGACA

HepC1a #3

Q I V G G V Y L L P R R G P R L G V R A T R K T S E R S Q P
CAGATTGTGGGAGGCTTACCTCCTGCCTAGGAGAGGCCCTAGGCTCGGCGTCAGGGCTACAGAAAGACAAGCGAAAGGTCCAGCCT

HepC1a #194

L H S Y S P G E I N R V A A C L R K L G V P P L R A W R H R
CTGCATAGCTATAGCCCTGGCGAAATCAATAGGGTCGCGCTTGCCCTCAGGAACTGGGAGTGCCCTCCCTCAGGGCTTGGAGACACAGA

HepC1a #189

T A R H T P V N S W L G N I I M F A P T L W A R M I L M T H
ACCGCTAGGCATACCCCTGTGAATAGCTGGCTGGGAAACATTATCATGTTGCTCCCACTGTGGGCCAGAATGATTCTGATGACCAT

HepC1a #81

E N L E T T M R S P V F T D N S S P P A V P Q S F Q V A H L
GAGAATCTGGAACCAATGAGAAGCCCTGTGTTTACCGATAACTCCAGCCCTCCCGCTGTGCCTCAGTCTTCCAAGTGGCTCACCTC

HepC1a #91

A T P P G S V T V P H P N I E E V A L S T T G E I P F Y G K

Figure 26 (Cont)

135/216

GCCACACCCCTGGCTCCGTGACAGTGCCTCACCCCTAACATTGAGGAAGTGGCTCTGTCCACCACAGGCGAAATCCCTTTCTATGGCAAA

HepC1a #60

L V F D I T K L L L A V F G P L W I L Q A S L L K V P Y F V
CTGGTCTTCGATATCAAAAGCTCCTGCTGCGCGTCTTCGGACCCCTCTGGATTCTGCAAGCCTCCCTGCTCAAGGTCCCTATTTCGTG

HepC1a #23

T A A L V M A Q L L R I P Q A I L D M I A G A H W G V L A G
ACCGTGCCTCGTGATGGCCCACTGCTCAGGATTCCCCAAGCCATTCTGGATATGATTGCCGGAGCCATTGGGGAGTGCTCGCCGGA

HepC1a #98

C N T C V T Q T V D F S L D P T F T I E T T T L P Q D A V S
TGCAATACCTGTGTGACACAGACAGTGGATTCTCCCTGGATCCCAATTCAATCGAAACCACAACCTCCCCAAGACGCTGTGTGCC

HepC1a #109

H G P T P L L Y R L G A V Q N E V T L T H P V T K Y I M T C
CACGGACCCACACCCCTCCTGTATAGGCTCGGCGCTGTGCAAAACGAAGTGACACTGACACACCCCTGTGACAAAGTATATCATGACCTGT

HepC1a #179

A R V A I K S L T E R L Y V G G P L T N S R G E N C G Y R R
GCCAGAGTGGCTATCAAAAGCCTCACGAAAGGCTCTACGTGCGCGGACCCCTACCAATAGCAGAGGCGAAAACTGTGGCTATAGGAGA

HepC1a #39

C V I G G A G N N T L H C P T D C F R K H P E A T Y S R C G
TGGTCTATCGGAGGCGCTGGCAATAACACACTGCATTGCCCTACCGATTGCTTTAGGAAACACCCCTGAGGCTACCTATAGCAGATGCCGA

HepC1a #76

T C G S S D L Y L V T R H A D V I P V R R R G D S R G S L L
ACCTGTGGCTCCAGCGATCTGTATCTGGTCACCAGACACGCTGACGTCTCCCTGTGAGAAGGAGAGGCGATAGCAGAGGCTCCCTGCTC

HepC1a #138

N M W S G T F P I N A Y T T G P C T P L P A P N Y T F A L W
AACATGTGGTCCGGCACATTCCCTATCAATGCCTATACCAAGGCCCTTGACACCCCTCCCCGCTCCCAATTACACATTGCTCTGTGG

HepC1a #89

H S T D A T S I L G I G T V L D Q A E T A G A R L V V L A T
CACTCCACCGATGCCACAAGCAATTCTGGGAATCGGAACCGTCTGGATCAGGCTGAGACAGCCGAGCCAGACTGGTCTGTGCTCGCCACA

HepC1a #130

Y V P E S D A A A R V T A I L S S L T V T Q L L R R L H Q W
TACGTCCCCGAAAGCGATGCCGCTGCCAGAGTGACAGCCATTCTGTCCAGCCTCACCGTCACCCACTGCTCAGGAGACTGCATCAGTGG

HepC1a #8

R P S W G P T D P R R R S R N L G K V I D T L T C G F A D L
AGGCCTAGCTGGGGCCCTACCGATCCCAAGGAGAAGCAGAAACCTCGGCAAAAGTGATTGACACACTGACATGCGGATTGCTGACCTC

HepC1a #33

G P D Q R P Y C W H Y P P K P C G I V P A K S V C G P V Y C
GGCCTGACCAAAGGCCTTACTGTTGGCATTACCTCCCAAAACCTGTGGCATTGTGCCTGCCAAAAGCGTCTCGGACCCGCTACTGT

HepC1a #115

E E C S Q H L P Y I E Q G M M L A E Q P K Q K A L G L L Q T
GAGGAATGCTCCAGCATCTGCCTTACATTGAGCAAGGCATGATGCTCGCCGAACAGTTTAAGCAAAAGGCTCTGGGACTGCTCCAGACA

HepC1a #107

Y Q A T V C A R A Q A P P P S W D Q M W K C L I R L K P T L
TACCAAGCCACAGTGTGTGCCAGAGCCCAAGCCCTCCCCCTAGCTGGGACCAATGTGGAAGTGTCTGATTAGGCTCAAGCCTACCCTC

HepC1a #34

C G I V P A K S V C G P V Y C F T P S P V V V G T T D R S G
TGCGGAATCGTCCCCGCTAAGTCCGTGTGTGGCCCTGTGTATTGCTTTACCCCTAGCCCTGTGGTCTGTGGGAACCACAGACAGAAGCGGA

HepC1a #131

S S L T V T Q L L R R L H Q W I S S E C T T P C S G S W L R
AGCTCCCTGACAGTGACACAGCTCCTGAGAAGGCTCCACCAATGGATTAGCTCCGAGTGTACCAACCCCTGTAGCGGAAGCTGGCTGAGA

HepC1a #161

D L S D G S W S T V S S E A G T E D V V C C S M S Y S W T G
GACCTCAGCGATGGCTCCTGGTCCACCGTCAGCTCCGAGGCTGGCACAGAGGATGTGGTCTGCTGTAGCATGAGCTATAGCTGGACCGGA

HepC1a #108

W D Q M W K C L I R L K P T L H G P T P L L Y R L G A V Q N
TGGGATCAGATGTGGAAATGCCTCATCAGACTGAAACCCACATGCATGGCCCTACCCCTCTGCTCTACAGACTGGGAGCCGCTCCAGAAT

Figure 26 (Cont)

136/216

HepC1a #116

L A E Q F K Q K A L G L L Q T A S R Q A E V I A P A V Q T N
CTGGCTGAGCAATTCAAACAGAAAGCCCTCGGCCTCTGTCAAACCGCTAGCAGACAGGCTGAGGTTCATCGCTCCCGCTGTGCAAAACCAAT

HepC1a #118

W Q K L E V F W A K H M W N F I S G I Q Y L A G L S T L P G
TGGCAAAAGCTCGAGGTCTTCTGGGCCAAACACATGTGGAATTTTCATTAGCGGAATCCAATACCTCGCCGACTGTCCACCCTCCCCGGA

HepC1a #129

L I A F A S R G N H V S P T H Y V P E S D A A A R V T A I L
CTGATTGCCTTTGCTCCAGGGGAAACCATGTGTCCCCACACACTATGTGCTGAGTCCGACGCTGCCGCTAGGGTCACCGCTATCCTCT

HepC1a #19

A T L C S A L Y V G D L C G S V F L V G Q L F T F S P R R H
GCCACACTGTGTAGCGCTCTGTATGTGGGAGACCTCTGCGGAAGCGTCTTCTCGTGGGACAGCTCTTCACATTCTCCCCCAGAAGGCAT

HepC1a #102

S S V L C E C Y D A G C A W Y E L T P A E T T V R L R A Y M
AGCTCCGTGCTCTGCGAATGCTATGACGCTGGCTGTGCTGGTACGAACTGACACCCGCTGAGACAACCGTCAAGGCTCAGGGCTTACATG

HepC1a #122

G W V A A Q L A A P G A A T A F V G A G L A G A A I G S V G
GGCTGGGTGGCTGCCCACTGGCTGCCCTGGCGCTGCCACAGCCTTTGTGGGAGCCGACTGGCTGGCGCTGCCATTGGCTCCGTGGGA

HepC1a #29

S W H I N S T A L N C N E S L N T G W L A G L F Y Q H K P N
AGCTGGCACATTAACTCCACCGCTCTGAATTGCAATGAGTCCCTGAATACCGGATGGCTCGCCGACTGTTTACCAACACAAATTCAAT

HepC1a #164

N A L S N S L L R H H N L V Y S T T S R S A C Q R Q K K V T
AAGCTCTGTCCAACCTCCCTGCTCAGGCATCACAATCTGGTCTACTCCACCACAAGCAGAAGCGCTTGCCAAAGGCAAAAGAAAGTGACA

HepC1a #1

A A M S T N P K P Q R K T K R N T N R R P Q D V K F P G G G
CGCGTATGTCCACCAATCCCAAACCCCAAGGAAAACCAAAAGGAATACCAATAGGAGACCCCAAGACGTCAAGTTTCCCGGAGGCGGA

HepC1a #106

S Q T K Q S G E N F P Y L V A Y Q A T V C A R A Q A P P P S
AGCCAAACCAACAGTCCGSGGAAAACCTTTCCTATCTGGTGGCTATCAGGCTACCGTCTGGCTAGGGCTCAGGCTCCCCCTCCCTCC

HepC1a #36

A P T Y S W G A N D T D V F V L N N T R P P L G N W F G C T
GCCCTACCTATAGCTGGGGCGCTAACGATACCGATGTGTTGTGTCTCAACAATACCAGACCCCTCTGGGAACTGGTTGGATGCACA

HepC1a #156

V P P P R K K R T V V L T E S T L S T A L A E L A T K S F G
GTGCTCCCCCTAGGAAAAGAGAACCGTGTGCTCACCGAAAGCACTGTCCACCGCTCTGGCTGAGCTCGCCACAAAGTCTTTCGGA

HepC1a #165

S T T S R S A C Q R Q K K V T F D R L Q V L D S H Y Q D V L
AGCACAACCTCCAGGTCCGCTGTGTCAGAGACAGAAAAGGTCACTTTGACAGACTGCAAGTGTGCTGACTCCCACTATCAGGATGTGCTC

HepC1a #90

D Q A E T A G A R L V V L A T A T P P G S V T V P H P N I E
GACCAAGCCGAAACCGCTGGCGCTAGGCTCGTGGTCTGGCTACCGTACCCCTCCCGGAAGCGTCACCGTCCCCCATCCAATATCGAA

HepC1a #141

F H Y V T G M T T D N L K C P C Q V P S P E F F T E L D G V
TTCCATTACGTACCGGAATGACAACCGATAACCTCAAGTGTCCCTGTGTCAGGTCCCTCCCCGAATTCTTTACCGAAGTGGATGGCGTC

HepC1a #198

L K L T P I A A A G R L D L S G W F T A G Y S G G D I Y H S
CTGAAACTGACACCCATTGCGCGTCCGGAAGGCTCGACCTCAGCGGATGGTTTACCGCTGGCTATAGCGGAGGCGATATCTATCACTCC

HepC1a #117

A S R Q A E V I A P A V Q T N W Q K L E V F W A K H M W N F
GCCTCCAGGCAAGCGAAGTGATTGCCCTGCGCTCCAGACAACTGGCAGAACTGGAAGTGTTTTGGGCTAAGCATATGTGGAACCTT

HepC1a #181

C R A S G V L T T S C G N T L T C Y I K A R A A C R A A G L
TGCAGAGCCTCCGCGTCTGTACAACCTCTGCGGAAACACTGACATGTCTATATCAAAGCCAGAGCCGCTTGCAGAGCCGCTGCGCTC

Figure 26 (Cont)

137/216

HepC1a #166

F D R L Q V L D S H Y Q D V L K E V K A A A S K V K A N L L
TTCGATAGGCTCCAGGTCCTGGATAGCCATTACCAAGACGTCCTGAAAGAGGTCAAGGCTGCCGCTAGCAAAGTGAAAGCCAATCTGCTC

HepC1a #180

G P L T N S R G E N C G Y R R C R A S G V L T T S C G N T L
GGCCCTCTGACAAACTCCAGGGGAGAGAATTGCGGATACAGAAGGTGTAGGGCTAGCGGAGTGCTCACCACAAGCTGTGGCAATACCCCTC

HepC1a #136

I M H T R C H C G A E I T G H V K N G T M R I V G P R T C R
ATCATGCACACAAGGTGTCACTGTGGCGCTGAGATTACCGGACACGTCAAGAATGGCACAATGAGAATCGTCGGCCCTAGGACATGCAGA

HepC1a #144

E V S F R V G L H E Y P V G S Q L P C E P E P D V A V L T S
GAGGTGAGCTTTAGGGTCGGCCTCCACGAATACCCGTGTGGGAAGCCAACCTGCTTGGCAACCGAACCCGATGTGGCTGTGCTCACTCTC

HepC1a #167

K E V K A A A S K V K A N L L S V E E A C S L T P P H S A K
AAGGAAGTGAAAGCCGCTGCCTCCAAGGTCAAGGCTAACCTCCTGTCCGTGGAAGAGGCTTGCTCCCTGACACCCCTCACTCCGCCAA

HepC1a #59

G R D A V I L L M C V V H P T L V F D I T K L L L A V F G P
GGCAGAGACGCTGTGATTCTGCTCATGTGTGTGGTCCACCCCTACCCCTGCTGTGTGACATTACCAAACCTCTCTGGCTGTGTTTGGCCCT

HepC1a #146

M L T D P S H I T A E A A G R R L A R G S P P S M A S S S A
ATGCTCACCGATCCCTCCACATTACCGCTGAGGCTGCCGGAAGGAGACTGGCTAGGGGAAGCCCTCCCTCCATGGCTAGCTCCAGCGCT

HepC1a #78

S P R P I S Y L K G S S G G P L L C P A G H A V G I F R A A
AGCCCTAGCCCTATCTCCTACCTCAAGGGAAGCTCCGGCGGACCCCTCCTGTGTCCGCTGGCCATGCCGTCCGCTTTTCAGAGCCGCT

HepC1a #32

D F D Q G W G P I S Y A N G S G P D Q R P Y C W H Y P P K P
GACTTTGACCAAGGCTGGGGCCCTATCTCCTACGCTAACGGAAGCGGACCCGATCAGAGACCCCTATTGCTGGCACTATCCCCCTAAGCCT

HepC1a #128

R H V G P G E G A V Q W M N R L I A F A S R G N H V S P T H
AGGCATGTGGGACCCGAGAGGAGCGCTCCAGTGGATGAATAGGCTCATCGCTTTCGCTAGCAGAGGCAATCAGCTCAGCCCTACCCAT

HepC1a #50

C L W M M L L I S Q A E A A L E N L V I L N A A S L A G T H
TGCTCTGGATGATGCTCCTGATTAGCCAAAGCCGAAGCCGCTCTGGAAAACCTCGTGATTCTGAATGCCGCTAGCCTCGCCGAACCCAT

HepC1a #114

I I P D R E V L Y R E P D E M E E C S Q H L P Y I E Q G M M
ATCATTTCCGATAGGGAAGTGCTCTACAGAGAGTTTGACGAAATGGAAGAGTGTAGCCAAACCTCCCTATATCGAACAGGGAATGATG

HepC1a #47

L I H L H Q N I V D V Q Y L Y G V G S S I A S W A I K W E Y
CTGATTCACCTCCACAAAACATTGTGGATGTGCAATACCTCTACGGAGTGGGAAGCTCCATCGCTAGCTGGGCCATTAAGTGGGAGTAT

HepC1a #200

V S H A R P R W F W F C L L L L A A G V G I Y L L P N R A A
GTGTCCACGCTAGGCCCTAGGTGGTCTGTCTGTCTGCTCGCGCTGGCGCTGGCAATTACCTCCTGCTTAACAGAGCCGCT

HepC1a #85

A A T L G F G A Y M S K A H G I D P N I R T G V R T I T T G
GCCGCTACCCCTCGGCTTTGGCGCTTACATGAGCAAAGCCCATGGCATTGACCCTAACATTAGGACAGGCGTCAGGACAATCACAACCGGA

HepC1a #62

R V Q G L L R I C A L A R K M I G G H Y V Q M A I I K L G A
AAGGTCCAGGAGTGTCTCAGGATTTCGCTCTGGCTAGGAAAATGATTGGCGGACACTATGTGCAAATGGCTATCATTAAAGCTCGGCGCT

HepC1a #153

R R F A Q A L P V W A R P D Y N P P L V E T W K K P D Y E P
AGGAGATTCCGCTCAGGCTCTGCCTGTGTGGGCGAGACCCGATTACAATCCCCCTCTGGTCGAGACATGGAAAAAGCCTGACTATGAGCCT

HepC1a #72

T A A Q T F L A T C I N G V C W T V Y H G A G T R T I A S P
ACCGCTGCCCAAACCTTTCTGGCTACCTGTATCAATGGCGTCTGCTGGACCGCTACCATGGCGCTGGCACAAGGACAATCGCTAGCCCT

HepC1a #65

Figure 26 (Cont)

138/216

W A H N G L R D L A V A V E P V V F S Q M E T K L I T W G A
TGGGCTCAAAATGGCTCAGGGATCTGGCTGTGGCTGTGGAACCCGTCGTGTTAGCCAAATGGAACCAAACCTGATTACCTGGGGCGCT

HepCla #74

K G P V I Q M Y T N V D Q D L V G W P A P Q G S R S L T P C
AAGGACCCGTCATCCAAATGTATACCAATGTGGATCAGGATCTGGTCGGCTGGCCCGCTCCCAAGGCTCCAGGTCCTGACACCCCTGT

HepCla #151

K V V I L D S F D P L V A E E D E R E I S V P A E I L R K S
AAGTCTGTGATTCTGGATAGCTTTGACCTCTGGTCGCCGAAGAGGATGAGAGAGAGATTAGCGTCCCGCTGAGATTCTGAGAAAGTCC

HepCla #64

L T G T Y V Y N H L T P L R D W A H N G L R D L A V A V E P
CTGACAGGCACATACGCTCTACAATCACCTCACCCCTCTGAGAGACTGGGCCCATAAACGGACTGAGAGACCTCGCCGTCGCGCTGAGCCT

HepCla #80

V C T R G V A K A V D F I P V E N L E T T M R S P V F T D N
GTGTGTACCAAGGCGTCGCCAAAGCCGTCGACTTTATCCCTGTGAAAACCTCGAGACAACCATGAGGTCCCGCTCTTACAGACAAT

HepCla #95

A L G I N A V A Y Y R G L D V S V I P T S G D V V V V A T D
GCCCTCGGCATTAAACGCTGTGGCTTACTATAGGGGACTGGATGTGTCGCTGATTCCCAACAGCGGAGAGCTGCTGGTCTGTGGCTACCGAT

HepCla #111

M S A D L E V V T S T W V L V G G V L A A L A A Y C L S T G
ATGTCCGCGCATCTGGAAGTGTACCTCCACCTGGGTCTGCTGGGAGGCGTCTGGCTGCCCTCGCGCTTACTGTCTGTCCACCGGA

HepCla #97

A L M T G Y T G D F D S V I D C N T C V T Q T V D F S L D P
GCCCTCATGACAGGCTATACCGGAGACTTTGACTCCGTGATTGACTGTAAACATGCGTCAACCAACCGTCTGACTTTAGCCTCGACCTT

HepCla #2

N T N R R P Q D V K F P G G G Q I V G G V Y L L P R R G P R
AACACAAACAGAAGGCTCAGGATGTGAAATTCCTGGCGGAGGCCAAATCGTCGGCGGAGTGATCTGCTCCCCAGAAAGGGGACCCAGA

HepCla #11

R A L A H G V R V L E D G V N Y A T G N L P G C S F S I F L
AGGGCTCTGGCTCACCGAGTGAGAGTGCTCGAGGATGGCGTCAACTATGCCACAGGCAATCTGCCTGGCTGTAGCTTTAGCATTTTCTCTC

HepCla #169

S K P G Y G A K D V R C H A R K A V A H I N S V W K D L L E
AGCAAAATTCGGATACGAGCCAAAGACGTGAGTGTACCGTAGGAAGCCGTCGCCCATATCAATAGCGTCTGGAAGACCTCTCTGGAA

HepCla #28

T P G A K Q N I Q L I N T N G S W H I N S T A L N C N E S L
ACCCCTGGCGTAAGCAAAACATTACGCTCATCAATACCAATGGCTCTCGGCATATCAATAGCACAGCCCTCAACTGTAAAGAAAGCCTC

HepCla #30

N T G W L A G L F Y Q H K F N S S G C P E R L A S C R R L T
AACACAGGCTGGCTGGCTGGCTCTTCTATCAGCATAGTTTAACTCCAGCGGATGCCCTGAGAGACTGGCTAGCTGTAGGAGACTGACA

HepCla #49

V V L L F L L L A D A R V C S C L W M M L L I S Q A E A A L
GTGGTCTGCTCTTCTCTCTGCTCGCCGATGCCAGAGTGTGTAGCTGTCTGTGGATGATGCTGCTCATCTCCAGGCTGAGGCTGCCCTC

HepCla #192

D C E I Y G A C Y S I E P L D L P P I I Q R L H G L S A F S
GACTGTGAGATTTACGGAGCCTGTTACTCCATCGAACCCCTCGACCTCCCCCTATCATTCAGAGACTGCATGGCCTCAGCGCTTCTCTC

HepCla #73

W T V Y H G A G G T R T I A S P K G P V I Q M Y T N V D Q D L
TGGACAGTGTATCACGGAGCCGGAACCAAGACCATTGCCCTCCCCAAAGGCCCTGTGATTGATGTACACAAACGTGACCAAGACCTC

HepCla #101

Y R F V A P G E R P S G M F D S S V L C E C Y D A G C A W Y
TACAGATTCTGCGCCCTGGCGAAAGGCTAGCGGAATGTTGACTCCAGCGTCTGTGTGAGTGTACGATGCCGGATGCGCTTGGTAT

HepCla #45

R S E L S P L L L S T T Q W Q V L P C S F T T L P A L S T G
AGGTCCGAGCTCAGCCCTCTGCTCTGTGCCACACAGTGGCAGGTCTGCTCTGCTCTTCAACCCCTCCCCGCTCTGTCCACCGGA

HepCla #195

L R K L G V P P L R A W R H R A R S V R A R L L A R G G R A

Figure 26 (Cont)

139/216

CTGAGAAAGCTCGGCGTCCCCCTCTGAGAGCCTGGAGGCATAGGGCTAGGTCCGTGAGAGCCAGACTGCTCGCCAGAGGCGGAAGGGCT

HepC1a #121
S P L T T S Q T L L F N I L G G W V A A Q L A A P G A A T A
AGCCCTCTGACAACTCCAGACACTGCTCTTCAATATCCTCGGCGGATGGTTCGCGCTCAGCTCGCCGCTCCCGGAGCCGCTACCGCT

HepC1a #61
L W I L Q A S L L K V P Y F V R V Q G L L R I C A L A R K M
CTGTGGATCCTCCAGGCTAGCCTCTGAAAGTGCCTTACTTTGTGAGAGTGCAAGGCCTCCTGAGAATCTGTGCCCTCGCCAGAAAGATG

HepC1a #137
V K N G T M R I V G P R T C R N M W S G T F P I N A Y T T G
GTGAAAAACGGAACCATGAGGATGTGGGACCCAGAACCTGTAGGAATATGTGGAGCGGAACCTTTCCCATTAACGCTTACACAACCGGA

HepC1a #92
E V A L S T T G E I P F Y G K A I P L E V I K G G R H L I F
GAGGTCGCCCTCAGCACAAACGGAGAGATTCCCTTTTACGGAAGGCTATCCCTCTGGAAGTGATTAAGGGAGGAGACACCTCATCTTT

HepC1a #188
L T R D P T T P L A R A A W E T A R H T P V N S W L G N I I
CTGACAGGGATCCCAACCCCTCTGGCTAGGGCTGCCCTGGGAGACAGCCAGACACACCCGTCAACTCTGGCTCGGCAATATCATTT

HepC1a #140
R V S A E E Y V E I R R V G D F H Y V T G M T T D N L K C P
AGGGTCAGCGCTGAGGAATACGTCGAGATTAGGAGAGTGGGAGACTTTCATATGTGACAGGCATGACCACAGACAACTCGAAATGCCCT

HepC1a #155
P V V H G C P L P P P R S P P V P P P R K K R T V V L T E S
CCCGTCGTGCATGGCTGTCCCTCCCCCTCCCAAGCCCTCCCGTCCCCCTCCCAAGAAAAGGACAGTGGTCTGACAGAGTCC

HepC1a #157
T L S T A L A E L A T K S F G S S S T S G I T G D N T T T S
ACCCCTCAGCACAGCCCTCGCCGAACCTGGCTACCAAAAGCTTTGGCTCCAGCTCCACCTCCGGCATTACCGGAGACAATACCACAACCTCC

HepC1a #135
V S C Q R G Y K G V W R G D G I M H T R C H C G A E I T G H
GTGTCTGCCAAAGGGGATACAAAGGCGTCTGGAGAGGCGATGGCATTATGCATACCAGATGCCATTGCGGAGCCGAAATCACAGGCCAT

HepC1a #20
V P L V G Q L F T F S P R R H W T T Q G C N C S I Y P G H I
GTGTTCTGGTTCGGCCAACTGTTTACCTTTAGCCCTAGGAGACTGGACCACACAGGGATGCAATTGCTCCATCTATCCCGGACACATT

HepC1a #123
F V G A G L A G A A I G S V G L G K V L V D I L A G Y G A G
TTCGTCGGCGCTGGCCTCGCCGAGCCGCTATCGGAAGCGTCCGCTCGGCAAGTCTCGTGGATATCCTCGCCGGATACGGAGCCGGA

HepC1a #133
D I W D W I C E V L S D F K T W L K A K L M P Q L P G I P F
GACATTTGGGATTGGATTTCGAAGTGCTCAGCGATTTCAAAACCTGGCTGAAAGCCAACTGATGCCCCAACTGCCTGGCATTCCCTTT

HepC1a #15
N S S I V Y E A A D A I L H T P G C V P C V R E G N A S R C
AACTCCAGCATGTGTATGAGGCTGCCGATGCCATTCTGCATACCCCTGGCTGTGTGCCTTGCCTCAGGGAAGGCAATGCCCTCCAGGTGT

HepC1a #31
S S G C P E R L A S C R R L T D F D Q G W G P I S Y A N G S
AGCTCCGCTGTCCCGAAAGGCTCGCCTCTGCAGAAGGCTCACCGATTTCGATCAGGGATGGGGACCCATTAGCTATGCCAATGGCTCC

HepC1a #178
R T E E A I Y Q C C D L D P Q A R V A I K S L T E R L Y V G
AGGACAGAGGAAGCCATTACCAATGCTGTGACCTCGACCCCTCAGGCTAGGGTCGCCATTAACTCCCTGACAGAGAGACTGTATGTGGGA

HepC1a #69
V S K G W R L L A P I T A Y A Q Q T R G L L G C I I T S L T
GTGTCCAAGGGATGGAGACTGCTCGCCCTATCACAGCCTATGCCCAACAGACAAGGGGACTGCTCGGCTGTATCATTACCTCCCTGACA

HepC1a #191
F F S V L I A R D Q L E Q A L D C E I Y G A C Y S I E P L D
TTCTTTAGCGTCTGATTCAGAGACCAACTGGAACAGGCTCTGGATTGCGAAATCTATGGCGCTTGCTATAGCATTGAGCCTCTGGAT

HepC1a #142
C Q V P S P E F F T E L D G V R L H R F A P P C K P L L R E
TGCCAAGTGCTAGCCCTGAGTTTTCACAGAGCTCGACGGAGTGAGACTGCATAGGTTTGGCCCTCCCTGTAAAGCCTCTGCTCAGGGAA

Figure 26 (Cont)

HepC1a #182
T C Y I K A R A A C R A A G L Q D C T M L V C G D D L V V I
ACCTGTTACATTAAGGCTAGGGCTGCTGTAGGGCTGCGGACTGCAAGACTGTACCATGCTGGTCTGCGGAGACGATCTGGTCTGTAT

HepC1a #86
I D P N I R T G V R T I T T G S P I T Y S T Y G K F L A D G
ATCGATCCCAATATCAGAACCGGAGTGAGAACCATTACCAAGGCTCCCCATTACCTATAGCACATACGGAAGATTCTGGCTGACGGA

HepC1a #44
C N W T R G E R C D L E D R D R S E L S P L L L S T T Q W Q
TGCAATTGGACAAGGGGAGAGAGATGCGATCTGGAAGACAGAGACAGAAGCGAACTGTCCCCCTCTGCTCAGCACAAACCAATGGCAA

HepC1a #22
T G H R M A W D M M M N W S P T A A L V M A Q L L R I P Q A
ACCGGACACAGAATGGCTTGGGATATGATGATGAATTGGTCCCCACAGCCGCTCTGGTCTATGGCTCAGCTCCTGAGAATCCCTCAGGCT

HepC1a #127
P G A L V V G V V C A A I L R R H V G P G E G A V Q W M N R
CCCGGAGCCCTCGTGGTGGGCGTCTGTGTGTGCGCTATCCTCAGGAGACAGTGGCCCTGGCGAAGGCGCTGTGCAATGGATGAACAGA

HepC1a #149
H D S P D A E L I E A N L L W R Q E M G G N I T R V E S E N
CAGCATAGCCCTGACGCTGAGCTCATCGAAGCCAATCTGCTCTGGAGACAGGAAATGGGAGGCAATATCAAGGGTCTGAGTCCGAGAAT

HepC1a #105
E G V F T G L T H I D A H F L S Q T K Q S G E N F P Y L V A
GAGGGAGTGTTTACCGGACTGACACACATTGACGCTCACTTTCTGTCCAGACAAAGCAAAGCGGAGAGAATTCCTCTTACCTCGTGGCT

HepC1a #5
R G R R Q P I P K A R R P E G R T W A Q P G Y P W P L Y G N
AGGGGAAGGAGACAGCCTATCCCTAAGGCTAGGAGACCCGAAGGAGAACTGGGCCCAACCCGGATACCCCTTGGCTCTGTATGGCAAT

HepC1a #173
L I V F P D L G V R V C E K M A L Y D V V S K L P L A V M G
CTGATTGTGTTTCCCGATCTGGGAGTGAGAGTGTGTGAGAAAATGGCTCTGTATGACGTCGTGTCCAAGCTCCCCCTCGCCGTCATGGGA

HepC1a #12
Y A T G N L P G C S F S I F L L A L L S C L T V P A S A Y Q
TACGCTACCGGAAACCTCCCGGATGCTCCTTCTCCATCTTTCTGCTCGCCCTCCTGTCTGCGCTCAACGCTCCCGCTAGCGCTTACCAA

HepC1a #124
L G K V L V D I L A G Y G A G V A G A L V A F K I M S G E V
CTGGGAAAGGTCTCTGGTGCACATCTGGCTGGCTATGGCGCTGGCGTGGCCGGAGCCCTCGTGGCTTTCAAATCATGACGGAGAGGTC

HepC1a #160
S Y S S M P P L E G E P G D P D L S D G S W S T V S S E A G
AGCTATAGCTCCATGCTCCCTCGAGGGAGAGCCTGGCGATCCCGATCTGTGCGAGCGAAGCTGGAGCACAGTGTCCAGCGAAGCCGGA

HepC1a #150
R Q E M G G N I T R V E S E N K V V I L D S F D P L V A E E
AGGCAAGAGATGGGCGGAAACATTACCAAGTGGAAAGCGAAACAAAGTGGTCATCCTCGACTCCTTCGATCCCTCGTGGCTGAGGAA

HepC1a #75
V G W P A P Q G S R S L T P C T C G S S D L Y L V T R H A D
GTGGGATGGCTGCCCTCAGGGAAGCAGAAGCCTCACCCCTTGACATGCGGAAGCTCCGACCTCTACCTCGTGACAGGCGATGCGGAT

HepC1a #88
G C S G G A Y D I I I C D E C H S T D A T S I L G I G T V L
GGCTGTAGCGGAGGCGCTTACGATATCATTATCTGTGACGAATGCCATAGCACAGACGCTACCTCCATCCTCGGCATTGGCACAGTGTCT

HepC1a #99
T F T I E T T T L P Q D A V S R T Q R R G R T G R G K P G I
ACCTTTACCAATTGAGACAACCACTGCCTCAGGATGCCGTGAGCAGAACCCAAAGGAGAGGAGAGAACCGGAAGGGGAAAGCTGGCATT

HepC1a #40
D C F R K H P E A T Y S R C G S G P W I T P R C L V D Y P Y
GACTGTTTCAGAAAGCATCCCGAAGCCACATACTCCAGGTGTGGCTCCGGCCCTTGGATTACCCCTAGGTGTCTGGTGCAGTATCCCTAT

HepC1a #201
L A A G V G I Y L L P N R A A
CTGGCTGCGGAGTGGGAATCTATCTGCTCCCCAATAGGGCTGCC

Figure 26 (Cont)

141/216

HepCla #163

A L V T P C A A E E Q K L P I N A L S N S L L R H H N L V Y
GCCCTCGTGACACCTGTGCGCGTGAGGAAACAGAACTGCCTATCAATGCCCTCAGCAATAGCCTCCTGAGACACCATAACCTCGTGTAT

HepCla #132

I S S E C T T P C S G S W L R D I W D W I C E V L S D F K T
ATCTCCAGCGAATGCACAACCCCTTGCTCCGCTCCTGGCTCAGGGATATCTGGGACTGGATCTGTGAGGTCTGTGCGACTTTAAGACA

HepCla #134

W L K A K L M P Q L P G I P F V S C Q R G Y K G V W R G D G
TGGCTCAAGGCTAAGCTCATGCCTCAGCTCCCCGGAATCCCTTTCGTGAGTGTGAGAGGCTATAAGGGAGTGTGAGGGGAGACGGA

HepCla #41

S G P N I T P R C L V D Y P Y R L W H Y P C T I N Y T I F K
AGCGGACCTGGATCAACCCAGATGCCTCGTGGATTACCCCTACAGACTGTGGCACTATCCCTGTACCATTAACTATACCATTTTCAAA

Artificial Protein:

VIPVRRRGDSRGSLLSPRPISYLGSSGGPARRGREILLGPADGMVSKGNLLAPITAYARLHRFAPPCKPLLREEVSFRVGLHEYPVGSVVFVSQMET
KLITWGADTAACGDIINGLPVSLLCFAGHAGVIFRAAVCTRGVAKAVDFIPVCVVIVGRIVLSGKPAIIPDREVLYREFDEMPCPLPAPNYTFALWR
VSAEYVEIRRVGDALYDVVSKLPLAVMGSSYGFQYSPGQVRVEFISWCLWNLQYFLTRVEAQLHVWVPLNVRGENLVILNAASLAGTHGLVSVFLVFP
CFAWYLLPPIIQRLHGLSAPSLHSYSPGIBNRVACNPPLVETWKKPDYEPVVGCPPLPPRSPPGVSSIASWAIKWEYVVLFLLLADARVCSLN
NTRPPLGNWFGCTMMNSTGTGFKVCGAPPFTTEAMTRYSAAPGDPQPEYDELELITSCSSWPLLLLLALLPQRAYALDTEVAASCGGVVLQQTGRLLGCI
ITSLTGRDKNQVEGEVQIVSSSPPAVPQSPQVAHLHAPTGSCKSTKVPAAANTPGLPVCQDHLFEWEGVFTGLTHIDAHFLVLLFAGVDAETHVTGGN
AGRTTSGLVSLLEVTTLHPVTKYIMTCSADLEVTSTWVLVGGVLAALAAAYCLSTGALMTGYTGDFSDVDCNTCVTQTVDFSLDPTFTIETTLTQDAVSHGFTPLLYRLGAVQ
LDLSIAYFSMVGNNAKVLVLLFAGVDAETHVTRLARGSPSPMASSASQLSAPSLKATCTANGLVSVFLVFPFAWYLKGRVWPGAVYALYGMQLPC
BEPEDVAVLTSMLTDPSHITABAGRDSVTPIDTTIMAKNEVFVCQPEKGGRRKPARYAAQGYKVLVNLNPSVAATLGFAGYMSKAHGVNRNSTGLYHVTN
DCPNSSIVYEAADAILHTSSYGFQYSPGQVRVEFLVQAWKSKTTPMGFSDTAACGDIINGLPVSARRGREILLGPADGMVSKGNLLAPITAYARLHRFAPPCKPLLREEVSFRVGLHEYPVGSVVFVSQMET
ABLIENANLWNPALIASLMAPTAAVTSPLTTSQTLFNLILGLVQAWKSKTTPMGFSDTRCFDSTVTESDIDEREISVPAEILKRSRRFAQALPVWARP
DYMFAPTLWARMILMTHFFSVLIARDQLEQALSVPITSGDVVVVATDALMTGYTGDFSDVDCNTCVTQTVDFSLDPTFTIETTLTQDAVSHGFTPLLYRLGAVQ
TTLPALSTGLIHLHQNIVDVQYLYKGRVWPGAVYALYGMQLPCBEPEDVAVLTSMLTDPSHITABAGRDSVTPIDTTIMAKNEVFVCQPEKGGRRKPARYAAQGYKVLVNLNPSVAATLGFAGYMSKAHGVNRNSTGLYHVTN
ELTPASTTTLRLAYMNTPGLPVCQDHLFEWEGVFTGLTHIDAHFLVLLFAGVDAETHVTRLARGSPSPMASSASQLSAPSLKATCTANGLVSVFLVFPFAWYLKGRVWPGAVYALYGMQLPC
GGRHLIFCHSKKKCDLAALKLVGGVLAALAAAYCLSTGCVVIVGRIVLSGKPACESAGVQEDAAASLRAFTEAMTRYSAAPGDPGWFTAGYSGGDIYHSV
SHARPWFPCLLSSSTSGITGNTTSSSEPAPSGCPSDASERTQRRRTGRGKPGIYRFVAPGERPSGMFDMVRMYVGGVEHRLAECNWTNRGERC
DLEDDAQLHVWVPLNVRGGRAVILLMCVHPTLGVRAKTRTSERSQPRGRQPIPKARRPEGNVSVAGHDGAKRVYLLTRDPTPLARAAWESE
PAPSGCPSDASAESYSSMPLEGEPPGPIGHHYVQMAIKLGAITGYTYVNHILTLPDSTEDLVNLLPALISPGALVGVVCAAILRLILDMIAGAHW
GVLGAIYFMSVGNNAKVLVVEGCGWAGNLLSPRGRSRPSWGPDPDRRRSRNWTTCGNCISYPGHITGHRMAWDMMMNWSFWWAMTPTVATRDGKLPAT
QLRRHIDLLVGSRLWHYPCTINITYIFKVRMYVGGVEHRLAFAVFCQPEKGGRRKPARLIVFPDLGVVRVCEKMGYIPLVGAPLGGAAALAHGVVRVLE
DGVNGGNAGRTTSGLVSLTLPAGAKQNIQLINTNGLALLSCLTPVPAAYQVRNSTGLYHVTNDCPGRDKNQVEGEVQIVSTAAQTFLATCINGVCPATQ
LRRHIDLLVGSATLCSALYVGDLCGSHAPTSGSKSTKVPAAAYAAQGYKVLVNLNPSVTRTWAQPGYWPPLYGNEGCGWAGNLLSPRGRSTEDVCCSMSYS
WTGALVTPCAABEQKLPALDTEVAASCGGVVLVGLMALTLSPYKYRYMNSTGTGFKVCGAPPVIGGAGNNTLHCPTSVEEACSLTPPHSAKSKFY
GAKDVRCHARIISGIVLAGLSTLPFNPAIASLMAPTAAVTSPLTTSQTLFNLILGLVQAWKSKTTPMGFSDTRCFDSTVTESDIDEREISVPAEILKRSRRFAQALPVWARP
HRTARHTPVNSWLGNIIMPAPTLWARMILMTHFFSVLIARDQLEQALSVPITSGDVVVVATDALMTGYTGDFSDVDCNTCVTQTVDFSLDPTFTIETTLTQDAVSHGFTPLLYRLGAVQ
KLLLAVFGLPWLILQASLLRYPYFVTAALVMAQLLRIPQAILDMIAGAHWGVLGAGNCTVCTQTVDFSLDPTFTIETTLTQDAVSHGFTPLLYRLGAVQ
NEVTLTHPTTKYIMTCAARVAIKSLTERLYVGGPLTNSRGENCGYRRRCRASGVLTSCGNTLIMHTRCHCGAETIGHVKNGTMRIVGPRTCREVSFRVGLHEYP
GDSRGSLLNMSGTFPINAYTTGCPCTPLPAPNYTFALWHSATDTSILIGTGLVDAQETAGARLVVLAATYVPESDAAARVTAISSLTIVTQLLRLHQQ
RPSWGPTDPRRRNRNLGKVIDTLTCGFADLGPDPQRPYCWHPYPPKCGIVPAKSVCGPVYCEECSSQHLPIYEQGMMLAEQFKQALGLLQTYQATVCAR
AQAPFPSPWQMKCLLRKLPKTLGCIIVPAKSVCGPVYCFPTSPVVGTTDRSGSSLTVTQLLRLHQNIISSCTTPCSCSWLRDLSDGSSWTSVSEAGT
EDVCCSMSYSWTGDMQWKLIRLKPTLHGPTPLLYRLGAVQNLAEQFKQALGLLQTLASRQAEVLAQVQTNWQKLEVPWAKHMMNFIISGIIYLAG
LSTLPLGLIAFASRGNHVSPHYVPESDAAARVTAIATLCSALYVGDLCGSVFLVQGLFTFSPRRHSSVLCCEYDAGCAWYELTPAETTVRLRAYMGW
VAAQLAAPGAATAFVGCAGLAGAAIGSVGSHINSTALNCNESLNTGVLLFLADARVCSLWMLLIISQAEALDCEIYGACYSIEPLDLPPIIQRLH
GLSAPSWTYHAGTRTIAAPKGFVIQMYTNVDQDLRYFVAPGERPSGMFSSVLCCEYDAGCAWYRSELSPLLLSTTQMQVLPSCSFTTLPALSTGLR
KLGVPPLRAWHRARSVRARLLARGGRASPLTTSQTLFNLILGLVQAWKSKTTPMGFSDTRCFDSTVTESDIDEREISVPAEILKRSRRFAQALPVWARP
PRTCRNMSSGTFPINAYTTGAEVALSTTGEIPFYGKAIPLVLEIKGRHLIFLTRDPTPLARAAWETARHTPVNSWLGNIIRVSAEYVEIRRVGDALYDVVSKLPLAVMGSSYGFQYSPGQVRVEFISWCLWNLQYFLTRVEAQLHVWVPLNVRGENLVILNAASLAGTHIIPDREVLYREFDEMPCPLPAPNYTFALWR
VTGHTDNLKCPVVGHCPLPPRSPPVPPPRKRTVVLTTESTLSTALAEALATSGFSSSTSGITGNTTTSVSCRQYKGVNRGDIHTRCHCGAE
ITGHVFLVGLFTFSPRRHWTTCGNCISYPGHIFVGCAGLAGAAIGSVGLGKVLVDILAGYAGDIWDNICEVLSDFKTLWAKLMPQLPGIPFNSSI
VYEAADAILHTPGVPCVREGNASRCSGCPERLASCRLTDFDQGWGPIISYANGSRTEBAIYQCCDLPQARVAIKSLTERLYVGVSKGNLLAPIT
AYAQTGRLLGCIITSLTFPSVLIARDQLEQALDCEIYGACYSIEPLDQVPSPEFFTELDGVRVLRHFAFPCKPLLRETCYIKARAACRAAGLQDCTM

Figure 26 (Cont)

142/216

LVCGDDLVVVIDPNIRITGVRTITTTGSPITYSTYGYKFLADGCNWRGBCDLEDNRDRSELSPLLLSTTQWQTGHRMADMMNWSPTAALVMAQLLRIP
QAPCALVGGVCAAILLRHHVGCPEGAGVCMNRHSDSPDAELIEANLLWRQEMGNITRVSENGEVFTGLTHIDAHFSLQTKQSGENFPYLVARGRRQP
IPKARRPBBGTWAPQGYMPWPLYGNLIVPDDLGRVRCMKWALYDVVSKLPAVMGYATGNLPGCSPSIFLALLSLCTVPSAPAYQLGKVLVDILAGYA
GVAGALVAFKIMSGEVSYSSMPPLEBPGDPLSDGSSWTVSSBAGRGCMGNITRVSENVKVVILDSDFLVAEEVGPWAPQGSRLTPTCTGSGDDL
YLVRHADGCSGGAYDIIICDCHSTDATSILGIGITVLTFTIETTLTPQDAVSRTORRGRTGRGKPGIDCFRKHPEATYSRCGSGFPWITPRCLVDYPY
LAAGVGIYLLPNRAAALVTPCAAEEQKLPINALSNSLLRRHNLVYISSECTTPCSGSLWRLDIWDWICEVLSDFKTLWAKLMPQLPGIPFVSCQRGYK
VVRGDCGSGPNIIPRCLVDYPTLRYLWHYPTCTINITYIFK

Artificial DNA:

[illegible]

Figure 26 (Cont)

143/216

CAGTCTCAGGAGACACATTGACCTCCCTGGTGGCTCCAGGCTCTGGCATTACCTTTGCACAATCAATTACACAATCTTTAAAGGTCAAGGATGTACGTGGC
CGGAGTGAACACAGACTGGAAGCCGCTGTGTTTTCGCTCCAGCCTGAGAAAGGCGGAAGGAAACCCGCTAGGCTCATCGTCTTCCCTGACCTCGGCG
TCAGGCTGGAACAAAGATGATGGGATACATTCCTCCGTGGGAGCCCTCTGGGAGGCGCTGCCAGAGCCCTCGCCCATGCGCTCAGGCTCTGGAA
GACGGAGTGAATGGCGGAAACGCTGGCAGAACCAAGCGGACTGTGACGCTCTGACACCGCGCAAACAGAAATATCAACATGTATTAACACA
CGGACTGGCTCTGCTCAGCTGTCTGACAGTGCTGCTCTCCGCTATCAGTCCAGGAATAGCACAGGCCCTTACCATTGTGACAAACGATTGCCCTGGCA
GAGACAAAACCAAGTGGGAAGCGGAAGTGCACAACTCGTCCAGCACCGCTCAGACATTTCTCTGCCACATGTCATTAAACGAGTGTGCTCCGCTACCCAA
CTGAGAAGGCATATCGATCTGCTGCTGGGAAGCGTACCTCTGCTCGCCCTTACGTCGGCGATCTGTGTGGCTTCCGCTCCACAGGCTCGCG
CAAAAGCACAAAGGTCCTCCGCTGCCATGCGCTCAGGGATACAAAGTGCTCGTGCTCAACCTTAGCCTCAGACATGGGCTCAGCTCTCCGCTCCGCTCGG
GGCCCTCTACGGAACGAGAGGCTGTGGCTGGGCGGATGCTGCTGCCCGCCAGAGGCTCCACCGAAGACGTCGTGTGTGCTCCATGTCTCTACTCC
TGGACAGGCGCTCTGGTCAACCTTGGCTGCCGAAGAGCAAAAGCTCCCCATGCTCCGCTCGACAGAGGTGCGGCTAGCTGTGGGAGGTGGTCTCT
GGTGGCCTCATGGCTCTGACACTGTCCCCATTTACAAAGGATTTGATGTAATCCCGGATTTCACAAAGGTTGCGGAGGCCCTCTCTGTGTGA
TTGGCGGAGCGGGAACAAATACCTCCACTGTCCCAAGCGTTCGAGGAAGCCTGTAGCCTCACCCCTCCGATAGCGCTAAGTCCAAGTTTGGCTA
GGCGCTAAGGATGTGAGATGGCATGCCAGAACTCTCCGGCTTCAGTATCTGGCTGGCTCAGCACATGCTCGTGGCAATCCCGCTAGCTGTGGGAGGTGGTCT
GGCTTTACACGCGCTGTGACAGATTTGTGGAGGCTCTACCTCTCGCTAGGAGGCGCTTAGGCTCGGCTCAGGCTACCGAAGACACGCG
AAGGCTCCCGCCTCTGCAATAGCTATAGCCTTGGGAAATCAATAGGCTCGCGCTTGGCTCAGGAACTGGGAGTGCTCTCCCTCAGGCTTGGAGA
CACAGACCGCTAGGCAATACCTCTGTAATAGTGTGGCTGGGAACATTATCATGTTCCGCTCCACATGCTGGGCGCAAGATGATTTCTGATGACCCATGA
GAATCTCGGAACCAATGAGAAGCCTGTGTTTACCGATAACTCGACCTCCCGCTGTGCTCAGTCTTCCAAGTGGCTCAGCTCGCCACACCC
CTGGCTCCGTGACAGTGCTCTACCTTAACATTGAGGAAGTGGCTCTGTCCACCACAGGCGAAATCCCTTTCTATGGCAAACTAGCTCTGCGATACACA
AAGCTCTCTGCTCGCGCTCTGGGACCCCTCTGATTTCTGCAAGCTCTCCCTGCTCAGGTTCCCTATTTCGTACACGCTGCGCTCTGATGCGCCAACT
GCTCAGGATTTCCCAAGCCATCTGATATGATGCTGGGAGCCCATTTGGGAGTGTGCGCGGATGCAATACCTGTGTGACACAGACAGTGGATTTCT
CCCTGGATCCCACTTCACAATCGAAACCAACCCCTCCCCAAGAGCTGTGTCCACGAGACCAACCCCTCTGTATAGGCTCGGCGCTGTGCA
AAGAGGTGACACATGACACCCCTGTGACAAAGTATATCATGACATGTGTGCCAGATGGCTATCAAAAGCCTACCGAAGGCTCTACGTGGCGGAGC
CTCACCAATAGCAGAGGCGAAATGTGGCTATAGGAGATGCGTCACTCGGAGGCGCTGGCAATAACACATGCTATGCCCTACCGATTTGCTTTAGGA
AACAACCTAGGCTTACCTATGACAGATGGGAACTGTGGCTCAGCGATCTGTATCTGTGACACAGACGCTGACGCTATCCCTGTGGAAGAGAGA
GGGATAGCAGAGGCTCCTGCTCAACATGTGTGTCGGGCAATCCCTATCAATGCTTATACCAAGGCCCTTGCAACCCCTCCCGCTCCCAATTA
CACATTGCTCTGTGGCTACCCAGATGCCACAGCATCTGGGAATCGGAACCGCTCTGGATCAGGTCAGACAGCGGAGCCAGATGCTGTGCTG
TCGCGACATAGCTCCCGAAGGAGTGCGCTGCGCAGGTGACGCTTCTGTGCTCAGCTCAGCTCAGCAACGCTGCTCAGGAGATGCTCATGTG
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Figure 26 (Cont)

Cassette A

Figure 26. (Cont)

146/216

GCTGGCAGAACCAAGCGGACTGGTCAGCCTCTGACACCCGGAGCCAAACAGAATATCCAAGTATTAAACACAAACGG
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ACGATTGCGCTGGCAGAGACAAACCAAGTGAAGGCGAAGTCAAAATCGTCAGCACAGCGCTCAGACATTCTCTCGCC
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Figure 26 (Cont)

147/216

Cassette C

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Figure 26 (Cont)

148/216

AACTGCCTATCAATGCCCTCAGCAATAGCCTCCTGAGACACCATAACCTCGTGTATATCTCCAGCGAATGCACAACCCCT
TGCTCCGGCTCCTGGCTCAGGGATATCTGGGACTGGATCTGTGAGGTCTGTCCGACTTTAAGACATGGCTCAAGGCTAA
GCTCATGCCCTCAGCTCCCGGAATCCCTTTTCGTGAGCTGTCAGAGAGGCTATAAGGGAGTGTGGAGGGGAGACGGAAGCG
GACCTGGATCACACCAGATGCCTCGTGGATTACCTTACAGACTGTGGCACTATCCCTGTACCATTAACTATACCATT
TTCAAAagatctTGAgtcgacgaattcgcc

Figure 26 (Cont)

149/216

Melanoma Savine design

- Two savines - one containing scrambled melanocyte differentiation Ags
 - one containing scrambled melanoma cancer specific Ags

Genes in melanocyte differentiation Savine**gp100**

MDLVLRCLLHLAVIGALLAVGATKVPNRNDWLGVSRQLRTKAWNRQLYPEWTEAQRLLDCWRGGQVSLKVSNDGPTLI
 GANASPSIALNFPQSQKVLDPDQVWVNNTIINGSQVWGGQPVYPQETDDACIFPDGGPCPSGSWSQKRSFVYVWKTW
 GQYVQLGPPVSGLSIGTGRAMLGTHMEVTVYHRRGSRSYVPLAHSSSAFTITDQVPFVSVSQRLRALDGGNKHFLR
 NQPLTFALQLHDPGSGYLAADLSYTWDFGDSSGTLISRALVVTHTYLEPGPVTAQVVLQAAIPLTSCGSSPVPGTTDG
 HRPTAEAPNTTAGQVPTTEVVGTTTGPQAPTAEPSGTTSVQVPTTEVISTAPVQMPTAESTGMTPEKVPVSEVMGTTLA
 EMSTPEATGMTPAEVSIVVLSGTTAAQVTTTEWVETTARELPIPEPEGPDASSIMSTESITGSLGPLLDGTATLRLVK
 RQVPLDCVLRYRGSFVTLDIVQGISAEILQAVPSGEGDAFELTVSCQGGPKPEACMBISSPGCQPPAQRQCQVPLP
 SPACQLVLHQLKGGSGTYCLNVSLADTNSLAVVSTQLIMPGQEAQGLQVPLIVGILLVLMVAVLASLIYRRRLMKQD
 FSVPLPHSSSHWLRLPRIFCSCPIGENSPLLSGQV

MART

MPREDAHFYGYPIKKGHGSYTTAEAAAGIGILTIVILGVLLIGCWYCRRRNGYRALMDKSLHVGTQCALTRCRPQEG
 FDHRDSKVSLEKNCEPVVNPAPPAYEKLSEQSPPPYSP

TRP-1

PAFLTWHRHYHLLRLEKDMQEMLEPSFSLPYWNFATGKNVCDICTDDLMGSRSNFDSLISPNSVFSQWRVVCDSLED
 YDTLGTLCNSTEDGPIRRNPAGNVARPMVQRLPEPQDVAQCLEVGLEFDTPPFYSNSTNSFRNTVEGYSDPTGKYDPAV
 RSLHNLALHFLNGTGCGQTHLSSQDPIFVLLHTFTDAVDEWLRRYNADISTFPLENAPIGHNRRQYNMVPFWPPVTNTE
 MFVTAPDNLGYTYE

Tyros

MLLAVLYCLLWSFQTSAGHFPRACVSSKNLMEKECCPPWSGDRSPCGQLSGRGSCQNILLSNAPLGPQFPFTGVDDRE
 SWPSVFFYNRTCQCSGNFMGFNCNCKFGFWGPNCTERRLLVRRNIFDLSAPEKDKFFAYLTLAKHTISSDYVPIGTY
 GQMKNGSTPMFNDINIYDLFVWMHYVSMALLGGSEIWRDIDFAHEAPAFLPWHRLFLLRWEQEIQKLTGDNFTIP
 YWDWRDAEKCDICTDEYMGQHPHTNPILLSPASFFSSWQIVCSRLEEYNHSHQSLCNGTPEGPLRRNPGNHDKSRTPLR
 PSSADVEFCLSLTQYESGSMKKAANPSFRNTLEGFASPLTGIADASQSSMHNALHIYMNMTMSQVQGSANDPIPLLHH
 AFVDSIFEQWLQRHRPLQEVYPEANAPIGHNRESYMPVFIPLYRNGDFFISSKDLGYDYSYLQSDPDSPQDYIKSYL
 EQASRIWSWLLGAAMVGAVLTALLAGLVSLLCRHKRQQLPEEKQPLLMEKEDYHSLYQSHL

TRP2

MSPLWWGFLSLCLGCKILPGAQQFPRVCMTVDSLNVKECCPRLGAESANVCGSQQGRGQCTEVRADTRPWSGPYILR
 NQDDRELWPRKFFHRTCKCTGNFAGYNCDCGKFGWTGPNCERKPPVIRQNIHSLSPQEREQFLGALDLAKKRVHPDY
 VITTHWLGLLPNGTQPPQFANCSVYDFFVWLHYYSVRDITLLGPRPYRAIDFSHQGPAFVTWHRYHLLCLERDLQRL
 IGNEFALPYWNFATGRNECDVCTDQLFGAARPDPTLISRNSRFSSWETVCDLDDYNHLVTLGNGTYEGLLRNQ
 GRNSMKLPTLKDIRDCLSLQKFDNPPFFQNSTFSFRNALEGFDKADGTLDLSQVMSLHNLVHSLFNGTNALPHSAANDP
 IFVVLHSFTDAIFDEWMKRFNPADAWPQELAPIGHNRMYNMVPFPPVPTNEELFLTSQDLGYSYAIPLPVSVETPG
 WPTTLLVVMGTLVALVGLFVLLAFLQYRRLRKGYTPLMETHLSSKRYTEA

MC1R

MAVQGSQRRLLGSLNSTPTAIPQLGLAANQTGARCLEVSIISDGLFSLGLVSLVENALVVATIKNRNLHSPMYCFIC
 CLALSDDLVSQTNVLETAVILLLEAGALVARAAVLQQLDNVIDVITCSSMLSSLCFLGAIAVDRIYISIPYALRYHSIV
 TLPAPRAVAAIIVASVVFSTLFIAYYDHVAVLLCLVFFFLAMLVLMVAVLYVHMLARACQHAQGIARLHKRQRPVHQG
 FGLKGAVTLTILLGIFFLCWGPFPLHLTLIVLCPEHPTCGCIPKNFNLFLALIICNAIIDPLIYAFHSQELRRTLKEV
 LTCSW

MUC1F

MTPGTQSPFFLLLLLTVLTVVTGSGHASSTPGGEKETSATORSSVPSSTEKNAVSMSSVLSSHSPGSGSSTTQGDV
 TLPATEPASGSAATWGQDVTSVPVTRPALGSTTPPAHDVTSAPDNK

Figure 27

150/216

MUC1R

NRPALGSTAPPVHNVTASAGSASGSASTLVHNGTSARATTTTPASKSTPFSIPSHHSDTPTTLASHSTKTDASSTHHSS
 VPPLTSSNHSTSPQLSTGVSTFFLSFHISNLQFNSSLEDPSDYYQELQORDISEMFLQIYKQGGFLGLSNIKFRPGSV
 VVQLTLAFREGTINVHDETQFNQYKTEAASRYNLTISDVSVSDVPPFSAQSGAGVPGWGIALLVLCVLVALAIVY
 LIALAVCQCRKNYQQLDIFPARDTYHPMSEYPTYHTHGRYVPPSSSTRSPYEKVSAGNGGSSLSYTNPAVAASANL

NB Muc 1 Repeat sequences in the middle of the gene were removed

Genes in melanoma specific Savine

BAGE

MAARAVFLALSAQLLQARLMKEESPVVSWRLEPEDGTALCFIF

GAGE-1

MSWRGRSTYRPRPRRYVEPPEMIGPMRPEQFSDEVEPATPEEGEPATQRQDPAAAQEGEGEGASAGQGPKPEADSQEQ
 GHPQTGCECEDGPDGQEMDPPNPPEVKTPPEEMRSHYVAQTGILWLLMNNCFNLSPRKP

gp100In4

SWSQKRSFVYVWKTWGEGLPSQPIIHTCVYFFLPDHLSTFGRPFHLNFCDFL

MAGE-1

MSLEQRSRLHCKPEEALQAQALGLVVCQAATSSSSPLVLGTLLEEVPTAGSTDPPQSPQGASAFPTTINFTRQRQPS
 GSSSREEEGPSTSCILESLFRAVITKKVADLVGFLLLKYRAREPVTKAEMLESVIKNYKCFPEIFGKASESLQLVFG
 IDVKADPTGHSYVLVTCLGLSYDGLLDGNQIMPKTGFLIIVLVMIAMEGGHAPEEEIWEELSVMEVYDGREHSAYGE
 PRKLLTQDLVQEKYLEYRQVPDSDPARYEFLWGPRALAETSYVKVLEYVIKVSARVRFFFPSSLREAALREEEGV

MAGE-3

MPLEQRSQHCKPEEGLEARGEALGLVGAQAPATEEQEAASSSTLVEVTLGEVPAESPDPQSPQGASSLPPTMNY
 LWSQSYEDSSNQEEGPSTFPDLESEFQAALSRKVAELVHFLLLKYRAREPVTKAEMLGSVVGNWQYFFPVI
 SKASS
 SLQLVFGIELMEVDPIGHLYIFATCLGLSYDGLLDGNQIMPAGLLIIVLAIAREGDCAPEEKIWEELSVLEVFEGR
 EDSILGDPKLLTQHVFQENYLEYRQVPGSDPACYEFLWGPRALVETSYVKVLHHMVKISGGPHISYPPLHEWVLR
 EE

PRAME

MERRRLWGSIQSRYISMSVWTSPPRLVELAQSLKDEALAIAALELLPRELFPPLFMAAFDGRHSQTLKAMVQAWPF
 TCLPLGLVMKGQHLHLETFKAVLDGLDVLLAQEVRPRRWKLQVLDLRKNSHQDFWTVWNGNRASLYSFPEPEAAQPM
 KKRKVDGLSTEAQPFIPVEVLVDLFLKEGACDELFSYLIKVKRKNVLRCLCKKLLKIFAMPMDIKMILKMVLDS
 IEDLEVTCTWKLPTLAKFSPYLGQMINLRLLLSHIHASSYISPEKEEQYIAQFTSQFLSLQCLQALYVDSLFFLRGR
 LDQLLRHVMNPLETSLITNCRLESDVMHLSQSPSVLSVLSLGVMLTDVSPPEPLQALLERASATLQDLVFDECGI
 TDDQLLALLPSLSHCSQLTTLSFYGNSISISALQSLQLHIGLSNLTHVLYPVPLESYEDIHGTLHLERLAYLHARLR
 ELLCELGRPSMVWLSANPCPHCGDRTFYDPEPILCPCFMPN

TRP2IN2

LMETHLSSKRYTEEAGFFPWLVVYVYRFVIGLRVWQWEVISCKLIKRRATTRQP

NYN501a

MQAEGRTGGSTGDADGPGGPGIPDGPAGNAGGPGEAGATGGRGPRGAGAARASGPGGAPRGPHGGAASGLNGCCRC
 GARGPESRLLEFYLAAMPFATPMEAEALARRSLAQDAPPLVPVGVLLKEFTVSGNILTIRLTAADHRQLQLSISCLQQL
 SLLMWITQCFLPVFLAQPPSGQRR

NYN501b

MLMAQEALAFMAQAMLAQERRVPRAAEVPGAQGGQGPGRGEEAPRGVRMAARLQG

LAGE1

Figure 27 (Cont)

151/216

MQAEGQGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRGPRGAGAARASGPRGGAPRGPHGGAASAQDGRCPG
 GARRPDSRLLQLHITMPFSSPMEAEVLVRRILSRDAAPLPRPGAVLKDFTVSGNLLFIRLTAADHRQLQLSISSCLQQL
 SLLMWITQCFLPVFLAQAAPSGQRR

Differentiation Savine Scramble process

Disease name : melanoma
 Input filename : Diffmucg.txt
 Output filename : Diffmucs.txt
 Number genes : 8
 Number segments : 187
 Segment length : 30
 Segment overlap : 15

Segments in original order:

 Gene : gp100
 Segment# : 1
 Offset : 1
 1st Codon : 1
 A A M D L V L K R C L L H L A V I G A L L A V G A T K V P R
 GCCGCTATGGATCTGGTCTCGTAAAGGTGTCTGCTCCACCTCGCGCTCATCGGAGCCCTCCTGGCTGTGGGAGCCACAAAGGTCCCCAGA

Gene : gp100
 Segment# : 2
 Offset : 16
 1st Codon : 1
 V I G A L L A V G A T K V P R N Q D W L G V S R Q L R T K A
 GTGATTGGCGCTCTGCTCGCGGTGGCGCTACCAAAGTGCCTAGGAATCAGGATTGGCTCGGCGTCAGCAGACAGCTCAGGACAAAGGCT

Gene : gp100
 Segment# : 3
 Offset : 31
 1st Codon : 1
 N Q D W L G V S R Q L R T K A W N R Q L Y P E W T E A Q R L
 AACCAAGACTGGCTGGGAGTGTCCAGGCACTGAGAACCAAGCCTGGAACAGACAGCTCTACCTGAGTGGAGCCGAAGCCCAAGGCTC

Gene : gp100
 Segment# : 4
 Offset : 46
 1st Codon : 1
 W N R Q L Y P E W T E A Q R L D C W R G G Q V S L K V S N D
 TGGATAGGCAACTGTATCCGAATGGACAGAGGCTCAGAGACTGGATTGCTGGAGGGGAGGCCAAGTGTCCCTGAAAGTGTCCAACGAT

Gene : gp100
 Segment# : 5
 Offset : 61
 1st Codon : 1
 D C W R G G Q V S L K V S N D G P T L I G A N A S F S I A L
 GACTGTTGGAGAGGCGGACAGGTCCAGCTCAAGTCAAGATGACGGACCCACACTGATTGGCGCTAACGCTAGCTTTAGCATTGCCCTC

Gene : gp100
 Segment# : 6
 Offset : 76
 1st Codon : 1
 G P T L I G A N A S F S I A L N F P G S Q K V L P D G Q V I
 GGCCCTACCCCTCATCGGAGCCCAATGCCTCCTTCTCCATCGCTCTGAATTCCTCGGCTCCAGAAAGTGTCCCGATGGCCAAGTGATT

Gene : gp100
 Segment# : 7
 Offset : 91
 1st Codon : 1
 N F P G S Q K V L P D G Q V I W V N N T I I N G S Q V W G G
 AACTTTCGGGAAGCCAAAGGTCTGCTGACGGACAGGTCTCTGGGTGAATAACACAATCATTAAACGGAAGCCAAAGTGTGGGGCGGA

Gene : gp100
 Segment# : 8
 Offset : 106
 1st Codon : 1

Figure 27 (Cont)

152/216

W V N N T I I N G S Q V W G G Q P V Y P Q E T D D A C I F P
TGGGTCAACAATACCATTATCAATGGCTCCCAGGTCTGGGGAGGCCAACCCGTCTACCTCAGGAAACCGATGACGCTTGCAITTTCCCT

Gene : gp100
Segment# : 9
Offset : 121
1st Codon : 1

Q P V Y P Q E T D D A C I F P D G G P C P S G S W S Q K R S
CAGCCTGTGTATCCCCAAGAGACAGACGATGCTGTATCTTTCCCGATGGCGGACCTGTCCCTCCGGCTCCTGGTCCCAGAAAAGGTCC

Gene : gp100
Segment# : 10
Offset : 136
1st Codon : 1

D G G P C P S G S W S Q K R S F V Y V W K T W G Q Y W Q V L
GACGGAGGCCCTTGCCCTAGCGGAAGCTGGAGCCAAAAGAGAAGCTTTGTGTATGTGTGAAGACATGGGACAGTATTGGCAAGTGCTC

Gene : gp100
Segment# : 11
Offset : 151
1st Codon : 1

F V Y V W K T W G Q Y W Q V L G G P V S G L S I G T G R A M
TTCGTCTACGCTCGGAAAACCTGGGGCCAATACTGGCAGGTCTGGGAGGCCCTGTGTCCGGCTCAGCATTTGGCACAGGCAGAGCCATG

Gene : gp100
Segment# : 12
Offset : 166
1st Codon : 1

G G P V S G L S I G T G R A M L G T H T M E V T V Y H R R G
GGCGGACCCGTGAGCGGACTGTCCATCGGAACCGGAAGGGCTATGCTCGGCACACACAATGGAAGTGACAGTGTATCACAGAAGGGGA

Gene : gp100
Segment# : 13
Offset : 181
1st Codon : 1

L G T H T M E V T V Y H R R G S R S Y V P L A H S S S A F T
CTGGGAACCCATACCATGGAGGTACCGTCTACCATAGGAGAGGCTCCAGGTCTACGTCCCCCTCGCCCATAGCTCCAGCGCTTTTACA

Gene : gp100
Segment# : 14
Offset : 196
1st Codon : 1

S R S Y V P L A H S S S A F T I T D Q V P P S V S V S Q L R
AGCAGAGCTATGTGCTCTGGCTCACTCCAGCTCCGCCTTTACCATTACCGATCAGTCCCTTTAGCGTCAGCGTCAGCCAACTGAGA

Gene : gp100
Segment# : 15
Offset : 211
1st Codon : 1

I T D Q V P P S V S V S Q L R A L D G G N K H F L R N Q P L
ATCACAGACCAAGTGCCCTTTCTCCGTGTCCTGCTCCAGCTCAGGGCTCTGGATGGCGGAAACAAACACTTTCTGAGAAACCAACCCCTC

Gene : gp100
Segment# : 16
Offset : 226
1st Codon : 1

A L D G G N K H F L R N Q P L T P A L Q L H D P S G Y L A E
GCCCTCGACGGAGGCAATAAGCATTTCTCAGGAATCAGCCTCTGACATTCGCTCTGCAACTGCATGACCTAGCGGATACCTCGCGGAA

Gene : gp100
Segment# : 17
Offset : 241
1st Codon : 1

T F A L Q L H D P S G Y L A E A D L S Y T W D F G D S S G T
ACCTTTGCCCTCCAGCTCCAGATCCCTCCGGCTATCTGGCTGAGGCTGACCTCAGCTATACCTGGGACTTTGGCGATAGCTCCGGCACA

Gene : gp100
Segment# : 18
Offset : 256
1st Codon : 1

A D L S Y T W D F G D S S G T L I S R A L V V T H T Y L E P
GCCGATCTGTCTACACATGGGATTTCCGGAGACTCCAGCGGAACCTCATCTCCAGGGCTCTGGTCTGACACACATACCTCGAGCCT

Figure 27 (Cont)

153/216

Gene : gp100
Segment# : 19
Offset : 271
1st Codon : 1
L I S R A L V V T H T Y L E P G P V T A Q V V L Q A A I P L
CTGATTAGCAGAGCCCTCGTGGTCACCCATACCTATCTGGAAACCGGACCCGTCACCGCTCAGGTCGTGCTCCAGGCTGCCATTCCCCTC

Gene : gp100
Segment# : 20
Offset : 286
1st Codon : 1
G P V T A Q V V L Q A A I P L T S C G S S P V P G T T D G H
GGCCCTGTGACAGCCCAAGTGGTCTGCAAGCCGCTATCCCTCTGACAAGCTGTGGCTCCAGCCCTGTGCCTGGCACAACCGATGGCCAT

Gene : gp100
Segment# : 21
Offset : 301
1st Codon : 1
T S C G S S P V P G T T D G H R P T A E A P N T T A G Q V P
ACCTCTGCGGAAGCTCCCCGTCACCGGAACCAAGACGACAGACCCACAGCCGAAGCCCTAACACAACCGCTGGCCAAGTGCCT

Gene : gp100
Segment# : 22
Offset : 316
1st Codon : 1
R P T A E A P N T T A G Q V P T T E V V G T T P G Q A P T A
AGGCTACCGCTGAGGCTCCCAATACCAAGCCGACAGGTCCTCCCAACCGAAGTGGTCGGCACAACCCCTGGCCAAGCCCTACCGCT

Gene : gp100
Segment# : 23
Offset : 331
1st Codon : 1
T T E V V G T T P G Q A P T A E P S G T T S V Q V P T T E V
ACCACAGAGGTCGTGGGAACCAACCCGACAGGTCCTCCACAGCCGAACCTCCGGCACAACCTCGTGCAAGTGCCTACCACAGAGGTC

Gene : gp100
Segment# : 24
Offset : 346
1st Codon : 1
E P S G T T S V Q V P T T E V I S T A P V Q M P T A E S T G
GAGCTAGCGGAACCAAGCGTCCAGTCCCAACCGAAGTGATTAGCAGCCCTGTGCAATGCCTACCGCTGAGTCCACCGGA

Gene : gp100
Segment# : 25
Offset : 361
1st Codon : 1
I S T A P V Q M P T A E S T G M T P E K V P V S E V M G T T
ATCTCCACCGCTCCCGTCCAGATGCCACAGCCGAAAGCAGGCGATGACCCCTGAGAAAGTGCTGTGTCGAGGTCATGGGAACCA

Gene : gp100
Segment# : 26
Offset : 376
1st Codon : 1
M T P E K V P V S E V M G T T L A E M S T P E A T G M T P A
ATGACACCCGAAAGTCCCGTCAGCGAAGTGATGGGCACAACCTCGCCGAAATGTCCACCCCTGAGGCTACCGGAATGACACCCGCT

Gene : gp100
Segment# : 27
Offset : 391
1st Codon : 1
L A E M S T P E A T G M T P A E V S I V V L S G T T A A Q V
CTGGCTGAGATGAGCACACCCGAAGCCACAGGCGATGACCCCTGCCGAAGTGTCATCGTCGTGCTCAGCGGAACCAAGCCGCTCAGGTC

Gene : gp100
Segment# : 28
Offset : 406
1st Codon : 1
E V S I V V L S G T T A A Q V T T T E W V E T T A R E L P I
GAGGTACGATTGTGGTCTGTCCGGCACAACCGCTGCCAAGTGACAACCAAGAGTGGGTGGAAACCAAGCCAGAGAGCTCCCAT

Gene : gp100

Figure 27 (Cont)

154/216

Segment# : 29
Offset : 421
1st Codon : 1
T T T E W V E T T A R E L P I P E P E G P D A S S I M S T E
ACCACAACCGAATGGTTCGAGACAACCGCTAGGGAACTGCCTATCCCTGAGCCTGAGGGACCCGATGCCTCCAGCATTATGTCCACCGAA

Gene : gp100
Segment# : 30
Offset : 436
1st Codon : 1
P E P E G P D A S S I M S T E S I T G S L G P L L D G T A T
CCCGAACCGGAAGGCCCTGACGCTAGCTCCATCATGAGCACAGAGTCCATCACAGGCTCCCTGGGACCCCTCTGGATGGCACAGCCACA

Gene : gp100
Segment# : 31
Offset : 451
1st Codon : 1
S I T G S L G P L L D G T A T L R L V K R Q V P L D C V L Y
AGCATTACCGAAGCCTCGGCCCTCTGCTCGACGGAACCGCTACCTCAGGCTCGTGAAAAGGCAAGTGCTCTGGATTGCGTCCGTGTAT

Gene : gp100
Segment# : 32
Offset : 466
1st Codon : 1
L R L V K R Q V P L D C V L Y R Y G S F S V T L D I V Q G I
CTGAGACTGGTCAAGAGACAGGTCCCCCTGACTGTGTCTCTACAGATACGGAAGCTTTAGCGTCACCTCGACATTGTGCAAGGCATT

Gene : gp100
Segment# : 33
Offset : 481
1st Codon : 1
R Y G S F S V T L D I V Q G I E S A E I L Q A V P S G E G D
AGGTATGGCTCCTTCTCCGTGACACTGGATATCGTCCAGGGAATCGAAAGCGCTGAGATTCTGCAAGCGTCCCTCCGGCGAAGGCGAT

Gene : gp100
Segment# : 34
Offset : 496
1st Codon : 1
E S A E I L Q A V P S G E G D A F E L T V S C Q G G L P K E
GAGTCCGCGAAATCCTCCAGGCTGTGCTAGCGGAGAGGAGACGCTTTCGAACTGACAGTGTCTGCCAAGGCGGACTGCCTAAGGAA

Gene : gp100
Segment# : 35
Offset : 511
1st Codon : 1
A F E L T V S C Q G G L P K E A C M E I S S P G C Q P P A Q
GCCTTTGAGCTCACCGTCAGCTGTGAGGAGGCCCTCCCAAGAGGCTTGATGAGATTAGCTCCCCCGGATGCCAACCCCTGCCCCAA

Gene : gp100
Segment# : 36
Offset : 526
1st Codon : 1
A C M E I S S P G C Q P P A Q R L C Q P V L P S P A C Q L V
GCCTGTATGGAATCTCCAGCCCTGGCTGTGAGCCTCCCGCTCAGAGACTGTGTGAGCCTGTGCTCCCTCCCCCGCTGCCACTGCTG

Gene : gp100
Segment# : 37
Offset : 541
1st Codon : 1
R L C Q P V L P S P A C Q L V L H Q I L K G G S G T Y C L N
AGGCTCTGCCAACCCGTCCTGCTAGCCCTGCTGTGAGCTGTGCTCCCAAAATCCTCAAGGAGGCTCCGGCACATACTGTCTGAAT

Gene : gp100
Segment# : 38
Offset : 556
1st Codon : 1
L H Q I L K G G S G T Y C L N V S L A D T N S L A V V S T Q
CTGCATCAGATTCTGAAAGCGGAAGCGGAACCTATTGCCTCAAGCTCAGCCTCGCGGATACCAATAGCCTCGCGCTGTGTCCACCCAA

Gene : gp100
Segment# : 39
Offset : 571

Figure 27 (Cont)

155/216

1st Codon : 1
V S L A D T N S L A V V S T Q L I M P G Q E A G L G Q V P L
GTGTCCCTGGCTGACACAACTCCCTGGCTGTGGTCAGCACACAGCTCATCATGCCCGACAGGAAGCCGGACTGGGACAGGTCCCCCTC

Gene : gp100
Segment# : 40
Offset : 586
1st Codon : 1
L I M P G Q E A G L G Q V P L I V G I L L V L M A V V L A S
CTGATTATGCCCTGGCCAAGAGGCTGGCCTCGGCCAAGTGCCCTCTGATTGTGGGAATCCTCCTGGTCCGTGATGGCCGTCTGCTCGCCTCC

Gene : gp100
Segment# : 41
Offset : 601
1st Codon : 1
I V G I L L V L M A V V L A S L I Y R R R L M K Q D F S V P
ATCGTCGGCAITCTGCTCGTGTCTATGGCTGTGGTCTGGCTAGCCTCATCTATAGGAGAAGGCTCATGAAACAGGATTCTCGTGCCT

Gene : gp100
Segment# : 42
Offset : 616
1st Codon : 1
L I Y R R R L M K Q D F S V P Q L P H S S S H W L R L P R I
CTGATTACAGAAGGAGACTGATGAAGCAAGACTTTAGCGTCCCCCAACTGCCTCACTCCAGCTCCCACTGGCTGAGACTGCCTAGGATT

Gene : gp100
Segment# : 43
Offset : 631
1st Codon : 1
Q L P H S S S H W L R L P R I F C S C P I G E N S P L L S G
CAGCTCCCCATAGCTCCAGCCATTGGCTCAGGCTCCCCAGAATCTTTTGCTCCTGCCCTATCGGAGAGAATAGCCCTCTGCTCAGCGGA

Gene : gp100
Segment# : 44
Offset : 646
1st Codon : 1
F C S C P I G E N S P L L S G Q Q V A A
TTCGTAGCTGTCCCATTTGGCGAAAACCTCCCCCTCCTGTCCGCCAACAGGTGCGCGCT

Gene : MART
Segment# : 1
Offset : 1
1st Codon : 1
A A M P R E D A H F I Y G Y P K K G H G H S Y T T A E E A A
GCCGTATGCCTAGGGAAGACGCTCACTTTATCTATGGCTATCCCAAAAGGGACACGGACACTCTACACAACCGCTGAGGAAGCCGCT

Gene : MART
Segment# : 2
Offset : 16
1st Codon : 1
K K G H G H S Y T T A E E A A G I G I L T V I L G V L L L I
AAGAAAGGCCATGGCCATAGCTATACCACAGCCGAAGAGGCTGCCGAATCGGAATCCTCACCGTCATCCTCGGCGTCTGCTCCTGATT

Gene : MART
Segment# : 3
Offset : 31
1st Codon : 1
G I G I L T V I L G V L L L I G C W Y C R R R N G Y R A L M
GGCATTGGCATTCTGACAGTGATTCTGGGAGTGCTCCTGCTCATCGGATGCTGGTACTGTAGGAGAAGGAATGGCTATAGGGCTCTGATG

Gene : MART
Segment# : 4
Offset : 46
1st Codon : 1
G C W Y C R R R N G Y R A L M D K S L H V G T Q C A L T R R
GGCTGTTGGTATTGCAGAAGGAGAAACGGATACAGAGCCCTCATGGATAAGTCCCTGCATGTGGGAACCAATGCGCTCTGACAAGGAGA

Gene : MART
Segment# : 5
Offset : 61
1st Codon : 1
D K S L H V G T Q C A L T R R C P Q E G F D H R D S K V S L

Figure 27 (Cont)

156/216

GACAAAAGCCTCCACGTCCGACACAGTGTGCCCTCACCAGAAGGTGTCCCCAAGAGGGATTGATCACAGAGACTCCAAGGTCAGCCTC

Gene : MART
Segment# : 6
Offset : 76
1st Codon : 1

C P Q E G F D H R D S K V S L Q E K N C E P V V P N A P P A
TGCCCTCAGGAAGGCTTTGACCATAGGGATAGCAAAGTGTCCCTGCAAGAGAAAACTGTGAGCCTGTGGTCCCAATGCCCTCCCGCT

Gene : MART
Segment# : 7
Offset : 91
1st Codon : 1

Q E K N C E P V V P N A P P A Y E K L S A E Q S P F P Y S P
CAGGAAAAGAATTGCGAACCCGTCGTGCCTAACGCTCCCCCTGCCTATGAGAACTGTCCGCGAACAGTCCCCCTCCCTATAGCCCT

Gene : MART
Segment# : 8
Offset : 106
1st Codon : 1

Y E K L S A E Q S P P P Y S P A A
TAGGAAAAGCTCAGCGCTGAGCAAAGCCCTCCCCCTTACTCCCCCGTGGC

Gene : TRP-1
Segment# : 1
Offset : 1
1st Codon : 1

A A P A F L T W H R Y H L L R L E K D M Q E M L Q E P S F S
GCCGCTCCCGCTTTCCTCACCTGGCACAGATACCATCTGCTCAGGCTCGAGAAAGACATGCAGGAAATGCTCCAGGAACCTCCTTCTCC

Gene : TRP-1
Segment# : 2
Offset : 16
1st Codon : 1

L E K D M Q E M L Q E P S F S L P Y W N F A T G K N V C D I
CTGGAAAAGGATATGCAAGAGATGCTGCAAGAGCCTAGCTTTAGCCTCCCCTATTGGAATTCGCTACCGGAAAGAATGTGTGTGACATT

Gene : TRP-1
Segment# : 3
Offset : 31
1st Codon : 1

L P Y W N F A T G K N V C D I C T D D L M G S R S N F D S T
CTGCTTACTGGAACCTTGCCACAGGCAAAAACGCTCGGATATCTGTACCGATGACCTCATGGGAAGCAGAAGCAATTCGATAGCACA

Gene : TRP-1
Segment# : 4
Offset : 46
1st Codon : 1

C T D D L M G S R S N F D S T L I S P N S V F S Q W R V V C
TGCACAGACGATCTGATGGGCTCCAGGTCCAACCTTGACTCCACCCTCATCTCCCCAATAGCGTCTTCTCCAGTGGAGGGTCTGTGT

Gene : TRP-1
Segment# : 5
Offset : 61
1st Codon : 1

L I S P N S V F S Q W R V V C D S L E D Y D T L G T L C N S
CTGATTAGCCCTAACTCCGTGTTTAGCCAATGGAGAGTGGTCTGCGATAGCCTCGAGGATTACGATACCTCGGCACACTGTGTAACTCC

Gene : TRP-1
Segment# : 6
Offset : 76
1st Codon : 1

D S L E D Y D T L G T L C N S T E D G P I R R N P A G N V A
GACTCCCTGGAGACTATGACACACTGGGAACCTCTGCAATAGCACAGAGGATGGCCCTATCAGAAGGAATCCCGCTGGCAATGTGGCT

Gene : TRP-1
Segment# : 7
Offset : 91
1st Codon : 1

T E D G P I R R N P A G N V A R P M V Q R L P E P Q D V A Q
ACCGAAGACGGACCCATTAGGAGAAACCTGCCGGAACGTCGCCAGACCCATGGTGCAGGCTCCCCGAACCCAGACGTCGCCCA

Figure 27 (Cont)

157/216

Gene : TRP-1
Segment# : 8
Offset : 106
1st Codon : 1
R P M V Q R L P E P Q D V A Q C L E V G L F D T P P F Y S N
AGGCCTATGGTCCAGAGACTGCCTGAGCCTCAGGATGTGGCTCAGTGTCTGGAAGTGGGACTGTTGACACACCCCTTTCTATAGCAAT

Gene : TRP-1
Segment# : 9
Offset : 121
1st Codon : 1
C L E V G L F D T P P F Y S N S T N S F R N T V E G Y S D P
TGCTCGAGGTCGGCTCTTCGATACCCCTCCCTTTTACTCCAACCTCCACCAATAGCTTTAGGAATACCGTCGAGGGGATACTCCGACCCT

Gene : TRP-1
Segment# : 10
Offset : 136
1st Codon : 1
S T N S F R N T V E G Y S D P T G K Y D P A V R S L H N L A
AGCACAACTCCTTCAGAAACACAGTGAAGGCTATAGCGATCCCAAGGCAAATACGATCCCGCTGTGAGAAGCCTCCACAATCTGGCT

Gene : TRP-1
Segment# : 11
Offset : 151
1st Codon : 1
T G K Y D P A V R S L H N L A H L F L N G T G G Q T H L S S
ACCGAAAGTATGACCTGCGCTCAGGTCCCTGCATAACCTCGCCCATCTGTTTCTGAATGGCACAGGCGGACAGACACCTCAGCTCC

Gene : TRP-1
Segment# : 12
Offset : 166
1st Codon : 1
H L F L N G T G G Q T H L S S Q D P I F V L L H T F T D A V
CACCTCTTCTCAACGGAACCGGAGGCCAAACCCATCTGTCCAGCCAAGACCTATCTTTGTGCTCCTGCATACCTTTACCGATGCCGCT

Gene : TRP-1
Segment# : 13
Offset : 181
1st Codon : 1
Q D P I F V L L H T F T D A V F D E W L R R Y N A D I S T F
CAGGATCCCATTTTCGTCTGCTCCACACATTACAGACGCTGTGTTGACGAATGGCTCAGGAGATACAATGCCGATATCTCCACCTTT

Gene : TRP-1
Segment# : 14
Offset : 196
1st Codon : 1
P D E W L R R Y N A D I S T F P L E N A P I G H N R Q Y N M
TTCGATGAGTGGCTGAGAAGGTATAACGCTGACATTAGCACATTCCCTCTGGAAAAAGCTCCCATTTGGCCATAACAGACAGTATAACATG

Gene : TRP-1
Segment# : 15
Offset : 211
1st Codon : 1
P L E N A P I G H N R Q Y N M V P F W P P V T N T E M F V T
CCCCTCGAGAATGCCCTATCGGACACAATAGGCAATACAATATGGTCCCTTTTGGCCTCCCGTCACCAATACCGAAATGTTTGTGACA

Gene : TRP-1
Segment# : 16
Offset : 226
1st Codon : 1
V P F W P P V T N T E M F V T A P D N L G Y T Y E A A
GTGCCTTTCTGGCCCCCTGTGACAAACACAGAGATGTTGCTACCGCTCCCGATAACCTCGGCTATACCTATGAGGCTGCC

Gene : Tyros
Segment# : 1
Offset : 1
1st Codon : 1
A A M L L A V L Y C L L N S F Q T S A G H F P R A C V S S K
GCCGCTATGCTCCTGGCTGTGCTCTACTGTCTGCTCTGGTCTTCCAAACCTCCGCGGACACTTCCAGAGCCTGTGTGTCCAGCAA

Gene : Tyros
Segment# : 2

Figure 27 (Cont)

158/216

Offset : 16
1st Codon : 1
Q T S A G H F P R A C V S S K N L M E K E C C P P W S G D R
CAGACAAGCGCTGGCCATTTCCTAGGGCTTGGTCAGCTCCAAGAATCTGATGGAGAAAGAGTGTTCCTCCCTGGAGCGGAGACAGA

Gene : Tyros
Segment# : 3
Offset : 31
1st Codon : 1
N L M E K E C C P P W S G D R S P C G Q L S G R G S C Q N I
AACCTCATGAAAAGGAATGCTGTCCCCCTTGGTCCGGCGATAGTCCCCCTGTGGCCAACTGTCCGGCAGAGGCTCCTGCCAAAACATT

Gene : Tyros
Segment# : 4
Offset : 46
1st Codon : 1
S P C G Q L S G R G S C Q N I L L S N A P L G P Q F P F T G
AGCCCTTGGCGAGCTCAGCGGAAGGGGAAGCTGTCAAGATATCCTCTGTCCAACGCTCCCTCGGCCCTCAGTTTCCTTTACCGGA

Gene : Tyros
Segment# : 5
Offset : 61
1st Codon : 1
L L S N A P L G P Q F P F T G V D D R E S W P S V F Y N R T
CTGCTCAGCAATGCCCTCTGGACCCCAATTCCCTTTACAGGCGTCGACGATAGGGAAAGCTGGCCCTCCGTGTTTTACAATAGGACA

Gene : Tyros
Segment# : 6
Offset : 76
1st Codon : 1
V D D R E S W P S V F Y N R T C Q C S G N F M G F N C G N C
GTGGATGACAGAGAGTCTGGCCTAGCGTCTTCTATAACAGAACCTGTCACTGTAGCGGAACTTTATGGGATTCAATTGCGGAAACTGT

Gene : Tyros
Segment# : 7
Offset : 91
1st Codon : 1
C Q C S G N F M G F N C G N C K F G F W G P N C T E R R L L
TGCCAAATGCTCCGGCAATTTTCATGGGCTTTAACTGTGGCAATTGCAAATTCGGATTCTGGGGCCCTAACTGTACCGAAAGGAGACTGCTC

Gene : Tyros
Segment# : 8
Offset : 106
1st Codon : 1
K F G F W G P N C T E R R L L V R R N I F D L S A P E K D K
AAGTTTGCTTTTGGGACCCAATTGCACAGAGAGAAGGCTCCTGGTCAGGAGAAACATTTTCGATCTGTCCGCCCTGAGAAAGACAAA

Gene : Tyros
Segment# : 9
Offset : 121
1st Codon : 1
V R R N I F D L S A P E K D K F F A Y L T L A K H T I S S D
GTGAGAAGGAATATCTTTGACCTCAGCGCTCCGAAAAGGATAAGTTTTTCGCTTACCTCACCTCGCCAAACACACAATCTCCAGCGAT

Gene : Tyros
Segment# : 10
Offset : 136
1st Codon : 1
F F A Y L T L A K H T I S S D Y V I P I G T Y G Q M K N G S
TCTTTGCTATCTGACACTGGCTAAGCATACCATAGCTCCGACTATGTGATTCCCATTTGGCACATACGGACAGATGAAGAATGGCTCC

Gene : Tyros
Segment# : 11
Offset : 151
1st Codon : 1
Y V I P I G T Y G Q M K N G S T P M F N D I N I Y D L F V W
TACGTCACTCATCGGAACCTATGGCCAAATGAAAAACGGAAGCACACCCATGTTCAATGACATTAACATTTACGATCTGTTGTGTGG

Gene : Tyros
Segment# : 12
Offset : 166
1st Codon : 1

Figure 27 (Cont)

159/216

T P M F N D I N I Y D L F V W M H Y Y V S M D A L L G G S E
ACCCCTATGTTTAACGATATCAATATCTATGACCTCTTCGTCCTGGATGCACTATTACGTCAGCATGGACGCTCTGCTCGGCGAAGCGAA

Gene : Tyros
Segment# : 13
Offset : 181
1st Codon : 1

M H Y Y V S M D A L L G G S E I W R D I D F A H E A P A F L
ATGCATTACTATGTGTCCATGGATGCCCTCCTGGGAGGCTCCGAGATTGGAGAGACATTGACTTTGCCCATGAGGCTCCCGCTTTCTCTC

Gene : Tyros
Segment# : 14
Offset : 196
1st Codon : 1

I W R D I D F A H E A P A F L P W H R L F L L R W E Q E I Q
ATCTGGAGGGATATCGAATTCGCTCACGAAGCCCTGCCTTCTGCCTTGGCATAGGCTCTTCTCTCTGAGATGGGAACAGGAAATCCAA

Gene : Tyros
Segment# : 15
Offset : 211
1st Codon : 1

P W H R L F L L R W E Q E I Q K L T G D E N F T I P Y W D W
CCCTGGCACAGACTGTTTCTGCTCAGGTGGGAGCAAGAGATTAGAACTGACAGGCGATGAGAATTCACAATCCCTTACTGGGACTGG

Gene : Tyros
Segment# : 16
Offset : 226
1st Codon : 1

K L T G D E N F T I P Y W D W R D A E K C D I C T D E Y M G
AAGCTCACGGGAGACGAAACTTTACCATTCCTTATGGGATTGGAGAGACGCTGAGAAATGCGATATCTGTACCGATGAGTATATGGGA

Gene : Tyros
Segment# : 17
Offset : 241
1st Codon : 1

R D A E K C D I C T D E Y M G G Q H P T N P N L L S P A S F
AGGGATGCCGAAAGTGTGACATTGACAGACGAATACATGGGCGGACAGCATCCCAACAAACCTAACCTCCTGTCCTCCCGCTAGCTTT

Gene : Tyros
Segment# : 18
Offset : 256
1st Codon : 1

G Q H P T N P N L L S P A S F F S S W Q I V C S R L E E Y N
GGCCAACCCCTACCAATCCCAATCTGCTCAGCCCTGCCTCCTTCTTAGCTCCTGGCAAATCGTCTGCTCCAGGCTCGAGGAATACAAT

Gene : Tyros
Segment# : 19
Offset : 271
1st Codon : 1

F S S W Q I V C S R L E E Y N S H Q S L C N G T P E G P L R
TTCTCCAGCTGGCAGATTGTGTAGCAGACTGGAAGAGTATACTCCCAACAAAGCCTCTGCAATGGCACACCCGAAGGCCCTCTGAGA

Gene : Tyros
Segment# : 20
Offset : 286
1st Codon : 1

S H Q S L C N G T P E G P L R R N P G N H D K S R T P R L P
AGCCATCAGTCCCTGTGTAAACGAACCCCTGAGGGACCCCTCAGGAGAAACCTGGCAATCAGGATAAGTCCAGGACACCCAGACTGCCT

Gene : Tyros
Segment# : 21
Offset : 301
1st Codon : 1

R N P G N H D K S R T P R L P S S A D V E F C L S L T Q Y E
AGGAATCCCGAAACCATGACAAAAGCAGAACCCCTAGGCTCCCTCCAGCGCTGACGTCGAGTTTTCCTCAGCCTCACCCAAATACGAA

Gene : Tyros
Segment# : 22
Offset : 316
1st Codon : 1

S S A D V E F C L S L T Q Y E S G S M D K A A N F S F R N T
AGCTCCCGCATGTGGAATTCGTCTGTCTGCTCCCTGACACAGTATGAGTCCGGCTCCATGGATAAGGCTGCCAATTTCTCCTTCAGAAACACA

Figure 27 (Cont)

160/216

Gene : Tyros
Segment# : 23
Offset : 331
1st Codon : 1
S G S M D K A A N P S F R N T L E G F A S P L T G I A D A S
AGCGGAAGCATGGACAAAGCCGCTAAGCTTTAGCTTTAGGAATACCCTCGAGGGATTGCTAGCCCTCTGACAGGCATTGCCGATGCCTCC

Gene : Tyros
Segment# : 24
Offset : 346
1st Codon : 1
L E G F A S P L T G I A D A S Q S S M H N A L H I Y M N G T
CTGGAAGGCTTTGCCTCCCCCTCACCGGAATCGCTGACGCTAGCCAAAGCTCCATGCATAACGCTCTGCATATCTATATGAATGGCACA

Gene : Tyros
Segment# : 25
Offset : 361
1st Codon : 1
Q S S M H N A L H I Y M N G T M S Q V Q G S A N D P I F L L
CAGTCCAGCATGCACAATGCCCTCCACATTACATGAACGGAACCATGAGCCAAGTCAAGGCTCCGCCAATGACCCTATCTTTCTGCTC

Gene : Tyros
Segment# : 26
Offset : 376
1st Codon : 1
M S Q V Q G S A N D P I F L L H H A F V D S I F E Q W L Q R
ATGTCCAGGTCAGGGAAGCGCTAACGATCCCATTTTCTCTGTCATCAGCTTTGTCGACTCCATCTTTGAGCAATGGCTCCAGAGA

Gene : Tyros
Segment# : 27
Offset : 391
1st Codon : 1
H H A F V D S I F E Q W L Q R H R P L Q E V Y P E A N A P I
CACCATGCCTTTGTGGATAGCATTTTCGAACAGTGGCTGCAAGGCATAGGCCCTCTGCAAGAGGTCTACCCCTGAGGCTAACGCTCCCAT

Gene : Tyros
Segment# : 28
Offset : 406
1st Codon : 1
H R P L Q E V Y P E A N A P I G H N R E S Y M V P F I P L Y
CACAGACCCCTCCAGGAAGTGATCCCGAAGCCAATGCCCTATCCGACACAATAGGGAAAGCTATATGGTCCCCTTTATCCCTCTGTAT

Gene : Tyros
Segment# : 29
Offset : 421
1st Codon : 1
G H N R E S Y M V P F I P L Y R N G D F F I S S K D L G Y D
GGCCATAACAGAGAGTCTACATGGTGCCTTTTCATTTCCCTCTACAGAAACGGAGACTTTTTCATTAGCTCCAAGGATCTGGGATACGAT

Gene : Tyros
Segment# : 30
Offset : 436
1st Codon : 1
R N G D F F I S S K D L G Y D Y S Y L Q D S D P D S F Q D Y
AGGAATGGCGATTTCTTTATCTCCAGCAAAGACCTCGGCTATGACTATAGCTATCTGCAAGACTCCGACCTGACTCCTTCCAAGACTAT

Gene : Tyros
Segment# : 31
Offset : 451
1st Codon : 1
Y S Y L Q D S D P D S F Q D Y I K S Y L E Q A S R I W S W L
TACTCCTACCTCCAGGATAGCGATCCCGATAGCTTTCAGGATTACATTAAGTCTACCTCGAGCAAGCCTCCAGGATTGGTCTGGCTC

Gene : Tyros
Segment# : 32
Offset : 466
1st Codon : 1
I K S Y L E Q A S R I W S W L L G A A M V G A V L T A L L A
ATCAAAGCTATCTGGAACAGGCTAGCAGAATCTGGAGCTGGCTGCTCGGCGCTGCCATGGTGGGAGCCGCTCTGACAGCCCTCCTGGCT

Gene : Tyros

Figure 27 (Cont)

161/216

Segment# : 33
Offset : 481
1st Codon : 1
L G A A M V G A V L T A L L A G L V S L L C R H K R K Q L P
CTGGAGCCGCTATGGTCGGCGCTGTGCTCACCCTCTGCTCGCCGACTGGTCAGCCTCCTGTGTAGGCATAAGAGAAAGCAACTGCCT

Gene : Tyros
Segment# : 34
Offset : 496
1st Codon : 1
G L V S L L C R H K R K Q L P E E K Q P L L M E K E D Y H S
GGCCTCGTGTCCCTGCTCTGCAGACACAAAAGGAAACAGCTCCCGAAGAGAAACAGCCTCTGCTCATGGAAGGAAGACTATCACTCC

Gene : Tyros
Segment# : 35
Offset : 511
1st Codon : 1
E E K Q P L L M E K E D Y H S L Y Q S H L A A
GAGGAAAGCAACCCCTCTGATGGAGAAAGAGGATTACCATAGCCTCTACCAAAGCCATCTGGCTGCC

Gene : TRP2
Segment# : 1
Offset : 1
1st Codon : 1
A A M S P L W W G F L L S C L G C K I L P G A Q G Q F P R V
GCCGCTATGTCCCCCTCTGGTGGGCTTTCTGCTCAGCTGTCTGGGATGCAAAATCCTCCCGGAGCCCAAGGCCAATCCCTAGGGTC

Gene : TRP2
Segment# : 2
Offset : 16
1st Codon : 1
G C K I L P G A Q G Q F P R V C M T V D S L V N K E C C P R
GGCTGTAAGATTCTGCCTGGCGCTCAGGACAGTTTCCAGAGTGTGTATGACAGTGGATAGCCTCGTGAATAAGGAATGCTGTCCCAGA

Gene : TRP2
Segment# : 3
Offset : 31
1st Codon : 1
C M T V D S L V N K E C C P R L G A E S A N V C G S Q Q G R
TGCATGACGCTCGACTCCCTGGTCAACAAAGAGTGTGGCCTAGGCTCGGCGCTGAGTCGCGCAATGTGTGTGGCTCCCAGCAAGGCAGA

Gene : TRP2
Segment# : 4
Offset : 46
1st Codon : 1
L G A E S A N V C G S Q Q G R G Q C T E V R A D T R P W S G
CTGGAGCCGAAAGCGCTAACGCTCTCGGAAGCCAACAGGGAAGGGGACAGTGTACCGAAGTGAGAGCCGATACCAGACCTGGAGCGGA

Gene : TRP2
Segment# : 5
Offset : 61
1st Codon : 1
G Q C T E V R A D T R P W S G P Y I L R N Q D D R E L W P R
GGCCATGCACAGAGGTGAGGGCTGACACAAGGCCTTGGTCCGGCCCTTACATTCTGAGAAACCAAGACGATAGGGAAGTGTGGCCCGA

Gene : TRP2
Segment# : 6
Offset : 76
1st Codon : 1
P Y I L R N Q D D R E L W P R K F F H R T C K C T G N F A G
CCCTATATCCTCAGGAATCAGGATGACAGAGAGCTCTGGCCTAGGAAATTCTTTACAGAACCTGTAAGTGTACCGGAAACTTTGCCGGA

Gene : TRP2
Segment# : 7
Offset : 91
1st Codon : 1
K F F H R T C K C T G N F A G Y N C G D C K F G W T G P N C
AAGTTTTTCCATAGGACATGCAAAATGCACAGGCAATTTGCTGCTATTAACGTGGCGATTGCAAAATTCGGATGGACAGGCCCTTAAGTGT

Gene : TRP2
Segment# : 8
Offset : 106

Figure 27 (Cont)

162/216

1st Codon : 1
Y N C G D C K F G W T G P N C E R K K P P V I R Q N I H S L
TACAATTGCGGAGACTGTAAGTTTGGCTGGACCGGACCCAATTGCGAAAGGAAAAGCCTCCCGTCATCAGACAGAATATCCATAGCCTC

Gene : TRP2
Segment# : 9
Offset : 121
1st Codon : 1
E R K K P P V I R Q N I H S L S P Q E R E Q F L G A L D L A
GAGAGAAAGAAACCCCTGTGATTAGGCAAAACATTCACCTCCCTGTCCCCCAAGAGAGAGAGCAATTCCTCGGCGCTCTGGATCTGGCT

Gene : TRP2
Segment# : 10
Offset : 136
1st Codon : 1
S P Q E R E Q F L G A L D L A K K R V H P D Y V I T T Q H W
AGCCCTCAGAAAGGGAACAGTTTCTGGGAGCCCTCGACCTCGCCAAAAGAGAGTGCATCCGATTACGTCATCAACCCCAACACTGG

Gene : TRP2
Segment# : 11
Offset : 151
1st Codon : 1
K K R V H P D Y V I T T Q H W L G L L G P N G T Q P Q F A N
AAGAAAGGTCACCCCTGACTATGTGATTACCACACAGCATTGGCTCGGCCTCCTGGGACCCAATGGCACACAGCCTCAGTTTGCCAAT

Gene : TRP2
Segment# : 12
Offset : 166
1st Codon : 1
L G L L G P N G T Q P Q F A N C S V Y D F F V W L H Y Y S V
CTGGGACTGCTCGGCCCTAACGGAAACCAACCCCAATTCGCTAACTGTAGCGTCTACGATTCTTTGTGTGGCTGCATTACTATAGCGTC

Gene : TRP2
Segment# : 13
Offset : 181
1st Codon : 1
C S V Y D F F V W L H Y Y S V R D T L L G P G R P Y R A I D
TGCTCCGTCATGACTTTTTCGTCTGGCTCCACTATTACTCCGTGAGAGACACACTGCTCGGCCCTGGCAGACCCCTATAGGGCTATCGAT

Gene : TRP2
Segment# : 14
Offset : 196
1st Codon : 1
R D T L L G P G R P Y R A I D F S H Q G P A F V T W H R Y H
AGGGATACCTCCTGGGACCCGGAAGGCCTTACAGAGCCATTGACTTTAGCCATCAGGGACCCGCTTCGTACCTGGCAGATACCAT

Gene : TRP2
Segment# : 15
Offset : 211
1st Codon : 1
F S H Q G P A F V T W H R Y H L L C L E R D L Q R L I G N E
TTCTCCCAAGGCCCTGCGCTTTGTGACATGGCATAGGTATCACCTCCTGTGTCTGGAAGGGATCTGCAAAGGCTCATCGGAAACGAA

Gene : TRP2
Segment# : 16
Offset : 226
1st Codon : 1
L L C L E R D L Q R L I G N E S F A L P Y W N F A T G R N E
CTGCTCTGCCTCGAGAGAGACCTCCAGAGACTGATTGGCAATGAGTCTTCGCTCTGCCTTACTGGAACCTTGCCACAGGCAGAAACGAA

Gene : TRP2
Segment# : 17
Offset : 241
1st Codon : 1
S F A L P Y W N F A T G R N E C D V C T D Q L F G A A R P D
AGCTTTGCCCTCCCTATTGGAAATTCGCTACCGGAAGGAATGAGTGTGACGTCTGCACAGACCAACTGTTTGGCGCTGCCAGACCCGAT

Gene : TRP2
Segment# : 18
Offset : 256
1st Codon : 1
C D V C T D Q L F G A A R P D D P T L I S R N S R F S S W E

Figure 27 (Cont)

163/216

TGCGATGTGTGTACCGATCAGCTCTTCGGAGCGCTAGGCGCTGACGATCCACACTGATTAGCAGAACTCCAGGTTTAGCTCCTGGGAA

Gene : TRP2

Segment# : 19

Offset : 271

1st Codon : 1

D P T L I S R N S R P S S W E T V C D S L D D Y N H L V T L
GACCTACCCATCTCCAGGAATAGCAGATTCTCCAGCTGGGAGACAGTGTGTGACTCCCTGGATGACTATAACCATCTGGTCACCCCTC

Gene : TRP2

Segment# : 20

Offset : 286

1st Codon : 1

T V C D S L D D Y N H L V T L C N G T Y E G L L R R N Q M G
ACCGTCTGCGATAGCCTCGACGATTACAATCACCTCGTGACACTGTGTAACGGAACCTATGAGGGACTGCTCAGGAGAAACCAAATGGGA

Gene : TRP2

Segment# : 21

Offset : 301

1st Codon : 1

C N G T Y E G L L R R N Q M G R N S M K L P T L K D I R D C
TGCAATGGCACATACGAAGGCCTCCTGAGAAGGAATCAGATGGGCAGAACTCCATGAACTGCCTACCCCTCAAGGATATCAGAGACTGT

Gene : TRP2

Segment# : 22

Offset : 316

1st Codon : 1

R N S M K L P T L K D I R D C L S L Q K F D N P P P F Q N S
AGGAATAGCATGAAGCTCCCCACACTGAAAGACATTAGGGATTGCGCTCAGCCTCCAGAAATTCGATAACCTCCCTTTTCCAAAACCTCC

Gene : TRP2

Segment# : 23

Offset : 331

1st Codon : 1

L S L Q K F D N P P P F Q N S T F S F R N A L E G F D K A D
CTGTCCCTGCAAAAGTTTGACAATCCCCCTTTCTTTTCAGAATAGCACATTCTCCTTCAGAAACGCTCTGGAAGGCTTTGACAAAGCCGAT

Gene : TRP2

Segment# : 24

Offset : 346

1st Codon : 1

T F S F R N A L E G F D K A D G T L D S Q V M S L H N L V H
ACCTTTAGCTTTAGGAATGCCCTCGAGGGATTGATAAGGCTGACGGAACCCCTCGACTCCAGGTCATGTCCCTGCATAACCTCGTGCAT

Gene : TRP2

Segment# : 25

Offset : 361

1st Codon : 1

G T L D S Q V M S L H N L V H S F L N G T N A L P H S A A N
GGCACACTGGATAGCCAAGTGATGAGCCTCCACAATCTGGTCCACTCCTTCCTCAACGGAACCAATGCCCTCCCATAGCGCTGCCAAT

Gene : TRP2

Segment# : 26

Offset : 376

1st Codon : 1

S F L N G T N A L P H S A A N D P I F V V L H S F T D A I F
AGCTTTCTGAATGGCACAAACGCTCTGCCTCACTCGCGCGTAACGATCCCATTTTCGTGCTGCTCCACTCCTTCACAGACGCTATCTTT

Gene : TRP2

Segment# : 27

Offset : 391

1st Codon : 1

D P I F V V L H S F T D A I F D E W M K R F N P P A D A W P
GACCTATCTTTGTGGTCTGCATAGCTTTACCGATGCCATTTTCGATGAGTGGATGAAAAGGTTTAAACCTCCCGCTGACGCTTGGCCT

Gene : TRP2

Segment# : 28

Offset : 406

1st Codon : 1

D E W M K R F N P P A D A W P Q E L A P I G H N R M Y N M V
GACGAATGGATGAAGAGATTCAATCCCCCTGCCGATGCCCTGGCCCCAAGAGCTCGCCCCCTATCGGACACAATAGGATGTACAATATGGTC

Figure 27 (Cont)

164/216

Gene : TRP2
Segment# : 29
Offset : 421
1st Codon : 1
Q E L A P I G H N R M Y N M V P P P P V T N E E L F L T S
CAGGAAGTGGCTCCCATTTGGCCATAACAGAATGTATAACATGGTGCCTTTCTTTCCCTGTGACAAACGAAGAGCTCTTCCTCACCTCC

Gene : TRP2
Segment# : 30
Offset : 436
1st Codon : 1
P P P P P V T N E E L F L T S D Q L G Y S Y A I D L P V S V
CCCTTTTCCCTCCCGTCACCAATGAGGAAGTGTCTGACAAGCGATCAGCTCGGCTATAGCTATGCCATTGACCTCCCGTCAGCGTC

Gene : TRP2
Segment# : 31
Offset : 451
1st Codon : 1
D Q L G Y S Y A I D L P V S V E E T P G W P T T L L V V M G
GACCAACTGGGATACTCTACGCTATCGATCTGCTGTCCGTGGAAGAGACACCGGATGGCTACCACTGCTCGTGGTCATGGGA

Gene : TRP2
Segment# : 32
Offset : 466
1st Codon : 1
E E T P G W P T T L L V V M G T L V A L V G L F V L L A F L
GAGGAAACCCCTGGCTGGCCACAAACCTCTGGTCGTGATGGGCACACTGGTCGCCCTCGTGGGACTGTTTGTGCTCCCTGGCTTTCTCT

Gene : TRP2
Segment# : 33
Offset : 481
1st Codon : 1
T L V A L V G L F V L L A F L Q Y R R L R K G Y T P L M E T
ACCTCGTGGCTCTGGTCGGCTCTTCGTCCTGCTCGCCTTTCTGCAATACAGAAGGCTCAGGAAAGGCTATACCCCTCTGATGGAGACA

Gene : TRP2
Segment# : 34
Offset : 496
1st Codon : 1
Q Y R R L R K G Y T P L M E T H L S S K R Y T E E A A A
CAGTATAGGAGACTGAGAAAGGATACACACCCCTCATGGAACCCATCTGTCCAGCAAAGGTATACCGAAGAGGGCTGCCGCT

Gene : MC1R
Segment# : 1
Offset : 1
1st Codon : 1
A A M A V Q G S Q R R L L G S L N S T P T A I P Q L G L A A
GCCGCTATGGCTGTGCAAGGCTCCAGAGAAGGCTCTGGGAAGCCTCACTCCACCCCTACCGCTATCCCTCAGCTCGGCCTCGCCGCT

Gene : MC1R
Segment# : 2
Offset : 16
1st Codon : 1
L N S T P T A I P Q L G L A A N Q T G A R C L E V S I S D G
CTGAATAGCACACCACAGCCATTCCCCAACTGGGACTGGCTGCCAATCAGACAGGCGCTAGGTGTCTGGAAGTGTCCATCTCCGACGGA

Gene : MC1R
Segment# : 3
Offset : 31
1st Codon : 1
N Q T G A R C L E V S I S D G L F L S L G L V S L V E N A L
AACCAAACCGAGCCAGATGCCTCGAGGTGAGCATTAGCGATGGCCTCTTCCTCAGCCTCGGCCTCGTGTCCCTGGTCGAGAATGCCCTC

Gene : MC1R
Segment# : 4
Offset : 46
1st Codon : 1
L F L S L G L V S L V E N A L V V A T I A K N R N L H S P M
CTGTTTCTGTCCCTGGGACTGGTCAGCCTCGTGGAAAAGCTCTGGTGGGCTACCATTTGCCAAAAACAGAACTCCACTCCCCCATG

Gene : MC1R
Segment# : 5

Figure 27 (Cont)

165/216

Offset : 61
1st Codon : 1
V V A T I A K N R N L H S P M Y C F I C C L A L S D L L V S
GTGGTCGCCACAATCGCTAAGAATAGGAATCTGCATAGCCCTATGTATTGCTTTATCTGTTCCTCGCCCTCAGCGATCTGCTCGTGTC

Gene : MC1R
Segment# : 6
Offset : 76
1st Codon : 1
Y C F I C C L A L S D L L V S G T N V L E T A V I L L L E A
TACTGTTTCATTGTCTGTCTGGCTCTGTCCGACCTCCTGGTCAGCGGAACCAATGTGCTCGAGACAGCCGTCATCCTCCTGCTCGAGGCT

Gene : MC1R
Segment# : 7
Offset : 91
1st Codon : 1
G T N V L E T A V I L L L E A G A L V A R A A V L Q Q L D N
GGCACAAACGTCCTGGAAACCGCTGTGATTCTGCTCCTGGAAGCCGAGCCCTCGTGGCTAGGGCTGCCGTCCTGCAACAGCTCGACAAT

Gene : MC1R
Segment# : 8
Offset : 106
1st Codon : 1
G A L V A R A A V L Q Q L D N V I D V I T C S S M L S S L C
GGCGCTCTGGTCGCCAGAGCCGCTGTGCTCCAGCAACTGGATAACGTCATCGATGTGATTACCTGTAGCTCCATGCTCAGCTCCCTGTGT

Gene : MC1R
Segment# : 9
Offset : 121
1st Codon : 1
V I D V I T C S S M L S S L C F L G A I A V D R Y I S I F Y
GTGATTGACGTCATCACATGCTCCAGCATGCTGTCCAGCCTCTGCTTTCTGGGAGCCATTGCCGTCGACAGATACATTAGCATTTTCTAT

Gene : MC1R
Segment# : 10
Offset : 136
1st Codon : 1
F L G A I A V D R Y I S I F Y A L R Y H S I V T L P R A P R
TTCTCGCGCTATCGCTGTGGATAGGTATATCTCCATCTTTTACGCTCTGAGATACCATAGCATGTGACACTGCCCTAGGGCTCCCGA

Gene : MC1R
Segment# : 11
Offset : 151
1st Codon : 1
A L R Y H S I V T L P R A P R A V A A I W V A S V V F S T L
GCCCTCAGGTATCACTCCATGCTCACCCTCCCGAGAGCCCTAGGGCTGTGGCTGCCATTGGGTGCGCTCCGTGGTCTTCTCCACCCCT

Gene : MC1R
Segment# : 12
Offset : 166
1st Codon : 1
A V A A I W V A S V V F S T L F I A Y Y D H V A V L L C L V
GCCGTCGCCGCTATCTGGGTGGCTAGCGTCGTGTTAGCACACTGTTTATCGCTTACTATGACCATGTGGCTGTGCTCCTGTGTCTGGTC

Gene : MC1R
Segment# : 13
Offset : 181
1st Codon : 1
F I A Y Y D H V A V L L C L V V F F L A M L V L M A V L Y V
TTCATGCTATTACGATCAGTCGCCGCTCCTGCTCTGCCTCGTGGTCTTCTTCTGGCTATGCTGCTGCTCATGGCTGTGCTCTACGTC

Gene : MC1R
Segment# : 14
Offset : 196
1st Codon : 1
V F F L A M L V L M A V L Y V H M L A R A C Q H A Q G I A R
GTGTTTTCTCTGCCATGCTGGTCCTGATGGCCGTCCTGTATGTGCATATGCTCGCCAGAGCCTGTCAGCATGCCAAGGCATTGCCAGA

Gene : MC1R
Segment# : 15
Offset : 211
1st Codon : 1

Figure 27 (Cont)

166/216

H M L A R A C Q H A Q G I A R L H K R Q R P V H Q G F G L K
C A C A T G C T G G C T A G G G C T T G C C A A C A C G C T C A G G G A A T C G C T A G G C T C C A C A A A G G C A A G G C C T G T G C A T C A G G A T T C G G A C T G A A A

Gene : MC1R
Segment# : 16
Offset : 226
1st Codon : 1

L H K R Q R P V H Q G F G L K G A V T L T I L L G I F F L C
C T G C A T A A G A G A C A G A G A C C C G T C C A C C A A G G C T T T G G C C T C A A G G G A G C C G T C A C C C T C A C C A T T C T G C T C G G C A T T T T C T T T C T G T G T

Gene : MC1R
Segment# : 17
Offset : 241
1st Codon : 1

G A V T L T I L L G I F F L C W G P F F L H L T L I V L C P
G G C G C T G T G A C A C T G A C A A T C C T C T G G G A A T C T T T T C C T C T G C T G G G G C C C T T T C T T T C T G C A T C T G A C A C T G A T T G T G C T C T G C C C T

Gene : MC1R
Segment# : 18
Offset : 256
1st Codon : 1

W G P F F L H L T L I V L C P E H P T C G C I F K N F N L F
T G G G A C C C T T T T T C C T C C A C C T C A C C C T C A T C G T C C T G T G T C C G A A C A C C C T A C C T G T G G C T G T A T C T T T A G A A T T T C A A T C T G T T

Gene : MC1R
Segment# : 19
Offset : 271
1st Codon : 1

E H P T C G C I F K N F N L F L A L I I C N A I I D P L I Y
G A C A T C C C A C A T G C G G A T G C A T T T T C A A A A C T T T A A C C T C T T C C T C G C C C T C A T C A T T T G C A A T G C C A T T A T G A T C C C C T C A T C T A T

Gene : MC1R
Segment# : 20
Offset : 286
1st Codon : 1

L A L I I C N A I I D P L I Y A F H S Q E L R R T L K E V L
C T G G C T C T G A T T A T C T G T A A C G C T A C A T T G A C C C T C T G A T T T A C G C T T T C C A T A G C C A A G A G C T C A G G A G A A C C C T C A A G G A A G T G C T C

Gene : MC1R
Segment# : 21
Offset : 301
1st Codon : 1

A F H S Q E L R R T L K E V L T C S W A A
G C C T T T C A C T C C C A G A A C T G A G A A G G A C A C T G A A A G A G T C C T G A C A T G C T C C T G G G C T G C C

Gene : MUC1F
Segment# : 1
Offset : 1
1st Codon : 1

A A M T P G T Q S P F F L L L L L T V L T V V T G S G H A S
G C C G C T A T G A C A C C C G G A A C C C A A G C C C T T C T T T C T G C T C C T G C T C C T G A C A G T G C T C A C C G T C G T G A C A G G C T C C G G C C A T G C C T C C

Gene : MUC1F
Segment# : 2
Offset : 16
1st Codon : 1

L L T V L T V V T G S G H A S S T P G G E K E T S A T Q R S
C T G C T A C C G T C C T G A C A G T G G T C A C C G A A G C G G A C A C G C T A G C T C C A C C C C T G G C G G A G A G A A A G A C A A G C G C T A C C C A A A G G T C C

Gene : MUC1F
Segment# : 3
Offset : 31
1st Codon : 1

S T P G G E K E T S A T Q R S S V P S S T E K N A V S M T S
A G C A C C C G G A G G C G A A A A G G A A A C C T C C G C C A C A G A G A A G C T C C G T G C C T A G C T C C A C C G A A A A G A A T G C C G T C A G C A T G A C C T C C

Gene : MUC1F
Segment# : 4
Offset : 46
1st Codon : 1

S V P S S T E K N A V S M T S S V L S S H S P G S G S S T T
A C G T C C C C T C C A G C A C A G A G A A A A C G C T G T G C C A T G A C A A G C T C C G T G C T C C A C C T C C C C C G G A A G C G A A G C T C C A C C A C A

Figure 27 (Cont)

167/216

Gene : MUC1F
Segment# : 5
Offset : 61
1st Codon : 1
S V L S S H S P G S G S S T T Q G Q D V T L A P A T E P A S
AGCGTCCGTGTCAGCCATAGCCCTGGCTCCGGCTCCAGCACAAACCAAGGCCAAGACGTACCCCTCGCCCTGCCACAGAGCCTGCCTCC

Gene : MUC1F
Segment# : 6
Offset : 76
1st Codon : 1
Q G Q D V T L A P A T E P A S G S A A T W G Q D V T S V P V
CAGGGACAGGATGTGACACTGGCTCCCGCTACCGAAACCCGCTAGCGGAAGCGCTGCCACATGGGGACAGGATGTGACAAGCGTCCCGCTC

Gene : MUC1F
Segment# : 7
Offset : 91
1st Codon : 1
G S A A T W G Q D V T S V P V T R P A L G S T T P P A H D V
GGCTCCGCCGTACCTGGGGCCAAGACGTACCTCCGTGCTGTGACAAGCGCTGCCCTCGGCTCCACCACACCCCTGCCCATGACGCTC

Gene : MUC1F
Segment# : 8
Offset : 106
1st Codon : 1
T R P A L G S T T P P A H D V T S A P D N K A A
ACCAGACCCGCTCTGGGAAGCACAAACCCCTCCCGCTCAGATGTGACAAGCGCTCCCGATAACAAAGCCGCT

Gene : MUC1R
Segment# : 1
Offset : 1
1st Codon : 1
A A N R P A L G S T A P P V H N V T S A S G S A S G S A S T
GCCGCTAACAGACCCGCTCTGGGAAGCACAGCCCTCCCGTCCCAATGTGACAAGCGCTAGCGGAAGCGCTAGCGGAAGCGCTAGCACACA

Gene : MUC1R
Segment# : 2
Offset : 16
1st Codon : 1
N V T S A S G S A S G S A S T L V H N G T S A R A T T T P A
AACGTACCTCCGCTCCGCTCCGCTCCGCTCCGCTCCACCTCGTGCATAACGGAACCTCCGCCAGAGCCACAACCACACCCGCT

Gene : MUC1R
Segment# : 3
Offset : 31
1st Codon : 1
L V H N G T S A R A T T T P A S K S T P P S I P S H H S D T
CTGGTCCCAATGGCACAAGCGCTAGGGCTACCACAACCCCTGCCTCCAAGTCCACCCCTTCTCCATCCCTAGCCATCACTCCGACACA

Gene : MUC1R
Segment# : 4
Offset : 46
1st Codon : 1
S K S T P P S I P S H H S D T P T T L A S H S T K T D A S S
AGCAAAAGCACACCCCTTAGCATTCCTCCACCATAGCGATACCCCTACCACTGGCTAGCCATAGCACAAAGACAGACGCTAGCTCC

Gene : MUC1R
Segment# : 5
Offset : 61
1st Codon : 1
P T T L A S H S T K T D A S S T H H S S V P P L T S S N H S
CCCACAACCTCGCTCCCACTCCACCAAAACCGATGCCTCCAGCACACCATAGCTCCGTGCCTCCCTCACCTCCAGCAATCACTCC

Gene : MUC1R
Segment# : 6
Offset : 76
1st Codon : 1
T H S S V P P L T S S N H S T S P Q L S T G V S F F F L S
ACCCATCACTCCAGCGTCCCGCTCTGACAAGCTCCACCATAGCACAGCCCTCAGCTCAGCACAGGCGTCAGCTTTTCTTTCTGTCTC

Gene : MUC1R

Figure 27 (Cont)

168/216

Segment# : 7
Offset : 91
1st Codon : 1
T S P Q L S T G V S F F F L S P H I S N L Q P N S S L E D P
ACCTCCCCCAACTGTCCACCGGAGTGTCTCTTTTCTCTCAGCTTTCACATTAGCAATCTGCAATTCAATAGCTCCCTGGAAGACCT

Gene : MUC1R
Segment# : 8
Offset : 106
1st Codon : 1
F H I S N L Q P N S S L E D P S T D Y Y Q E L Q R D I S E M
TTCCATATCTCCAACCTCCAGTTTAACTCCAGCCTCGAGGATCCCTCCACGATTACTATCAGGAACCTGCAAAGGGATATCTCCGAGATG

Gene : MUC1R
Segment# : 9
Offset : 121
1st Codon : 1
S T D Y Y Q E L Q R D I S E M F L Q I Y K Q G G F L G L S N
AGCACAGACTATTACCAAGAGCTCCAGAGAGACATTAGCGAAATGTTTCTGCAATCTATAAGCAAGGCGGATTCTCGGCCTCAGCAAT

Gene : MUC1R
Segment# : 10
Offset : 136
1st Codon : 1
F L Q I Y K Q G G F L G L S N I K F R P G S V V V Q L T L A
TTCTCCAGATTACAAACAGGGAGGCTTCTGGGACTGTCCAACATTAAGTTTAGGCCTGGCTCCGTGGTCTGTGCAACTGACACTGGCT

Gene : MUC1R
Segment# : 11
Offset : 151
1st Codon : 1
I K F R P G S V V V Q L T L A F R E G T I N V H D V E T Q F
ATCAAATTACAGCCCGGAAGCGTCTGTGGTCCAGCTCACCTCGCCTTTAGGGAAGGCACAATCAATGTGCTGACGCTCGAGACACAGTTT

Gene : MUC1R
Segment# : 12
Offset : 166
1st Codon : 1
F R E G T I N V H D V E T Q F N Q Y K T E A A S R Y N L T I
TTCAGAGAGGAACCATTAACGTCCAGATGTGGAAACCCATTCAATCAGTATAAGACAGAGGCTGCCTCCAGGTATAACCTCACCAIT

Gene : MUC1R
Segment# : 13
Offset : 181
1st Codon : 1
N Q Y K T E A A S R Y N L T I S D V S V S D V P F P F S A Q
AACCAATACAAACCGAAGCCGTAGCAGATACAATCTGACAATCTCCGACGTCAGCGTCAGCGATGTGCCTTTCCCTTTCTCCGCCCAA

Gene : MUC1R
Segment# : 14
Offset : 196
1st Codon : 1
S D V S V S D V P F P F S A Q S G A G V P G W G I A L L V L
AGCGATGTGTCCGTGTCGACGTCCCTTTCCCTTTAGCGCTCAGTCCGGCGCTGGCGTCCCGGATGGGAATCGCTCTGCTCGTGCTC

Gene : MUC1R
Segment# : 15
Offset : 211
1st Codon : 1
S G A G V P G W G I A L L V L V C V L V A L A I V Y L I A L
AGCGGAGCCGAGTGCCCTGGCTGGGGCATGCCCCTCCTGGTCTGGTCTGGTCCCTCGCCATTGTGTATCTGATTGCCCTC

Gene : MUC1R
Segment# : 16
Offset : 226
1st Codon : 1
V C V L V A L A I V Y L I A L A V C Q C R R K N Y G Q L D I
GTGTGTGTGCTCGTGGCTCTGGCTATCGTCTACCTCATCGCTCTGGCTGTGTGTGTCAGTGTAGGAGAAAGAATTACGGACAGCTCGACATT

Gene : MUC1R
Segment# : 17
Offset : 241

Figure 27 (Cont)

169/216

1st Codon : 1
 A V C Q C R R K N Y G Q L D I F P A R D T Y H P M S E Y P T
 GCCGCTGCTCCAATGCAGAAGGAAAACTATGGCCAACCTGGATATCTTTCCCGCTAGGGATACCTATCACCTATGTCCGAGTATCCACACA

Gene : MUC1R

Segment# : 18

Offset : 256

1st Codon : 1

F P A R D T Y H P M S E Y P T Y H T H G R Y V P P S S T D R
 TTCCTGCGAGAGACATACCATCCCATGAGCGAATACCTACCTATCACACACCGGAAGGTATGTGCTCCCTCCAGCACAGACAGA

Gene : MUC1R

Segment# : 19

Offset : 271

1st Codon : 1

Y H T H G R Y V P P S S T D R S P Y E K V S A G N G G S S L
 TACCATACCCATGGCAGATACGTCCCCCTAGCTCCACCGATAGGTCCCCCTATGAGAAAGTGTCCGCCGGAACGGAGGCTCCAGCCTC

Gene : MUC1R

Segment# : 20

Offset : 286

1st Codon : 1

S P Y E K V S A G N G G S S L S Y T N P A V A A A S A N L A
 AGCCCTTACGAAAAGGTGAGCGCTGGCAATGGCGGAAGCTCCCTGTCTACACAAACCTGCGCTGCGCGCTGCTCCGCCAATCTGGCT

Gene : MUC1R

Segment# : 21

Offset : 301

1st Codon : 1

S Y T N P A V A A A S A N L A A
 AGCTATACCAATCCCGCTGTGGCTGCCGCTAGCGCTAACCTGCGCGCT

Segments in scrambled order:

gp100 #4

W N R Q L Y P E W T E A Q R L D C W R G G Q V S L K V S N D
 TGGAATAGGCAACTGTATCCGAATGGACAGAGGCTCAGAGACTGGATTGCTGGAGGGGAGGCCAAGTGTCCCTGAAAGTGTCCAACGAT

TRP2 #6

P Y I L R N Q D D R E L W P R K F F H R T C K C T G N F A G
 CCTATATCTCTCAGGAATCAGGATGACAGAGAGCTCTGGCCTAGGAAATCTTTACAGAACCTGTAAGTGTACCGGAACTTTGCCGGA

Tyros #30

R N G D F F I S S K D L G Y D Y S Y L Q D S D P D S F Q D Y
 AGGAATGGCGATTCTTTATCTCCAGCAAAGACCTCGGCTATGACTATAGCTATCTGCAAGACTCCGACCCTGACTCCTTCCAAGACTAT

TRP-1 #1

A A P A F L T W H R Y H L L R L E K D M Q E M L Q E P S F S
 GCCGCTCCCGCTTTCTCTACCTGGCAGACATACCATCTGCTCAGGCTCGAGAAAGACATGCAGGAAATGCTCCAGGAACCTCCTTCTCTC

Tyros #29

G H N R E S Y M V P F I P L Y R N G D F F I S S K D L G Y D
 GGCCATAACAGAGAGTCTTACATGGTGCCCTTTCAITCCCTCTACAGAAACGGAGACTTTTTTCATTAGCTCCAAGGATCTGGGATACGAT

TRP2 #16

L L C L E R D L Q R L I G N E S F A L P Y W N F A T G R N E
 CTGCTCTGCCTCGAGAGAGACCTCCAGAGACTGATTGGCAATGAGTCCTTCGCTCTGCCTTACTGGAACCTTGCCACAGGCAGAAACGAA

gp100 #23

T T E V V G T T P G Q A P T A E P S G T T S V Q V P T T E V
 ACCACAGAGGTCGTGGGAACACACCCGGACAGGCTCCACAGCCGAACCTCCGGCACAACTCCGTGCAAGTGCTACCCACAGAGGTC

MUC1R #9

S T D Y Y Q E L Q R D I S E M F L Q I Y K Q G G F L G L S N
 AGCAGAGTATTACCAAGAGCTCCAGAGAGACATTAGCGAAATGTTCTGCAAACTATAAGCAAGGCGGATTCTCGGCCCTCAGCAAT

gp100 #36

A C M E I S S P G C Q P P A Q R L C Q P V L P S P A C Q L V
 GCCTGTATGGAAATCTCCAGCCCTGGCTGTGAGCTCCCGCTCAGAGACTGTGTGAGCTGTGCTCCCTCCCCCGCTTGCCAACTGGTC

TRP2 #31

D Q L G Y S Y A I D L P V S V E E T P G W P T T L L V V M G

Figure 27 (Cont)

170/216

GACCAACTGGGATACTCCTACGCTATCGATCTGCCCTGTGTCCGTGGAAGAGACACCGGATGGCCTACCACACTGCTCGTGGTCATGGGA

TRP-1 #7
T E D G P I R R N P A G N V A R P M V Q R L P E P Q D V A Q
ACCGAAGACGGACCCATTAGGAGAAACCCTGCCGGAACGTCGCCAGACCCATGGTGCAAAGGCTCCCCGAACCCCAAGACGTCGCCCAA

TRP2 #3
C M T V D S L V N K E C C P R L G A E S A N V C G S Q Q G R
TGCAATGACGTCGACTCCCTGGTCAACAAAGAGTGTGGCCCTAGGCTCGGCGCTGAGTCCGCCAATGTGTGTGGCTCCAGCAAGGCAGA

MUC1R #13
N Q Y K T E A A S R Y N L T I S D V S V S D V P F P F S A Q
AACCAATACAAAACGAAGCCGCTAGCAGATACAATCTGACAATCTCCGACGTCAGCGTCAGCGATGTGCCCTTCCCTTTCTCCGCCAA

TRP2 #1
A A M S P L W W G F L L S C L G C K I L P G A Q G Q F P R V
GCCGCTATGTCCCCCTCTGGTGGGCTTTCTGCTCAGCTGTCTGGGATGCAAAATCCTCCCGGAGCCCAAGGCCAATTCCTAGGGTC

gp100 #18
A D L S Y T W D F G D S S G T L I S R A L V V T H T Y L E P
GCCGATCTGTCTACACATGGGATTTCGGAGACTCCAGCGGAACCTCATCTCCAGGGCTCTGGTCTGTGACACACATACCTCGAGCCT

gp100 #27
L A E M S T P E A T G M T P A E V S I V V L S G T T A A Q V
CTGGCTGAGATGAGACACCCGAAGCCACAGGCATGACCCCTGCCGAAGTGTCCATCGTGTCTCAGCGGAACACAGCCGCTCAGGTC

MUC1R #11
I K F R P G S V V V Q L T L A F R E G T I N V H D V E T Q P
ATCAAATTCAGACCCGGAAGCGTCTGGTCCAGCTCACCCTCGCCTTTAGGGAAGGCACAATCAATGTGATGACGTCGAGACACAGTTT

MUC1F #7
G S A A T W G Q D V T S V P V T R P A L G S T T P P A H D V
GGCTCCGCGCTACCTGGGGCCAAGACGTCACCTCCGTGCCCTGTGACAAGGCCCTCGCCTCGGCTCCACCACACCCCTGCCCATGACGTC

MC1R #16
L H K R Q R P V H Q G F G L K G A V T L T I L L G I F F L C
CTGCATAAGAGACAGAGACCCGTCACCAAGGCTTTGGCCCTCAAGGGAGCCGTCACCCCTCACCATTCTGTCTCGGCATTTCTTTCTGTGT

MC1R #20
L A L I I C N A I I D P L I Y A F H S Q E L R R T L K E V L
CTGGCTCTGATTATCTGTAACGCTATCATTGACCCCTCTGATTTACGCTTTTCCATAGCCAAGAGCTCAGGAGAACCCTCAAGGAAGTGCTC

TRP2 #7
K F P H R T C K C T G N F A G Y N C G D C K F G W T G P N C
AAGTTTTTCCATAGGACATGCAATGCACAGGCAATTTCCGTGGCTATACTGTGGCGATTGCAAATTCGGATGGACAGGCCCTAACTGT

TRP2 #23
L S L Q K F D N P P F F Q N S T F S P R N A L E G F D K A D
CTGTCCCTGCAAAGTTTGACAATCCCCCTTTCTTTGAGAATAGCACAATCTCTCTCAGAAAACGCTCTGGAAGGCTTTGACAAGCCGAT

MUC1R #4
S K S T P F S I P S H H S D T P T T L A S H S T K T D A S S
AGCAAAAGCACACCCCTTTAGCATTCCCTCCACCATAGCGATACCCCTACCACACTGGCTAGCCATAGCACAAAGACAGACGCTAGCTCC

MUC1R #1
A A N R P A L G S T A P P V H N V T S A S G S A S G S A S T
GCCGCTAACAGACCCGCTCTGGGAAGCACAGCCCTCCCGTCCACAATGTGACAAGCGCTAGCGGAAGCGCTAGCGGAAGCGCTAGCACA

TRP2 #21
C N G T Y E G L L R R N Q M G R N S M K L P T L K D I R D C
TGCAATGGCACATACGAAGCCCTCTGAGAAGGAATCAGATGGGCAGAACTCCATGAAACTGCCTACCCCTCAAGGATATCAGAGACTGT

MUC1R #6
T H H S S V P P L T S S N H S T S P Q L S T G V S F F F L S
ACCCATCACTCCAGCGTCCCCCTCTGACAAGCTCCAACCATAGCACAAAGCCCTCAGCTCAGCACAGGCGTCAGCTTTTCTTTCTGTCTC

MC1R #13
F I A Y Y D H V A V L L C L V V F F L A M L V L M A V L Y V
TTCATTGCCTATTACGATCAGTCGCGCTCTGTCTGCTCGTGGTCTTTCTTTCTGGCTATGCTCGTGCTCATGGCTGTGCTCTACGTC

Tyros #16
K L T G D E N F T I P Y W D N R D A E K C D I C T D E Y M G

Figure 27 (Cont)

171/216

AAGCTCACCGGAGACGAAAACCTTTACCATTCCCTATTGGGATTGGAGAGACGCTGAGAAATGCGATATCTGTACCGATGAGTATATGGGA

gp100 #32
L R L V K R Q V P L D C V L Y R Y G S F S V T L D I V Q G I
CTGAGACTGGTCAAGAGACAGGTCCCCCTCGACTGTGTGCTCTACAGATACGGAAGCTTTAGCGTCACCCCTCGACATTGTGCAAGGCATT

MUC1R #10
F L Q I Y K Q G G F L G L S N I K F R P G S V V V Q L T L A
TTCCTCCAGATTACAAACAGGGAGGCTTTCTGGGACTGTCCAACATTAAGTTTAGGCCTGGCTCCGTGGTGGTCAACTGACACTGGCT

MC1R #9
V I D V I T C S S M L S S L C F L G A I A V D R Y I S I F Y
GTGATTGACGTCATCATGTCTCCAGCATGCTGTCCAGCCTCTGCTTTCTGGGAGCCATTGCCGTGACAGATACATTAGCATTCTCTAT

Tyros #21
R N P G N H D K S R T P R L P S S A D V E F C L S L T Q Y E
AGGAATCCCGAAACCATGACAAAAGCAGAACCCCTAGGCTCCCTCCAGCGCTGACGTGAGTTTTCCTCAGCCTCACCCAATACGAA

TRP-1 #14
F D E W L R R Y N A D I S T F P L E N A P I G H N R Q Y N M
TTCGATGAGTGGCTGAGAAGGTATAACGCTGACATTAGCACATTCCCTCTGGAAAACGCTCCCATTTGGCCATAACAGACAGTATAACATG

gp100 #39
V S L A D T N S L A V V S T Q L I M P G Q E A G L G Q V P L
GTGTCCCTGGCTGACACAACTCCCTGGCTGTGGTCAGCACACAGCTCATCATGCCCGACAGGAAGCCGGAAGTGGGACAGGTCCCCCTC

gp100 #20
G P V T A Q V V L Q A A I P L T S C G S S P V P G T T D G H
GGCCCTGTGACAGCCCAAGTGGTCTGCAAGCCGCTATCCCTCTGACAAGCTGTGGCTCCAGCCCTGTGCTGGCAACCGATGGCCAT

Tyros #8
K F G F W G P N C T E R R L L V R R N I F D L S A P E K D K
AAGTTTGGCTTTTGGGGACCAATTGCACAGAGAGAAGGCTCCTGGTCAGGAGAAAATTTTCGATCTGTCCGCCCTGAGAAAGACAAA

gp100 #13
L G T H T M E V T V Y H R R G S R S Y V P L A H S S S A F T
CTGGGAACCCATACCATGGAGGTACCGTCTACCATAGGAGAGGCTCCAGGTCTACGTCCCCCTCGCCCATAGCTCCAGCGCTTTTACA

MC1R #12
A V A A I W V A S V V F S T L F I A Y Y D H V A V L L C L V
GCCGTGCGCTATCTGGGTGGCTAGCGTCTGTGTTAGCACACTGTTTATCGCTTACTATGACCATGTGGCTGTGCTCCTGTGTCTGGCT

TRP2 #25
G T L D S Q V M S L H N L V H S F L N G T N A L P H S A A N
GGCACACTGGATAGCCCAAGTGATGAGCCTCCCAATCTGGTCCACTCCTTCTCAACGGAAACCAATGCCCTCCCCCATAGCGCTGCCAAT

MART #4
G C W Y C R R R R N G Y R A L M D K S L H V G T Q C A L T R R
GGCTGTGGTATTGCAGAAGGAGAAACGGATACAGAGCCCTCATGGATAAGTCCCTGCAATGTGGGAACCAATGCGCTCTGACAAGGAGA

Tyros #15
P W H R L F L L R W E Q E I Q K L T G D E N F T I P Y N D W
CCCTGGCACAGACTGTTTCTGCTCAGGTGGGAGCAAGAGATTAGAAAAGTACAGGCGATGAGAATTTACAAATCCCTTACTGGGACTGG

MC1R #1
A A M A V Q G S Q R R L L G S L N S T P T A I P Q L G L A A
GCCGCTATGGCTGTGCAAGGCTCCAGAGAAGGCTCCTGGGAAGCCTCAACTCCACCCCTACCGCTATCCCTCAGCTCGGCTCGCCGCT

MC1R #5
V V A T I A K N R N L H S P M Y C F I C C L A L S D L L V S
GTGGTGGCCACAATCGCTAAGAATAGGAATCTGCATAGCCCTATGTATTGCTTTATCTGTTGCTCGCCCTCAGCGATCTGCTCGTGTCC

Tyros #25
Q S S M H N A L H I Y M N G T M S Q V Q G S A N D P I F L L
CAGTCCAGCATGCACAATGCCCTCCACATTTACATGAACGGAACCATGAGCAAGTGAAGGCTCCGCCAATGACCCCTATCTTTCTGTCT

Tyros #18
G Q H P T N P N L L S P A S F F S S W Q I V C S R L E E Y N
GGCCAAACCCCTACCAATCCCAATCTGCTCAGCCCTGCCTCTCTTTAGCTCTGGCAAATCGTCTGCTCCAGGCTCGAGGAATACAA

MC1R #6
Y C F I C C L A L S D L L V S G T N V L E T A V I L L L E A

Figure 27 (Cont)

172/216

TACTGTTTCATTGCTGCTGGCTCTGTCCGACCTCCTGGTCAGCGGAACCAATGTGCTCGAGACAGCCGTCACTCTCTGCTCGAGGCT

TRP2 #19
D P T L I S R N S R F S S W E T V C D S L D D Y N H L V T L
GACCTACCTCATCTCCAGGAATAGCAGATTCTCCAGCTGGGAGACAGTGTGTGACTCCCTGGATGACTATAACCATCTGGTCACCCCTC

MUC1F #8
T R P A L G S T T P P A H D V T S A P D N K A A
ACCAGACCCGCTCTGGGAAGCACAAACCCCTCCCGCTCAGATGTGACAGCGCTCCCGATAACAAAGCCGCT

Tyros #17
R D A E K C D I C T D E Y M G G Q H P T N P N L L S P A S F
AGGGATGCCGAAAAGTGTGACATTTGACACAGCAATACATGGGCGGACAGCATCCCAAAACCTAACCTCCTGTCCCCCGCTAGCTTT

gp100 #17
T F A L Q L H D P S G Y L A E A D L S Y T W D F G D S S G T
ACCTTTGCCCTCCAGCTCCAGATCCCTCCGGCTATCTGGCTGAGGCTGACCTCAGCTATACCTGGGACTTTGGCGATAGCTCCGGCACA

Tyros #22
S S A D V E F C L S L T Q Y E S G S M D K A A N F S F R N T
AGCTCCGCGGATGTGGAATTCTGTCTGTCCCTGACACAGTATGAGTCCGGCTCCATGGATAAGGCTGCCAATTCTCCTTCAGAAACACA

gp100 #6
G P T L I G A N A S F S I A L N F P G S Q K V L P D G Q V I
GGCCCTACCTCATCGGAGCCAATGCCCTCTTCCATCGCTCTGAATTTCCCTGGCTCCCAAGAGTGTCTCCCGATGGCCAAGTGATT

MC1R #18
W G P F F L H L T L I V L C P E H P T C G C I F K N F N L F
TGGGACCCCTTTTCTCCACCTCACCTCATCGTCTGTGTCCCGAACCCCTACCTGTGGCTGTATCTTTAAGAATTTCAATCTGTTT

Tyros #7
C Q C S G N F M G F N C G N C K F G F W G P N C T E R R L L
TGCCAATGCTCCGGCAATTTTCATGGGCTTTAACTGTGGCAATTGCAAAATTCGGATTCTGGGGCCCTAACTGTACCGAAAGGAGACTGCTC

TRP2 #34
Q Y R R L R K G Y T P L M E T H L S S K R Y T E E A A A
CAGTATAGGAGACTGAGAAAGGGATACACACCCCTCATGGAAACCCATCTGTCCAGCAAAAGGTATACCGAAGAGGCTGCGCT

TRP-1 #15
P L E N A P I G H N R Q Y N M V P F W P P V T N T E M F V T
CCCCTCGAGAATGCCCTATCGGACACAATAGGCAATACAATATGGTCCCTTTTGGCCTCCCGTCACCAATACCGAAATGTTTGTGACA

gp100 #7
N F P G S Q K V L P D G Q V I W V N N T I I N G S Q V W G G
AATTTCCCGGAAGCCAAAGGTCCTGCCTGACGGACAGGTATCTGGGTGAATAACACAATCATTAAACGGAAGCCAAGTGTGGGGCGGA

gp100 #22
R P T A E A P N T T A G Q V P T T E V V G T T P G Q A P T A
AGGCTACCGCTGAGGCTCCCAATACACAGCCGGACAGGTCCCCACAACCGAAGTGGTCGGCACAAACCCCTGGCCAAGCCCTACCGCT

MUC1F #3
S T P G G E K E T S A T Q R S S V P S S T E K N A V S M T S
AGCACCCCGGAGGCGAAAAGGAAACCTCCGCCACACAGAGAAGTCCGTGCCTAGCTCCACCGAAAAGAATGCCGTGAGCATGACCTCC

gp100 #42
L I Y R R R L M K Q D F S V P Q L P H S S S H W L R L P R I
CTGATTTACAGAAGGAGACTGATGAAGCAAGACTTTAGCGTCCCCCAACTGCCTCACTCCAGCTCCCACTGGCTGAGACTGCCTAGGATT

TRP2 #12
L G L L G P N G T Q P Q F A N C S V Y D F F V W L H Y Y S V
CTGGGACTGCTCGGCCCTAACGGAACCCCAACCCCAATTGCTAACTGTAGCGTCTACGATTTCTTTGTGTGGCTGCATTACTATAGCGT

TRP-1 #9
C L E V G L P D T P P F Y S N S T N S F R N T V E G Y S D P
TGCTCGAGGTGGGCTCTTCGATACCCCTCCCTTTTACTCCAACCTCACCAATAGCTTTAGGAATACCGTCGAGGGTACTCCGACCCCT

gp100 #1
A A M D L V L K R C L L H L A V I G A L L A V G A T K V P R
GCGCTATGATCTGGTCTGAAAAGGTGTCTGCTCCACCTCGCGTCATCGGAGCCCTCCTGGCTGTGGGAGCCACAAGGTCCCCAGA

MC1R #3
N Q T G A R C L E V S I S D G L F L S L G L V S L V E N A L

Figure 27 (Cont)

173/216

AACCAAAACCGAGCCAGATGCCTCGAGGTCAGCATTAGCGATGGCCTCTTCTCAGCCTCGGCCTCGTGTCCCTGGTCGAGAATGCCTC

Tyros #23

S G S M D K A A N F S F R N T L E G F A S P L T G I A D A S
AGCGGAAGCATGGACAAAGCCGCTAACTTTAGCTTTAGGAATACCTCGAGGGATTCGCTAGCCCTCTGACAGGCATTGCCGATGCCTCC

Tyros #4

S P C G Q L S G R G S C Q N I L L S N A P L G P Q F P F T G
AGCCCTTGCGGACAGCTCAGCGGAAGGGAAGCTGTGAGAATATCCTCCTGTCCAACGCTCCCTCGGCCCTCAGTTTCCCTTTACCGGA

Tyros #13

M H Y Y V S M D A L L G G S E I W R D I D F A H E A P A F L
ATGCATTACTATGTGTCCATGGATGCCCTCCTGGGAGGCTCCGAGATTGGAGAGACATTGACTTTGCCCATGAGGCTCCCGCTTTCCCTC

Tyros #35

E E K Q P L L M E K E D Y H S L Y Q S H L A A
GAGGAAAGCAACCCCTCCTGATGGAGAAGAGGATTACCATAGCCTCTACCAAAGCCATCTGGCTGCC

TRP2 #5

G Q C T E V R A D T R P W S G P Y I L R N Q D D R E L W P R
GGCCAATGCACAGAGGTCAGGGCTGACACAAGGCCTTGGTCCGGCCCTTACATTCTGAGAAACCAAGACGATAGGGAACTGTGGCCCGA

MUC1F #4

S V P S S T E K N A V S M T S S V L S S H S P G S G S S T T
AGCGTCCCCCTCCAGCACAGAGAAAAACGCTGTGTCCATGACAAGCTCCGTGCTCAGCTCCCACTCCCCCGGAAGCGGAAGCTCCACCACA

Tyros #12

T P M F N D I N I Y D L F V W M H Y Y V S M D A L L G G S E
ACCCCTATGTTTAAAGCATATCAATATCTATGACCTCTCGTCTGGATGCACTATTACGTGAGCATGGACGCTCTGCTCGGCGGAAGCGAA

gp100 #9

Q P V Y P Q E T D D A C I F P D G G P C P S G S W S Q K R S
CAGCCTGTGTATCCCCAAGAGACAGACAGATGCCTGTATCTTTCCCGATGGCGGACCCCTGTCCCTCGGCTCCTGGTCCCAGAAAAGGTCC

TRP-1 #6

D S L E D Y D T L G T L C N S T E D G P I R R N P A G N V A
GACTCCCTGGAAGACTATGACACACTGGGAACCCCTCTGCAATAGCACAGAGGATGGCCCTATCAGAAGGAATCCCGCTGGCAATGTGGCT

gp100 #8

W V N N T I I N G S Q V W G G Q P V Y P Q E T D D A C I F P
TGGGTCAACAATACCATTATCAATGGCTCCAGGTCTGGGGAGGCCAACCCGCTCTACCCCTCAGGAAACCGATGACGCTTGCAATTTCCCT

MART #7

Q E K N C E P V V P N A P P A Y E K L S A E Q S P P P Y S P
CAGGAAAAGAAATGCGAACCCTCGTGCCTAACGCTCCCCCTGCCTATGAGAACTGTCCGCCGAACAGTCCCCCTCCCTATAGCCCT

gp100 #14

S R S Y V P L A H S S S A F T I T D Q V P F S V S V S Q L R
AGCAGAAGCTATGTGCCTCTGGCTCACTCCAGCTCCGCTTTACCATTACCGATCAGGTCCCTTTAGCGTCAGCGTCAGCCAACCTGAGA

TRP-1 #2

L E K D M Q E M L Q E P S F S L P Y W N F A T G K N V C D I
CTGGAAAAGGATATGCAAGAGATGCTGCAAGAGCCTAGCTTTAGCCTCCCCCTATTGGAATTTGCTACCGGAAAGAAATGTGTGTGACATT

TRP-1 #16

V P F W P P V T N T E M F V T A P D N L G Y T Y E A A
GTGCTTTCTGGCCCCCTGTGACAAACACAGAGATGTTGTCACCGCTCCCGATAACCTCGGCTATACCTATGAGGCTGCC

TRP2 #13

C S V Y D F F V W L H Y Y S V R D T L L G P G R P Y R A I D
TGCTCCGTGTATGACTTTTTCTGTCTGGCTCCACTATTACTCCGTGAGAGACACTGTCTCGGCCCTGGCAGACCCTATAGGCTATCGAT

Tyros #9

V R R N I F D L S A P E K D K F F A Y L T L A K H T I S S D
GTGAGAAGGAATATCTTTGACCTCAGCGCTCCCGAAAAGGATAAGTTTTCTGCTTACCTCACCTCGCCAAACACACAATCTCCAGCGAT

MART #2

K K G H G H S Y T T A E E A A G I G I L T V I L G V L L L I
AAGAAAGGCCATGGCCATAGCTATACCACAGCCGAAGAGGCTGCCGAATCGGAATCCTCACCGTCATCCTCGCGCTCTGCTCCTGATT

gp100 #11

F V Y V W K T W G Q Y W Q V L G G P V S G L S I G T G R A M

Figure 27 (Cont)

174/216

TTCGTCTACGTCTGGAAAACTGGGGCCAATACTGGCAGTCTCTGGAGGCCCTGTGTCCGGCCTCAGCATTGGCACAGGCAGAGCCATG

gp100 #12

G G P V S G L S I G T G R A M L G T H T M E V T V Y H R R G
GGCGGACCCGTCAGCGACTGTCCATCGGAACCGGAAGGGCTATGCTCGGCACACACAATGGAAGTGACAGTGTATCACAGAAGGGGA

gp100 #25

I S T A P V Q M P T A E S T G M T P E K V P V S E V M G T T
ATCTCCACCGCTCCCGTCCAGATGCCACAGCCGAAAGCACAGGCATGACCCCTGAGAAAGTGCTGTGTCCGAGGTGATGGGAACCACA

Tyros #19

F S S W Q I V C S R L E E Y N S H Q S L C N G T P E G P L R
TTCTCCAGCTGGCAGATTGTGTGTAGCAGACTGGAAGAGTATAACTCCACCAAGCCTCTGCAATGGCACACCCGAAGGCCCTCTGAGA

TRP2 #27

D P I F V V L H S F T D A I F D E W M K R F N P P A D A W P
GACCTATCTTTGTGGTCTGCTAGCTTTACCGATGCCATTTTCGATGAGTGGATGAAAAGGTTTAACCCCTCCCGCTGACGCTTGGCCT

MC1R #15

H M L A R A C Q H A Q G I A R L H K R Q R P V H Q G F G L K
CACATGCTGGCTAGGGCTTGCCAAACGCTCAGGGAATCGTAGGCTCCACAAAAGGCAAGGCTGTGCATCAGGGATTGGGACTGAAA

MUC1F #2

L L T V L T V V T G S G H A S S T P G G E K E T S A T Q R S
CTGCTCACCGTCTGACAGTGGTCACCGAAGCGGACACGCTAGCTCCACCCCTGGCGGAGAGAAAGAGACAAGCGCTACCCAAAGGTCC

gp100 #44

F C S C P I G E N S P L L S G Q Q V A A
TTCTGTAGCTGTCCATTGGCGAAAACCTCCCCCTCTGTCCGGCCAACAGGTGCGCGCT

TRP2 #24

T F S F R N A L E G F D K A D G T L D S Q V M S L H N L V H
ACCTTTAGCTTTAGGAATGCCCTCGAGGGATTGATAAGGCTGACGGAACCCCTCGACTCCAGGTGATGTCCCTGCATAACCTCGTGAT

Tyros #20

S H Q S L C N G T P E G P L R R N P G N H D K S R T P R L P
AGCCATCAGTCCCTGTGTAAACGGAACCCCTGAGGGACCCCTCAGGAGAAACCTGGCAATCAGATAAGTCCAGGACACCCAGACTGCGCT

TRP2 #30

P F F P P V T N E E L F L T S D Q L G Y S Y A I D L P V S V
CCCTTTTCCCTCCCGTCACCAATGAGGAAGTGTCTGACAAGCGATCAGCTCGGCTATAGCTATGCCATTGACCTCCCGCTCAGCGTC

TRP2 #9

E R K K P P V I R Q N I H S L S P Q E R E Q F L G A L D L A
GAGAGAAAGAAACCCCTGTGATTAGGCAAAACATTCACTCCCTGTCCCCCAAGAGAGAGCAATTCTCGCGCTCTGGATCTGGCT

TRP2 #29

Q E L A P I G H N R M Y N M V P F P P V T N E E L F L T S
CAGGAAGTGGCTCCCATGCGCATACAGAAATGATAACATGGTGCTTTCTTTCCCCCTGTGACAAAAGAGAGCTCTTCCCTCACCTCC

gp100 #28

E V S I V V L S G T T A A Q V T T T E W V E T T A R E L P I
GAGGTGAGCATTGTGGTCTGTCCGGCACAACCGCTGCCCAAGTGACAACCACAGAGTGGGTGGAAACCAAGCCAGAGAGCTCCCCATT

MUC1R #7

T S P Q L S T G V S F F F L S F H I S N L Q F N S S L E D P
ACCTCCCCCAACTGTCCACCGAGTGTCTTCTTTTCTCAGCTTTCACATTAGCAATCTGCAATTCAATAGCTCCCTGGAAGACCTT

MUC1R #19

Y H T H G R Y V P P S S T D R S P Y E K V S A G N G G S S L
TACCATACCCATGGCAGATACGTCCCCCTAGCTCCACCGATAGGTCCCCCTATGAGAAAGTGTCGGCCGGAACGGAGGCTCCAGCCTC

MC1R #4

L F L S L G L V S L V E N A L V V A T I A K N R N L H S P M
CTGTTCTGTCCCTGGGACTGGTCAGCCTCGTGGAAAACGCTCTGGTGGTGTACCATTGCCAAAACAGAAACCTCCACTCCCCCATG

TRP2 #26

S F L N G T N A L P H S A A N D P I F V V L H S F T D A I F
AGCTTTCTGAATGGCACAACGCTCTGCCTCACTCCGCGGTAACGATCCCATTTTGTGTGTGTCCACTCCTTCACAGACGCTATCTTT

MUC1R #17

A V C Q C R R K N Y G Q L D I P P A R D T Y H P M S E Y P T

Figure 27 (Cont)

175/216

GCCGCTGCGCAATGCAGAAGGAAAACTATGGCCAACCTGGATATCTTTCCGCTAGGGATACCTATCACCCCTATGTCGAGTATCCACACA

MC1R #14

V P F L A M L V L M A V L Y V H M L A R A C Q H A Q G I A R
GTGTTTTCTCGCCATGCTGGTCCTGATGGCCGCTCTGTATGTGCATATGCTCGCCAGAGCCTGTTCAGCATGCCCAAGGCATTGCCAGA

TRP-1 #10

S T N S F R N T V E G Y S D P T G K Y D P A V R S L H N L A
AGCACAACTCCTTCAGAAACACAGTGAAGGCTATAGCGATCCCACAGGCAATACGATCCCGCTGTGAGAAGCCTCCACAATCTGGCT

TRP-1 #3

L P Y W N F A T G K N V C D I C T D D L M G S R S N F D S T
CTGCCTTACTGGAACCTTGGCCACAGGCAAAAACGCTCGCGATATCTGTACCGATGACCTCATGGGAAGCAGAAGCAATTCGATAGCACACA

gp100 #15

I T D Q V P F S V S V S Q L R A L D G G N K H F L R N Q P L
ATCACAGACCAAGTGCCCTTTCTCCGTGTCCGTGTCCAGCTCAGGGCTCTGGATGGCGGAAACAAACACTTTCTGAGAAACCAACCCCTC

MUC1R #8

F H I S N L Q F N S S L E D P S T D Y Y Q E L Q R D I S E M
TTCATATCTCCAACCTCCAGTTTAACTCCAGCCTCGAGGATCCCTCCACGATTACTATCAGGAACTGCAAAGGGATATCTCCGAGATG

MUC1R #20

S P Y E K V S A G N G G S S L S Y T N P A V A A A S A N L A
AGCCCTTACGAAAAGGTACGCGCTGGCAATGGCGGAAGCTCCCTGTCTACACAAACCTGCGGTGCGCGCTGCGCTCGCCAATCTGGCT

Tyros #11

Y V I P I G T Y G Q M K N G S T P M F N D I N I Y D L F V W
TAGCTCATCCCTATCGGAACCTATGGCCAAATGAAAAACGGAAGCACACCCATGTTCAATGACATTAACATTTACGATCTGTTTGTGTGG

gp100 #37

R L C Q P V L P S P A C Q L V L H Q I L K G G S G T Y C L N
AGGCTCTGCCAACCCTCTGCTAGCCCTGCTGTCTGCTGCTCCACCAATCCTCAAGGGAGGCTCCGGCACATACTGTCTGAAT

gp100 #33

R Y G S F S V T L D I V Q G I E S A E I L Q A V P S G E G D
AGGTATGGCTCCTTCTCCGTGACACTGGATATCGTCCAGGGAATCGAAAGCGCTGAGATTCTGCAAGCCGTCCCCTCCGGCGAAGGCGAT

Tyros #27

H H A F V D S I F E Q W L Q R H R P L Q E V Y P E A N A P I
CACCATGCCCTTTGTGGATAGCATTTTCGAACAGTGGCTGCAAAGGCATAGGCCTCTGCAAGAGGTCTACCTGAGGCTAACGCTCCCAT

TRP-1 #4

C T D D L M G S R S N F D S T L I S P N S V F S Q W R V V C
TGCACAGACGATCTGATGGCTCCAGGTCCAACTTTGACTCCACCCCTCATCTCCCCAATAGCGTCTTCTCCCAGTGGAGGGTCTGTGT

MUC1R #18

P P A R D T Y H P M S E Y P T Y H T H G R Y V P P S S T D R
TTCCCTGCCAGAGACACATACCATCCCATGAGCGAATACCCTACCTATCACACACGGAAGGTATGTGCCTCCCTCCAGCACAGACAGA

MUC1R #21

S Y T N P A V A A A S A N L A A
AGCTATACCAATCCCCTGTGGCTGCCGCTAGCGCTAACCTCGCCGCT

MC1R #19

E H P T C G C I F K N F N L F L A L I I C N A I I D P L I Y
GAGCATCCACATGCGGATGCATTTTCAAAAACCTTAACTCTTCTCGCCCTCATCATTTGCAATGCCATTATCGATCCCCTCATCTAT

Tyros #26

M S Q V Q G S A N D P I F L L H H A F V D S I F E Q W L Q R
ATGTCCCAGGTCCAGGGAAGCGCTAACGATCCCATTTTCTCTCTGCATCAGCTTTTCGTGCACTCCATCTTTGAGCAATGGCTCCAGAGA

TRP2 #22

R N S M K L P T L K D I R D C L S L Q K F D N P P F F Q N S
AGGAATAGCATGAAGCTCCCCACACTGAAAGACATTAGGGATTGCCTCAGCCTCCAGAAATTCGATAACCCCTCCCTTTTTCCAAAACCTCC

gp100 #19

L I S R A L V V T H T Y L E P G P V T A Q V V L Q A A I P L
CTGATTAGCAGAGCCCTCGTGGTCAACCATACCTATCTGGAACCCGGAACCGTCAACGCTCAGGTCTGTCTCCAGGCTGCCATTCCCTCT

TRP2 #17

S F A L P Y W N F A T G R N E C D V C T D Q L F G A A R P D

Figure 27 (Cont)

176/216

AGCTTTGCGCTCCCCTATTGGAATTTGCTACCGGAAGGAATGAGTGTGACGCTGCACAGACCAACTGTTTGGCGCTGCCAGACCCGAT

gp100 #2
V I G A L L A V G A T K V P R N Q D W L G V S R Q L R T K A
GTGATTGGCGCTCTGCTCGCGCTCGGCGCTACCAAAGTGCCCTAGGAATCAGGATTGGCTCGGCGTCAGCAGACAGCTCAGGACAAAGGCT

gp100 #16
A L D G G N K H F L R N Q P L T F A L Q L H D P S G Y L A E
GCGCTCGACGGAGGCAATAAGCATTTCCTCAGGAATCAGCCTCTGACATTGCTCTGCAACTGCATGACCCCTAGCGGATACCTCGCGGAA

TRP2 #18
C D V C T D Q L F G A A R P D D P T L I S R N S R F S S W E
TGGATGTGTGTACCGATCAGCTCTTCGGAGCCGCTAGGCGCTGACGATCCCACTGATTAGCAGAACTCCAGGTTTAGCTCTCGGGAA

MART #1
A A M P R E D A H F I Y G Y P K K G H G H S Y T T A E E A A
GCGCTATGCTTAGGGAAGACGCTCACTTTATCTATGGCTATCCCAAAAGGGACACGGACACTCCTACACAACCGCTGAGGAAGCCGCT

TRP-1 #11
T G K Y D P A V R S L H N L A H L F L N G T G G Q T H L S S
ACCGGAAAGTATGACCCCTGCGCTCAGGTCCTGCATAACCTCGCCCATCTGTTTCTGAATGGCACAGGCGGACAGACACCTCAGCTCC

MUC1R #14
S D V S V S D V P P P F S A Q S G A G V P G W G I A L L V L
AGCGATGTGTCCGTGTCCGACGTCCCTTTCCCTTTAGCGCTCAGTCCGGCGCTGGCGTCCCGGATGGGGAATCGCTCTGCTCGTGCTC

TRP2 #10
S P Q E R E Q F L G A L D L A K K R V H P D Y V I T T Q H W
AGCCCTCAGGAAAGGGAACAGTTTCTGGGAGCCCTCGACCTCGCCAAAAGAGAGTGCATCCCGATTAGCTCATCACAACCCACACTGG

Tyros #10
F F A Y L T L A K H T I S S D Y V I P I G T Y G Q M K N G S
TTCTTTGCTATCTGACACTGGCTAAGCATACCATTAGCTCCGACTATGTGATTCCCATTTGGCACATACGGACAGATGAAGATGGCTCC

MC1R #7
G T N V L E T A V I L L L E A G A L V A R A A V L Q Q L D N
GGCACAACGTCCTGGAAACCGCTGTGATTCTGCTCCTGGAAGCCGGAGCCCTCGTGGCTAGGGCTGCGCTCCTGCAACAGCTCGACAAAT

MUC1R #16
V C V L V A L A I V Y L I A L A V C Q C R R K N Y G Q L D I
GTGTGTGTGCTCGTGCTCTGGCTATCGTCTACCTCATCGCTCTGGCTGTGTGTCTAGTGTAGGAGAAAGAATTACGGACAGCTCGACATT

MART #6
C P Q E G F D H R D S K V S L Q E K N C E P V V P N A P P A
TGCCCTCAGGAAGGCTTTGACCATAGGGATAGCAAAAGTGTCCTGCAAGAGAAAACTGTGAGCCTGTGGTCCCCAATGCCCTCCCGCT

MUC1F #5
S V L S S H S P G S G S S T T Q G Q D V T L A P A T E P A S
AGCGTCTGTCCAGCCATAGCCCTGGCTCCGGCTCCAGCACAACCCAAGGCAAGACGTACCCCTCGCCCTGCCACAGAGCTGCCTCC

TRP2 #28
D E W M K R F N P P A D A N P Q E L A P I G H N R M Y N M V
GACGAATGGATGAAGAGATTCAATCCCCCTGCCGATGCTGGCCCCAAGAGCTCGCCCTATCGGACACAATAGGATGTACAATATGGTC

MC1R #21
A F H S Q E L R R T L K E V L T C S W A A
GCCTTTCACTCCAGGAACCTGAGAAGGACACTGAAAGAGGTCCTGACATGCTCTGGGCTGCC

TRP2 #15
F S H Q G P A F V T W H R Y H L L C L E R D L Q R L I G N E
TTCTCCCAAGGCGCTGCTTTGTGACATGGCATAGGTATCACCTCCTGTGTCTGGAAAGGGATCTGCAAAGGCTCATCGGAAACGAA

TRP-1 #8
R P M V Q R L P E P Q D V A Q C L E V G L F D T P P F Y S N
AGGCCTATGGTCCAGAGACTGCTGAGCCTCAGGATGTGGCTCAGTGTCTGGAAGTGGGACTGTTTGACACACCCCTTTCTATAGCAAT

TRP-1 #13
Q D P I F V L L H T F T D A V F D E W L R R Y N A D I S T F
CAGGATCCCATTTTGTCTCTGCTCCACACATTACAGACGCTGTGTTTACGAATGGCTCAGGAGATACAATGCCGATATCTCCACCTTT

TRP2 #4
L G A E S A N V C G S Q Q G R G Q C T E V R A D T R P W S G

Figure 27 (Cont)

CTGGGAGCCGAAAGCGCTAACGTCCTGCGGAAGCCAA CAGGGAAGGGGACAGTGTACCGAAGTGAGAGCCGATACCAGACCTGGAGCGGA

T V C D S L D D Y N H L V T L C N G T Y E G L L R R N Q M G

Figure 27 (Cont)

178/216

ACCGTCTGCGATAGCCTCGACGATTACAATCACCTCGTGACACTGTGTAACGGAACCTATGAGGGACTGCTCAGGAGAAACCAAATGGGA

Tyros #5

L L S N A P L G P Q F P P T G V D D R E S W P S V F Y N R T
CTGCTCAGCAATGCCCTCTGGGACCCCAATTCCCTTTACAGGCGTCGACGATAGGGAAGCTGGCCCTCCGTGTTTTACAATAGGACA

MART #8

Y E K L S A E Q S P P P Y S P A A
TACGAAAAGCTCAGCGCTGAGCAAAGCCCTCCCTTACTCCCCCGCTGCC

gp100 #41

I V G I L L V L M A V V L A S L I Y R R R L M K Q D F S V P
ATCGTCGGCATTCTGCTCGTGCTCATGGCTGTGGTCTGGCTAGCCTCATCTATAGGAGAAGGCTCATGAAACAGGATTTCTCCGTGCT

MART #3

G I G I L T V I L G V L L L I G C W Y C R R R N G Y R A L M
GGCATTGGCATTCTGACAGTGATTCTGGAGTGCTCCTGCTCATCGGATGCTGGTACTGTAGGAGAAGGAATGGCTATAGGGCTCTGATG

Tyros #31

Y S Y L Q D S D P D S F Q D Y I K S Y L E Q A S R I W S W L
TACTCCTACCTCCAGGATAGCGATCCCGATAGCTTTCAGGATTACATTAAGTCTTACCTCGAGCAAGCCCTCCAGGATTTGGTCTGGCTC

MUC1F #6

Q G Q D V T L A P A T E P A S G S A A T W G Q D V T S V P V
CAGGGACAGGATGTGACACTGGCTCCCGCTACCGAACCCTAGCGGAAGCGCTGCCACATGGGGACAGGATGTGACAAGCGTCCCGCTC

gp100 #21

T S C G S S P V P G T T D G H R P T A E A F N T T A G Q V P
ACCTCTCGGGAAGCTCCCGCTCCCGGAACCACAGACGGACACAGACCACAGCGAAGCCCTAACACAACCGCTGGCCAAGTGCT

MUC1R #3

L V H N G T S A R A T T T P A S K S T P F S I P S H H S D T
CTGGTCCACATGGCACAAGCGCTAGGGCTACCACAACCCTGCCTCCAAGTCCACCCCTTTCTCCATCCCTAGCCATCACTCCGACACA

TRP2 #32

E E T P G W P T T L L V V M G T L V A L V G L F V L L A P L
GAGGAAACCCTGGCTGGCCACAACCCTCCTGGTCTGATGGGCACACTGGTGCCTCTGTTGGACTGTTTGTGCTCCTGGCTTTCCTC

gp100 #29

T T T E N V E T T A R E L P I P E P E G P D A S S I M S T E
ACCACAACCGAATGGGTCGAGACAACCGCTAGGGAACTGCCTATCCCTGAGCTGAGGGACCCGATGCCTCCAGCATTATGTCCACCGAA

MUC1R #17

G A V T L T I L L G I P F L C W G P F F L H L T L I V L C P
GGCGCTGTGACACTGACAATCCTCCTGGGAATCTTTTCTCTGCTGGGGCCCTTTCTTCTGCTGACACTGATGTGCTCTGCCCT

Tyros #33

L G A A M V G A V L T A L L A G L V S L L C R H K R K Q L P
CTGGAGCCGCTATGGTCGGCGCTGTGCTCACCGCTCTGCTCGCCGACTGGTCAGCCTCCTGTGTAGGCATAAGAGAAGCAACTGCCT

MUC1R #8

G A L V A R A A V L Q Q L D N V I D V I T C S S M L S S L C
GGCGCTCTGGTCCGAGCCGCTGTGCTCCAGCAACTGGATAACGTCATCGATGTGATTACCTGTAGCTCCATGCTCAGCTCCCTGTGT

gp100 #26

M T P E K V P V S E V M G T T L A E M S T P E A T G M T P A
ATGACACCCGAAAGGTCCCGCTCAGCGAAGTGATGGGCACAACCTCGCCGAAATGTCCACCCCTGAGGCTACCGGAATGACACCCGCT

Tyros #2

Q T S A G H P P R A C V S S K N L M E K E C C P P W S G D R
CAGACAAGCGCTGGCCATTTCCCTAGGGCTTGCGTCAGTCCAAGAATCTGATGGAGAAAGAGTGTTGCCCTCCCTGGAGCGGAGACAGA

MUC1R #11

A L R Y H S I V T L P R A P R A V A A I W V A S V V F S T L
GCCCTCAGGTATCACTCCATCGTCACCTCCCGAGAGCCCTAGGGCTGTGGCTGCCATTTGGGTGCGCTCCGTGGTCTTCTCCACCCCTC

MUC1R #12

F R E G T I N V H D V E T Q F N Q Y K T E A A S R Y N L T I
FTCAGAGAGGGAACCATTAACGTCCACGATGTGGAAACCAATTCAATCAGTATAAGACAGAGGCTGCCTCCAGGTATAACCTCACCAT

Tyros #3

N L M E K E C C P P W S G D R S P C G Q L S G R G S C Q N I

Figure 27 (Cont)

AACCTCATGGAAGGAATGCTGTCCCCCTTGGTCCGGCGATAGGTCCCCCTGTGGCCAACTGTCCGGCAGAGGCTCCTGCCAAACATT

I K S Y L E Q A S R I W S W L L G A A M V G A V L T A L L A
ATCAAAGCTATCTGGAAACAGGCTAGCAGAATCTGGAGCTGGCTGCTCGGCGCTGCCATGGTGGGAGCCGCTCTGACAGGCCCTCTGGCT

P T T L A S H S T K T D A S S T H H S S V P P L T S S N H S
 CCCACAACCCCTCGCTCCCACTCCACCAAAACCGATGCTCCAGCACACACCATAGCTCGTGGCTCCCTCACCTCCAGCAATCACTCC

S G A G V P G W G I A L L V L V C V L V A L A I V Y L I A L
AGCGGAGCGGAGTGCCTGGCTGGGCGATTGCCCTCCTGGTCTGGTCTCGCTCTGGTGGCCCTCGCCATTGTGTATCTGATTGCCCTC

F L G A I A V D R Y I S I F Y A L R Y H S I V T L P R A P R
 TTCTCGGCGCTATCGCTGTGGATAGGTATATCTCCATCTTTACGCTCTGAGATACCATAGCATTGTGACACTGCCTAGGGCTCCGAGA

L I M P G Q E A G L G Q V P L I V G I L L V L M A V V L A S
CTGATTATGCCTGGCCAAGAGGCTGGCCCTGGCCAAGTGCCCTCTGATTGTGGGAATCCTCCTGGTCTCATGGCGCTCGTGCTCGCCCTCC

T L V A L V G L F V L L A F L Q Y R R L R K G Y T P L M E T
ACCCCTCGTGGCTCTGGTCGGCCTCTTCGTCCTGCTCGCCTTTCTGCAATACAGAAGGCTCAGGAAAGGCTATACCCCTCTGATGGAGACA

L I S P N S V F S Q W R V V C D S L E D Y D T L G T L C N S
CTGATTAGCCCTAACTCCGTGTTTAGCCAAATGGAGAGTGGTCTGCGATAGCCCTCGAGGATTACGATACCCCTGGGCACACTGTGTAACCTCC

LNSTPTAIPQLGLAANQTGARCLVSVISDGTCTGAATAGCACACCCACAGCCATTCCCCAACCTGGGACTGGCTGCCAATCAGACAGGGCGCTAGGTGTCTGGAAGTGTCCATCTCCGACGGA

H R P L Q E V Y P E A N A P I G H N R E S Y M V P F I P L Y
CACAGACCCCTCCAGGAAGTGTATCCCGAAGCCAATGCCCTATCGGACACAATAGGGAAAGCTATATGGTCCCTTTATCCCTCTGTAT

K P S G T T S V Q V P T T E V I S T A P . V Q M P T A E S T G
GAGCCTAGCGGAACCAAGCGTCCAGGTCCCCACAACCGAAGTGATTAGCACAGCCCCGTGTCAAATGCCTACCGCTGAGTCCACCGGA

K K R V H P D Y V I T T Q H W L G L L G P N G T Q P Q F A N
AAGAAAAGGGTCCACCTGACTATGTGATTACCAACAGCATTGGCTCGGCCCTCTGGGACCCAATGGCACAGCCTCAGTTTGCCAAT

L H Q I L K G G S G T Y C L N V S L A D T N S L A V V S T Q
TGCATCAGATTCTGAAGGCGGAAGCGGAACCTATTGCCTCAACGTCAGCCTCGCGGATACCAATAGCCTCGCGGTGCTGCCACCCAA

P E P E G P D A S S I M S T E S I T G S L G P L L D G T A T
 CCGGAACCCGAAGGCCCTGACGCTAGCTCCATCATGAGCACAGAGTCCATCACAGGCTCCCTGGGACCCCTCTGGATGGCCACAGCCACA

S I T G S L G P L L D G T A T L R L V K R Q V P L D C V L Y
AGCATTACGGGAAGCCTCGGCCCTCGCTCGACGGAACGCTACCCCTCAGGCTCGTGAAGAAGCAAGTGCCTCTGGATTGCGTCTGTAT

D C N R G G Q V S L K V S N D G P T L I G A N A S F S I A L
TACGTGTGGAGAGGGCGGACAGGTGAGCCTCAAGGTGAGCAATGACGGACCCACACTGATTGGCGCTAACGCTAGCTTTAGCATTGCCCTC

NRRLQYLEWTEAQRLLDCNRGGQVSLKVSNDPIYLIRNQDDRELMPRKFPHRTCKCTGNFAGRNGDFFISSKDLGYDYSYLQSDPDPSQDYAAPAFLTW
NRYHLLRLKEDKMQLBQPSFSGHNRESYVMVFTPLRYNRNGDFFISSKDLGYDLLCLLERLLQLIGNESFALPVALFATGRNETTEVGTTPCQAPTAEB
SYGTTSSVQVPTTEVSTDYQYBLQRDLISEMFLQYIKQGGFLGSLNACHETSSPCQPPAQRCLKPVLPSFPAQLVDQLGYSYAIDLPSVSEETPGWPT
LLVMVGTGQFPIRRNPAGNVAWRMPQRLPEPQDVAQCMTVDLSVNKECCPRLGAESANVCSSQGRNGQYKTEASRYNLLTSDVSVDVPPFPFPAQSA
ISEPLWGGFLLSCLGKLLPGAQGPFRVADLSYTNDFGDSSTGLISRALVYLITLYEFLAEMSTPEATGHTPAEVSIVVLGTTAAQVIFKRPQSGVV
ILTLAFREGTINVHDVETQFGSAATWGQDVTSVPVTRPALGSTTPPAHDVLHQRQRPVHGGFGLKGAVTTLTLILGIFFVLCTALICNAIDPLIYAFH
QELRLTLKEVLFKFFHRTCKCTGNFAGRNGCDKCPGFTGNCLSLQKPDNPFPQNSTFSFRNALGFKDASKSTPSPISHSIDSTPTTLASHSTKT
SSAANRAPALGSTAPPVHNVTASGASAGSNASTNGYEGLLRNMGGRNSNMKPLTKIDRCTHSSVPEPLTSSNHSSTPOLSTGVSFPFLFSFLIA

Figure 27 (Cont)

181/216

[illegible]

Figure 27 (Cont)

182/216

[illegible]

Figure 27 (Cont)

183/216

ATATGGTCCCCTTTATCCCTCTGTATGAGCCTAGCGGAACCACAAGCGTCCAGTCCCCACAACCGAAGTGATTAGCACAGCCCCCTGTGCAAATGCCT
ACCGCTGAGTCCACCGAAAGAAAAGGGTCCACCTGACTATGTGATTACACACAGCATGGCTCGGCCCTCCTGGGACCCCAATGGCACACAGCCTCA
GTTTGCCCAATCTGCATCAGATTCTGAAAGGCGGAAGCGGAACCTATTGCCTCAACGTGAGCCTCGCGGATACCAATAGCCTCGCCGTCTGTGCCACCC
AACCGAACC CGAAGGCCCTGACGCTAGCTCCATCATGAGCACAGAGTCCATCACAGGCTCCCTGGGACCCCTCCTGGATGGCACAGCCACAAGCATT
ACCGGAAGCCTCGGCCCTCTGCTCGACGGAACCGTACCCTCAGGCTCGTGAAAAGGCAAGTGCCTCTGGATTGCGTCTGTATGACTGTGGAGAGG
CGGACAGGTGAGCCTCAAGGTGAGCAATGACGGACCCACACTGATTGGCGCTAACGCTAGCTTTAGCATTGCCCTC

Melanoma cancer Specific Savine Scramble process

Scramble - Output File

Scramble version : 0.1 beta, 08/02/1999

Num. genes : 10

Num. segments : 121

Segment length : 30

Segment overlap : 15

Segments in original order:

Gene : BAGE

Segment# : 1

Offset : 1

1st Codon : 1

A A M A A R A V F L A L S A Q L L Q A R L M K E E S P V V S
GCCGCTATGGCTGCCAGAGCCGCTCTTCCTCGCCCTCAGCGCTCAGCTCTGCAAGCCAGACTGATGAAGGAAGAGTCCCCGTCGTGTCC

Gene : BAGE

Segment# : 2

Offset : 16

1st Codon : 1

L L Q A R L M K E E S P V V S W R L E P E D G T A L C F I F
CTGCTCCAGGCTAGGCTCATGAAGAGGAAAGCCCTGTGGTCAGCTGGAGGCTCGAGCCTGAGGATGGCACAGCCCTCTGCTTTATCTTT

Gene : BAGE

Segment# : 3

Offset : 31

1st Codon : 1

W R L E P E D G T A L C F I F A A
TGGAGACTGGAACCGAAGACGGAACCGCTCTGTGTTTCATTTTCGCTGCC

Gene : GAGE-1

Segment# : 1

Offset : 1

1st Codon : 1

A A M S W R G R S T Y R P R P R R Y V E P P E M I G P M R P
GCCGCTATGTCTGGAGAGGCAGAACACATACAGACCCAGACCCAGAGGTATGTGGAACCCCTGAGATGATCGGACCCATGAGGCCT

Gene : GAGE-1

Segment# : 2

Offset : 16

1st Codon : 1

R R Y V E P P E M I G P M R P E Q F S D E V E P A T P E E G
AGGAGATACGTGAGCCTCCCGAAATGATTGGCCCTATGAGACCCGAACAGTTAGCGATGAGGTGAGCCTGCCACACCCGAAGAGGGA

Gene : GAGE-1

Segment# : 3

Offset : 31

1st Codon : 1

E Q F S D E V E P A T P E E G E P A T Q R Q D P A A A Q E G
GAGCAATTCTCCGACGAAGTGGAACCCGCTACCCCTGAGGAAGGCGAACCCTGAGCTACCCAAAGGCAAGACCCCTGCCGCTGCCCAAGAGGGA

Gene : GAGE-1

Segment# : 4

Offset : 46

1st Codon : 1

E P A T Q R Q D P A A A Q E G E D E G A S A G Q G P K P E A
GAGCCTGCCACACAGAGACAGGATCCCGCTGCCGCTCAGGAAGGCGAAGACGAAGGCGCTAGCGCTGGCCAAAGGCCCTAAGCCTGAGGCT

Gene : GAGE-1

Segment# : 5

Offset : 61

1st Codon : 1

Figure 27 (Cont)

184/216

E D E G A S A G Q G P K P E A D S Q E Q G H P Q T G C E C E
GAGGATGAGGGAGCCTCCGCCGACAGGGACCCAAACCCGAAGCCGATAGCCAAGAGCAAGGCCATCCCCAAACCGGATGCGAATGCGAA

Gene : GAGE-1

Segment# : 6

Offset : 76

1st Codon : 1

D S Q E Q G H P Q T G C E C E D G P D G Q E M D P P N P E E
GACTCCAGGAACAGGGACACCTCAGACAGGCTGTGAGTGTGAGGATGGCCCTGACGGACAGGAAATGGATCCCCCTAACCCCTGAGGAA

Gene : GAGE-1

Segment# : 7

Offset : 91

1st Codon : 1

D G P D G Q E M D P P N P E E V K T P E E E M R S H Y V A Q
GACGGACCCGATGGCCAAGAGATGGACCTCCCAATCCCGAAGAGGTCAAGACACCCGAAGAGGAAATGAGAAGCCATTACGTGCGCCCAA

Gene : GAGE-1

Segment# : 8

Offset : 106

1st Codon : 1

V K T P E E E M R S H Y V A Q T G I L W L L M N N C F L N L
GTGAAAACCCCTGAGGAAGAGATGAGGTCCCACTATGTGGCTCAGACAGGCATTCTGTGGCTGCTCATGAATAACTGTTTCTCAACCTC

Gene : GAGE-1

Segment# : 9

Offset : 121

1st Codon : 1

T G I L W L L M N N C F L N L S P R K P A A
ACCGGAATCCTCGGCTCCTGATGAACAATTGCTTTCTGAATCTGTCCCCAGAAAGCCTGCCGCT

Gene : gp100In4

Segment# : 1

Offset : 1

1st Codon : 1

A A S W S Q K R S F V Y V W K T W G E G L P S Q P I I H T C
CCCCTAGCTGGAGCCAAAAGAGAAGCTTTGTGTATGTGTGGAAGACATGGGGAGAGGGACTGCCTAGCCAACCCATTATCCATACCTGT

Gene : gp100In4

Segment# : 2

Offset : 16

1st Codon : 1

T W G E G L P S Q P I I H T C V Y F F L P D H L S F G R P F
ACCTGGGGCGAAGGCCTCCCTCCAGCCTATCATTCACACATGCGTCTACTTTTTCTCCTCCCGATCACCTCAGCTTTGGCAGACCCCTT

Gene : gp100In4

Segment# : 3

Offset : 31

1st Codon : 1

V Y F F L P D H L S F G R P F H L N F C D F L A A
GTGTATTTCCTTCGCTGACCATCTGTCTCTCGGAAGGCCCTTCCATCTGAATTCTGTGACTTTCTGGCTGCC

Gene : MAGE-1

Segment# : 1

Offset : 1

1st Codon : 1

A A M S L E Q R S L H C K P E E A L E A Q Q E A L G L V C V
GCGCTATGTCCCTGGAACAGAGAAGCCTCCACTGTAGCCTGAGGAAGCCCTCGAGGCTCAGCAAGAGGCTCTGGGACTGGTCTGCGTC

Gene : MAGE-1

Segment# : 2

Offset : 16

1st Codon : 1

E A L E A Q Q E A L G L V C V Q A A T S S S S P L V L G T L
GAGGCTCTGGAAGCCCAACAGGAAGCCCTCGGCCTCGTGTGTGTGCAAGCCGCTACCTCCAGCTCCAGCCCTCTGGTCTCGGGAACCCCTC

Gene : MAGE-1

Segment# : 3

Offset : 31

1st Codon : 1

Q A A T S S S S P L V L G T L E E V P T A G S T D P P Q S P
CAGGCTGCCACAAGCTCCAGCTCCCCCTCGTGTCTGGCACACTGGAAGAGGTCCCCACAGCCGGAAGCACAGACCCTCCCCAAAGCCCTC

Figure 27 (Cont)

185/216

Gene : MAGE-1
Segment# : 4
Offset : 46
1st Codon : 1
E E V P T A G S T D P P Q S P Q G A S A F P T T I N F T R Q
GAGGAAGTGCTACCGCTGGCTCCACCGATCCCCCTCAGTCCCCCAAGGCGCTAGCGCTTCCCTACCAATCAATTTACAAGGCAA

Gene : MAGE-1
Segment# : 5
Offset : 61
1st Codon : 1
Q G A S A F P T T I N F T R Q R Q P S E G S S S R E E E G P
CAGGGAGCCTCGCCTTCCCAACCATTAACCTTTACAGACAGAGACAGCCTAGCGAAGGCTCCAGCTCCAGGGAAGAGGAAGGCCCT

Gene : MAGE-1
Segment# : 6
Offset : 76
1st Codon : 1
R Q P S E G S S S R E E E G P S T S C I L E S L F R A V I T
AGGCAACCCCTCGAGGGAAGCTCCAGCAGAGAGGAAGAGGGACCCCTCCACCTCCTGCATTCTGGAAGCCTCTTCAGAGCCGTCATCACA

Gene : MAGE-1
Segment# : 7
Offset : 91
1st Codon : 1
S T S C I L E S L F R A V I T K K V A D L V G F L L L K Y R
AGCACAAAGCTGTATCCTCGAGTCCCTGTTTAGGGCTGTGATTACCAAAAAGGTGCGCGATCTGGTCGGCTTTCTGCTCCTGAAATACAGA

Gene : MAGE-1
Segment# : 8
Offset : 106
1st Codon : 1
K K V A D L V G F L L L K Y R A R E P V T K A E M L E S V I
AAGAAAGTGCTGACCTCGTGGGATTCTCTGCTCAAGTATAGGGCTAGGGAACCCGTACCAAGCGAAATGCTCGAGTCCGTGATT

Gene : MAGE-1
Segment# : 9
Offset : 121
1st Codon : 1
A R E P V T K A E M L E S V I K N Y K H C F P E I F G K A S
GCCAGAGAGCTGTGACAAAGGCTGAGATGCTGGAAGCGTCATCAAAAATATAAGCATTGCTTCCCGAAATCTTTGGCAAAGCCCTC

Gene : MAGE-1
Segment# : 10
Offset : 136
1st Codon : 1
K N Y K H C F P E I F G K A S E S L Q L V F G I D V K E A D
AAGAATTACAAACATGTTTCCCTGAGATTTTCGGAAGGCTAGCGAAGCCCTCCAGCTCGTGTGTCATTGACGTCAAGGAAGCCGAT

Gene : MAGE-1
Segment# : 11
Offset : 151
1st Codon : 1
E S L Q L V F G I D V K E A D P T G H S Y V L V T C L G L S
GAGTCCTGCAACTGGTCTTCGGAATCGATGTGAAAGAGGCTGACCCCTACGGACACTCCTACGTCTGGTCACCTGTCTGGGACTGTCC

Gene : MAGE-1
Segment# : 12
Offset : 166
1st Codon : 1
P T G H S Y V L V T C L G L S Y D G L L G D N Q I M P K T G
CCCACAGGCCATAGCTATGTGCTCGTGACATGCCTCGGCCTCAGCTATGACGGACTGCTCGGCGATAACCAATCATGCCCAAACCGGA

Gene : MAGE-1
Segment# : 13
Offset : 181
1st Codon : 1
Y D G L L G D N Q I M P K T G F L I I V L V M I A M E G G H
TACGATGGCCTCCTGGGAGACAATCAGATTATGCCTAAGACAGGCTTTCTGATTATCGTCTGGTCATGATTGCCATGGAGGGAGGCCAT

Gene : MAGE-1

Figure 27 (Cont)

186/216

Segment# : 14
Offset : 196
1st Codon : 1
F L I I V L V M I A M E G G H A P R E E I W E E L S V M E V
TTCCTCATCTGTGCTCGTGATGATCGCTATGGAAGGCGGACACGCTCCCGAAGAGGAAATCTGGGAGGAACTGTCCGTGATGGAGGTC

Gene : MAGE-1
Segment# : 15
Offset : 211
1st Codon : 1
A P E E E I W E E L S V M E V Y D G R E H S A Y G E P R K L
GCCCTGAGGAAGAGATTGGGAAGAGCTCAGCGTCATGGAAGTGTATGACGGAAGGGAACACTCCGCCTATGGCGAACCAGAAAGCTC

Gene : MAGE-1
Segment# : 16
Offset : 226
1st Codon : 1
Y D G R E H S A Y G E P R K L L T Q D L V Q E K Y L E Y R Q
TACGATGGCAGAGAGCATAGCGCTTACGGAGAGCCTAGGAACTGCTCACCCAGACCTCGTGCAAGAGAAATACCTCGAGTATAGGCAA

Gene : MAGE-1
Segment# : 17
Offset : 241
1st Codon : 1
L T Q D L V Q E K Y L E Y R Q V P D S D P A R Y E F L W G P
CTGACACAGGATCTGTGTCAGGAAAAGTATCTGGAATACAGACAGGTCCCGGATAGCGATCCCGCTAGGTATGAGTTTCTGTGGGGCCCT

Gene : MAGE-1
Segment# : 18
Offset : 256
1st Codon : 1
V P D S D P A R Y E F L W G P R A L A E T S Y V K V L E Y V
GTGCCTGACTCCGACCCTGCCAGATACGAATTCCTCTGGGGACCCAGAGCCCTCGCCGAAACCTCTACGTCAAGGTCTTGAATACGTC

Gene : MAGE-1
Segment# : 19
Offset : 271
1st Codon : 1
R A L A E T S Y V K V L E Y V I K V S A R V R F F P P S L R
AGGCTCTGGCTGAGACAGCTATGTGAAAGTGCTCGAGTATGTGATTAAAGTCAGCGCTAGGGTCAGGTTTTCTTTCCCTCCCTGAGA

Gene : MAGE-1
Segment# : 20
Offset : 286
1st Codon : 1
I K V S A R V R F F P P S L R E A A L R E E E E G V A A
ATCAAAGTGTCCGCAGAGTGAGATTCTTTTCCCTAGCCTCAGGGAAGCCGCTCTGAGAGAGGAAGAGGAAGCGCTCGCCGCT

Gene : MAGE-3
Segment# : 1
Offset : 1
1st Codon : 1
A A M P L E Q R S Q H C K P E E G L E A R G E A L G L V G A
GCCGCTATGCCTCTGGAACAGAGAAGCCAACTGTAGCCTGAGGAAGGCTCGAGGCTAGGGGAGAGGCTCTGGGACTGGTCGGCGCT

Gene : MAGE-3
Segment# : 2
Offset : 16
1st Codon : 1
E G L E A R G E A L G L V G A Q A P A T E E Q E A A S S S S
GAGGGACTGGAAGCCAGAGGCGAAGCCCTCGGCCTCGTGGGAGCCCAAGCCCTGCCACAGAGGAACAGGAAGCCGCTAGCTCCAGCTCC

Gene : MAGE-3
Segment# : 3
Offset : 31
1st Codon : 1
Q A P A T E E Q E A A S S S S S T L V E V T L G E V P A A E S
CAGGCTCCCGCTACCGAAGAGCAAGAGGCTGCCTCCAGCTCCAGCACACTGGTCGAGGTCAACCTCGGGGAAGTGCTCGCGCTGAGTCC

Gene : MAGE-3
Segment# : 4
Offset : 46

Figure 27 (Cont)

187/216

1st Codon : 1
T L V E V T L G E V P A A E S P D P P Q S P Q G A S S L P T
ACCCTCGTGAAGTGACACTGGGAGAGGTCCCGCTGCCGAAAGCCCTGACCCTCCCCAAAGCCCTCAGGGAGCCTCCAGCCTCCCCACA

Gene : MAGE-3
Segment# : 5
Offset : 61
1st Codon : 1
P D P P Q S P Q G A S S L P T T M N Y P L W S Q S Y E D S S
CCCGATCCCCCTCAGTCCCCCAAGGCGTAGCTCCCTGCCTACCACAATGAATTACCTCTGTGGAGCCAAAGCTATGAGGATAGCTCC

Gene : MAGE-3
Segment# : 6
Offset : 76
1st Codon : 1
T M N Y P L W S Q S Y E D S S N Q E E E G P S T F P D L E S
ACCATGAATATCCCCCTCTGGTCCAGTCTCTACGAAGACTCCAGCAATCAGGAAGAGGAAGGCCCTAGCACATTCCCTGACCTCGAGTCC

Gene : MAGE-3
Segment# : 7
Offset : 91
1st Codon : 1
N Q E E E G P S T F P D L E S E F Q A A L S R K V A E L V H
AACCAGAGGAAGAGGGACCTCCACCTTTCCCGATCTGGAAGCGAATTCAGCCGCTCTGTCCAGGAAAGTGCTGAGCTCGTGCAT

Gene : MAGE-3
Segment# : 8
Offset : 106
1st Codon : 1
E F Q A A L S R K V A E L V H F L L L K Y R A R E P V T K A
GAGTTTCAGGCTGCCCTCAGCAGAAAGTCCCGAAGTGGTCCACTTTCTGCTCCTGAAATACAGAGCCAGAGAGCCTGTGACAAAGGCT

Gene : MAGE-3
Segment# : 9
Offset : 121
1st Codon : 1
F L L L K Y R A R E P V T K A E M L G S V V G N W Q Y F F P
TTCTCCTGCTCAAGTATAGGGCTAGGGAACCCGTCACCAAAGCCGAAATGCTCGGCTCCGTGGTCCGCAATTGGCAATACTTTTCCCT

Gene : MAGE-3
Segment# : 10
Offset : 136
1st Codon : 1
E M L G S V V G N W Q Y F F P V I F S K A S S S L Q L V F G
GAGATGCTGGGAAGCGTCTGGGAAACTGGCAGTATTCTTTCCCGTCATCTTTAGCAAAGCCTCCAGCTCCCTGCAACTGGTCTTCGGA

Gene : MAGE-3
Segment# : 11
Offset : 151
1st Codon : 1
V I F S K A S S S L Q L V F G I E L M E V D P I G H L Y I F
GTGATTTTCTCAAGGCTAGCTCCAGCCTCCAGCTCGTGTCTGGCATTGAGCTCATGGAAGTGGATCCCATGGCCATCTGTATATCTTT

Gene : MAGE-3
Segment# : 12
Offset : 166
1st Codon : 1
I E L M E V D P I G H L Y I F A T C L G L S Y D G L L G D N
ATCGAACTGATGGAGGTGACCCCTATCGGACACCTCTACATTTTCGCTACCTGTCTGGGACTGTCTACGATGGCCTCCTGGGAGACAAAT

Gene : MAGE-3
Segment# : 13
Offset : 181
1st Codon : 1
A T C L G L S Y D G L L G D N Q I M P K A G L L I I V L A I
GCCACATGCCCTCGGCCTCAGCTATGACGGACTGCTCGGCGATAACCAAATCATGCCAAAGCCGGACTGCTCATCATTTGTGCTCGCCATT

Gene : MAGE-3
Segment# : 14
Offset : 196
1st Codon : 1
Q I M P K A G L L I I V L A I I A R E G D C A P E E K I W E

Figure 27 (Cont)

188/216

CAGATTATGCCTAAGGCTGGCCTCCTGATTATCGTCTGGCTATCATTTGCCAGAGAGGGAGACTGTGCCCTGAGGAAAAGATTGGGAA

Gene : MAGE-3
Segment# : 15
Offset : 211
1st Codon : 1

I A R E G D C A P E E K I W E E L S V L E V F E G R E D S I
ATCGCTAGGGAAGGCGATTGCGCTCCCGAAGAGAAAATCTGGGAGGAACGTCCGTGCTCGAGGTCTTCCAAGGCAGAGAGGATAGCATT

Gene : MAGE-3
Segment# : 16
Offset : 226
1st Codon : 1

E L S V L E V F E G R E D S I L G D P K K L L T Q H F V Q E
GAGCTCAGCGTCTGGAAGTGTGAGGGAAGGGAAGACTCCATCTCGGCGATCCCAAAAAGCTCCTGACACAGCATTTCGTCCAGGAA

Gene : MAGE-3
Segment# : 17
Offset : 241
1st Codon : 1

L G D P K K L L T Q H F V Q E N Y L E Y R Q V P G S D P A C
CTGGGAGACCCTAAGAACTGTCTACCCAACACTTTGTGCAAGAGAATTACCTCGAGTATAGGCAAGTGCCTGGCTCCGACCCCTGCCTGT

Gene : MAGE-3
Segment# : 18
Offset : 256
1st Codon : 1

N Y L E Y R Q V P G S D P A C Y E F L W G P R A L V E T S Y
AACTATCTGGAATACAGACAGGTCCCGGAAGCGATCCCGCTTGCTATGAGTTTCTGTGGGGCCCTAGGGCTCTGGTCGAGACAAGCTAT

Gene : MAGE-3
Segment# : 19
Offset : 271
1st Codon : 1

Y E F L W G P R A L V E T S Y V K V L H H M V K I S G G P H
TACGAATTCCTCTGGGGACCCAGAGCCCTCGTGGAAACCTCTACGTCAAGGTCCTGCATCACATGGTGAAAATCTCCGGCGGACCCCTAT

Gene : MAGE-3
Segment# : 20
Offset : 286
1st Codon : 1

V K V L H H M V K I S G G P H I S Y P P L H E W V L R E G E
GTGAAATGTGCTCCACCATATGGTCAAGATTAGCGGAGGCCCTCACATTAGCTATCCCCCTCTGCATGAGTGGGTGCTCAGGGAAGGCGAA

Gene : MAGE-3
Segment# : 21
Offset : 301
1st Codon : 1

I S Y P P L H E W V L R E G E E A A
ATCTCCTACCTCCCTCCACGAATGGGTCTGAGAGAGGGAGAGGAAGCCGCT

Gene : PRAME
Segment# : 1
Offset : 1
1st Codon : 1

A A M E R R R L W G S I Q S R Y I S M S V W T S P R R L V R
GCCGCTATGGAAGGAGAAGGCTCTGGGAAGCATTGAGTCCAGGTATATCTCCATGTCGCTGTGGACCTCCCCAGAGGCTCGTGGAA

Gene : PRAME
Segment# : 2
Offset : 16
1st Codon : 1

Y I S M S V W T S P R R L V E L A G Q S L L K D E A L A I A
TACATTAGCATGAGCGTCTGGACAAGCCCTAGGAGACTGGTCGAGCTGCGCGGACAGTCCCTGCTCAAGGATGAGGCTCTGGCTATCGCT

Gene : PRAME
Segment# : 3
Offset : 31
1st Codon : 1

L A G Q S L L K D E A L A I A A L E L L P R E L F P P L F M
CTGGCTGGCCAAAGCCTCTGAAAGACGAAGCCCTCGCCATTGCCGCTCTGGAAGTCTCCCCAGAGAGCTCTTCCCTCCCTCTTCATG

Figure 27 (Cont)

189/216

Gene : PRAME
Segment# : 4
Offset : 46
1st Codon : 1
A L E L L P R E L F P P L F M A A F D G R H S Q T L K A M V
GCCCTCGAGCTCCTGCCTAGGGAACGTGTTCCCTCTGTTATGGCTGCCTTTGACGGAAGGCATAGCCAAACCTCAAGGCTATGGTC

Gene : PRAME
Segment# : 5
Offset : 61
1st Codon : 1
A A F D G R H S Q T L K A M V Q A W P P T C L P L G V L M K
GCCGCTTCGATGGCAGACACTCCAGACACTGAAAGCCATGGTGCAAGCCTGGCCCTTACCTGTCTGCCTCTGGGAGTGCTCATGAAA

Gene : PRAME
Segment# : 6
Offset : 76
1st Codon : 1
Q A W P P T C L P L G V L M K G Q H L H L E T F K A V L D G
CAGGCTTGGCCTTTACATGCTCCCTCGGCGTCTGATGAAGGGACAGCATCTGCATCTGGAACCTTTAAGGCTGTGCTCGACGGA

Gene : PRAME
Segment# : 7
Offset : 91
1st Codon : 1
G Q H L H L E T F K A V L D G L D V L L A Q E V R P R R W K
GGCCAACACTCCACCTCGAGACATTCAAAGCCGTCTGGATGGCTCGACGTCTGCTCGCCCAAGAGGTCAGGCTAGGAGATGGAAA

Gene : PRAME
Segment# : 8
Offset : 106
1st Codon : 1
L D V L L A Q E V R P R R W K L Q V L D L R K N S H Q D F W
CTGGATGTGCTCCTGGCTCAGGAAGTGAGACCCAGAAGGTGAAGCTCCAGGTCTGGATCTGAGAAAGATAGCCATCAGGATTTCTGG

Gene : PRAME
Segment# : 9
Offset : 121
1st Codon : 1
L Q V L D L R K N S H Q D F W T V W S G N R A S L Y S F P E
CTGCAAGTCTCGACCTCAGGAAAACTCCCAACCAAGACTTTGGACAGTGTGGAGCGGAAACAGAGCCTCCCTGTATAGCTTTCCCGAA

Gene : PRAME
Segment# : 10
Offset : 136
1st Codon : 1
T V W S G N R A S L Y S F P E P E A A Q P M T K K R K V D G
ACCGTCTGGTCCGGCAATAGGGCTAGCCTTACTCTCTCCCTGAGCCTGAGGCTGCCCAACCCATGACCAAAAAGAGAAAGGTGACGGA

Gene : PRAME
Segment# : 11
Offset : 151
1st Codon : 1
P E A A Q P M T K K R K V D G L S T E A E Q P F I P V E V L
CCCGAAGCGCTCAGCCTATGACAAAGAAAAGGAAAGTGATGGCTCAGCACAGAGGCTGAGCAACCTTTATCCCTGTGGAAGTGCTC

Gene : PRAME
Segment# : 12
Offset : 166
1st Codon : 1
L S T E A E Q P F I P V E V L V D L F L K E G A C D E L F S
CTGTCCACCGAAGCCGAACAGCCTTTCATTCCTCGAGGTCCTGGTCGACCTCTTCCTCAAGGAAGGCGCTTGCGATGAGCTCTTCTCC

Gene : PRAME
Segment# : 13
Offset : 181
1st Codon : 1
V D L F L K E G A C D E L F S Y L I E K V K R K K N V L R L
GTGGATCTGTTTCTGAAAGAGGGAGCCTGTGACGAACGTGTTAGCTATCTGATTGAGAAAGTAAAAGGAAAAAGATGTGCTCAGGCTC

Gene : PRAME
Segment# : 14

Figure 27 (Cont)

190/216

Offset : 196
1st Codon : 1
Y L I E K V K R K K N V L R L C C K K L K I F A M P M Q D I
TACCTCATCGAAAAGGTCAAGAGAAAAGAAACGTCCTGAGACTGTGTTGCAAAAAGCTCAAGATTTTCGCTATGCCTATGCAAGACATT

Gene : PRAME
Segment# : 15
Offset : 211
1st Codon : 1
C C K K L K I F A M P M Q D I K M I L K M V Q L D S I E D L
TGCTGTAAGAAACTGAAAATCTTTGCCATGCCCATGCAGGATATCAAAATGATTCTGAAAATGGTCCAGCTCGACTCCATCGAAGACCTC

Gene : PRAME
Segment# : 16
Offset : 226
1st Codon : 1
K M I L K M V Q L D S I E D L E V T C T W K L P T L A K F S
AAGATGATCCTCAAGATGGTGCAACTGGATAGCATGAGGATCTGGAAGTGACATGCACATGGAACTGCCTACCTCGCCAAATCTCC

Gene : PRAME
Segment# : 17
Offset : 241
1st Codon : 1
E V T C T W K L P T L A K F S P Y L G Q M I N L R R L L L S
GAGGTACCTGTACCTGGAAGCTCCCCACACTGGCTAAGTTTAGCCCTTACCTCGGCCAAATGATTAACTCAGGAGACTGCTCCTGTCC

Gene : PRAME
Segment# : 18
Offset : 256
1st Codon : 1
P Y L G Q M I N L R R L L L S H I H A S S Y I S P E K E E Q
CCCTATCTGGGACAGATGATCAATCTGAGAAGGCTCCTGCTCAGCCATATCCATGCCTCCAGCTATATCTCCCCGAAAAGGAAGAGCAA

Gene : PRAME
Segment# : 19
Offset : 271
1st Codon : 1
H I H A S S Y I S P E K E E Q Y I A Q F T S Q F L S L Q C L
CACATTACGCTAGCTCCTACATTAGCCCTGAGAAAGAGGAACGATATATCGCTCAGTTTACCTCCCAGTTTCTGTCCCTGCAATGCCTC

Gene : PRAME
Segment# : 20
Offset : 286
1st Codon : 1
Y I A Q F T S Q F L S L Q C L Q A L Y V D S L F F L R G R L
TACATTGCCCAATTCAAGCCCAATTCCTCAGCCTCCAGTGTCTGCAAGCCCTCTAGCTCGACTCCCTGTTTTCTCAGGGGAAGGCTC

Gene : PRAME
Segment# : 21
Offset : 301
1st Codon : 1
Q A L Y V D S L F F L R G R L D Q L L R H V M N P L E T L S
CAGGCTCTGTATGTGGATAGCCTCTTCTTTCTGAGAGGCAGACTGGATCAGCTCCTGAGACACGTCATGAATCCCTCGAGACACTGTCC

Gene : PRAME
Segment# : 22
Offset : 316
1st Codon : 1
D Q L L R H V M N P L E T L S I T N C R L S E G D V M H L S
GACCACTGCTCAGGCATGTGATGAACCTCTGGAAACCTCAGCATTACCAATTGCAGACTGTCCGAGGGAGACGTCATGCATCTGTCC

Gene : PRAME
Segment# : 23
Offset : 331
1st Codon : 1
I T N C R L S E G D V M H L S Q S P S V S Q L S V L S L S G
ATCAAACTGTAGGCTCAGCGAAGGCGATGTGATGCACCTCAGCCAAAGCCCTAGCGTCAGCCAACGTCCGTGCTCAGCCTCAGCGGA

Gene : PRAME
Segment# : 24
Offset : 346
1st Codon : 1

Figure 27 (Cont)

191/216

Q S P S V S Q L S V L S L S G V M L T D V S P E P L Q A L L
CAGTCCCCCTCCGTGTCCAGCTCAGCGTCTGTCCCTGTCCGGCGTCATGCTACCGATGTGTCCCCGAACCCCTCCAGGCTCTGCTC

Gene : PRAME
Segment# : 25
Offset : 361
1st Codon : 1

V M L T D V S P E P L Q A L L E R A S A T L Q D L V F D E C
GTGATGCTGACAGACGTGAGCCCTGAGCCTCTGCAAGCCCTCCTGAAAGGGCTAGCGCTACCCCTCCAGGATCTGGTCTTCGATGAGTGT

Gene : PRAME
Segment# : 26
Offset : 376
1st Codon : 1

E R A S A T L Q D L V F D E C G I T D D Q L L A L L P S L S
GAGAGAGCCTCCGCCCACTGCAAGACCTCGTGTGACGAATCGGGAATCACAGACGATCAGCTCCTGGCTCTGCTCCCTCCCTGTGCTC

Gene : PRAME
Segment# : 27
Offset : 391
1st Codon : 1

G I T D D Q L L A L L P S L S H C S Q L T T L S F Y G N S I
GGCATTACCGATGACCAACTGCTCGCCCTCCTGCTAGCCTCAGCCATTGCTCCAGCTCACCACACTGTCTTCTATGGCAATAGCAT

Gene : PRAME
Segment# : 28
Offset : 406
1st Codon : 1

H C S Q L T T L S F Y G N S I S I S A L Q S L L Q H L I G L
CACTGTAGCCAACTGACAACTCAGCTTTTACGGAACTCCATCTCCATCTCCGCCCTCCAGTCCCTGCTCCAGCATCTGATTGGCCTC

Gene : PRAME
Segment# : 29
Offset : 421
1st Codon : 1

S I S A L Q S L L Q H L I G L S N L T H V L Y P V P L E S Y
AGCATTAGCGCTCTGCAAGCCTCCTGCAACACCTCATCGGACTGTCCAACTCACCCATGTGCTCTACCCTGTGCTCTGGAAAGCTAT

Gene : PRAME
Segment# : 30
Offset : 436
1st Codon : 1

S N L T H V L Y P V P L E S Y E D I H G T L H L E R L A Y L
AGCAATCTGACACAGTCTGTATCCGTCCTCCCTCGAGTCTACGAAGACATTACGGAACTCCACCTCGAGAGACTGGCTTACCTC

Gene : PRAME
Segment# : 31
Offset : 451
1st Codon : 1

E D I H G T L H L E R L A Y L H A R L R E L L C E L G R P S
GAGGATATCCATGGCACACTGCATCTGGAAGGCTCGCCTATCTGCATGCCAGACTGAGAGAGCTCCTGTGTGAGCTCGGCAGACCCCTC

Gene : PRAME
Segment# : 32
Offset : 466
1st Codon : 1

H A R L R E L L C E L G R P S M V W L S A N P C P H C G D R
CAGCTAGGCTCAGGGAAGTCTCTGCGAACTGGGAAGGCTAGCATGGTGTGGCTGTCCGCCAATCCCTGTCCCCATTGCGGAGACAGA

Gene : PRAME
Segment# : 33
Offset : 481
1st Codon : 1

M V W L S A N P C P H C G D R T F Y D P E P I L C P C F M P
ATGGTCTGGCTCAGCGCTAACCTTGCCCTCACTGTGGCGATAGGACATTCTATGACCTGAGCCTATCCTCTGCCCTTGCTTTATGCTT

Gene : PRAME
Segment# : 34
Offset : 496
1st Codon : 1

T F Y D P E P I L C P C F M P N A A
ACCTTTTACGATCCGAACCATCTGTGTCCCTGTTTCATGCCAATGCCGCT

Figure 27 (Cont)

192/216

Gene : TRP2IN2
Segment# : 1
Offset : 1
1st Codon : 1
A A L M E T H L S S K R Y T E E A G G F F P W L K V Y Y Y R
GCCGCTCTGATGGAGACACACCTCAGCTCCAAGAGATACACAGAGGAAGCCGGAGGCTTTTCCCTTGGCTCAAGGTCTACTATTACAGA

Gene : TRP2IN2
Segment# : 2
Offset : 16
1st Codon : 1
E A G G F F P W L K V Y Y Y R F V I G L R V W Q W E V I S C
GAGGCTGGCCGATTCCTTCCCTGGCTGAAAGTGTATTACTATAGGTTTGTGATTGGCTCAGGGTCTGGCAATGGGAAGTGATTAGCTGT

Gene : TRP2IN2
Segment# : 3
Offset : 31
1st Codon : 1
F V I G L R V W Q W E V I S C K L I K R A T T R Q P A A
TTCGTCATCGGACTGAGAGTGTGGCAGTGGGAGGTCATCTCTGCAAACTGATTAAAGAGAGCCACAACCAGACAGCCTGCCGCT

Gene : NYNS01a
Segment# : 1
Offset : 1
1st Codon : 1
A A M Q A E G R G T G G S T G D A D G P G G P G I P D G P G
GCCGCTATGCAAGCCGAAGGCAGAGGCACAGGCGGAAGCACAGGCGATGCCGATGGCCCTGGCGGACCCGGAATCCCTGACGGACCCGGA

Gene : NYNS01a
Segment# : 2
Offset : 16
1st Codon : 1
D A D G P G G P G I P D G P G G N A G G P G E A G A T G G R
GACGCTGACGGACCCCGAGGCCCTGGCATTCCCGATGGCCCTGGCGGAACCGCTGGCGGACCCGGAGAGGCTGGCGCTACCGGAGGCAGA

Gene : NYNS01a
Segment# : 3
Offset : 31
1st Codon : 1
G N A G G P G E A G A T G G R G P R G A G A A R A S G P G G
GGCAATGCCGAGGCCCTGGCGAAGCCGAGGCCACAGGCGGAAGGGGACCCAGAGGCGCTGGCGCTGCCAGAGCCTCCGGCCCTGGCGGA

Gene : NYNS01a
Segment# : 4
Offset : 46
1st Codon : 1
G P R G A G A A R A S G P G G G A P R G P H G G A A S G L N
GGCCTAGGGGAGCCCGAGCCGCTAGGGCTAGCGGACCCGGAGGCGGAGCCCTAGGGGACCCATGGCGGAGCCGCTAGCGGACTGAAT

Gene : NYNS01a
Segment# : 5
Offset : 61
1st Codon : 1
G A P R G P H G G A A S G L N G C C R C G A R G P E S R L L
GGCGCTCCAGAGGCCCTACCGAGGCGCTGCCCTCCGGCCCTCAACGGATGCTGTAGGTGTGGCGCTAGGGGACCCGAAAGCAGACTGCTC

Gene : NYNS01a
Segment# : 6
Offset : 76
1st Codon : 1
G C C R C G A R G P E S R L L E F Y L A M P F A T P M E A E
GGCTGTTGCAGATGCGGAGCCAGAGGCCCTGAGTCCAGGCTCCTGGAATTCATCTGGCTATGCCCTTTCGCTACCCCTATGGAAGCCGAA

Gene : NYNS01a
Segment# : 7
Offset : 91
1st Codon : 1
E F Y L A M P F A T P M E A E L A R R S L A Q D A P P L P V
GAGTTTACCTCGCATGCCCTTTGCCACACCCATGGAGGCTGAGCTGCCAGAGGTCCTGGCTCAGGATGCCCTCCCTCCCTCCCGCTC

Gene : NYNS01a

Figure 27 (Cont)

193/216

Segment# : 8
Offset : 106
1st Codon : 1
L A R R S L A Q D A P P L P V P G V L L K E F T V S G N I L
CTGGCTAGGAGAAGCCTCGCCCAAGACGCTCCCCCTCTGCCTGTGCCTGGCGTCTGCTCAAGGAATTACAGTGTCCGGCAATATCCTC

Gene : NYNS01a
Segment# : 9
Offset : 121
1st Codon : 1
P G V L L K E F T V S G N I L T I R L T A A D H R Q L Q L S
CCCGAGTGTCTCTGAAAGAGTTTACCGTCAGCGGAACATTCTGACAATCAGACTGACAGCGCTGACCATAGGCAACTGCAACTGTCC

Gene : NYNS01a
Segment# : 10
Offset : 136
1st Codon : 1
T I R L T A A D H R Q L Q L S I S S C L Q Q L S L L M W I T
ACCATTAGGCTACCGCTGCGGATCAGACAGCTCCAGCTCAGCATTAGCTCTGCTCCAGCAACTGTCCCTGCTCATGTGGATCACA

Gene : NYNS01a
Segment# : 11
Offset : 151
1st Codon : 1
I S S C L Q Q L S L L M W I T Q C F L P V F L A Q P P S G Q
ATCTCCAGTGTCTGCAAGAGCTCAGCCTCTGATGTGGATTACCAATGCTTTCTGCTGTGTTCTGGCTCAGCCTCCCTCCGGCCAA

Gene : NYNS01a
Segment# : 12
Offset : 166
1st Codon : 1
Q C F L P V F L A Q P P S G Q R R A A
CAGTGTTTCTCCCGTCTTCTCGCCCAACCCCTAGCGGACAGAGAAGGGCTGCC

Gene : NYNS01b
Segment# : 1
Offset : 1
1st Codon : 1
A A M L M A Q E A L A F L M A Q G A M L A A Q E R R V P R A
GCCGCTATGCTCGGCTCAGGAAGCCCTCGCCTTTCTGATGGCCCAAGGCGCTATGCTCGCCGCTCAGGAAAGGAGAGTGCCTAGGGCT

Gene : NYNS01b
Segment# : 2
Offset : 16
1st Codon : 1
Q G A M L A A Q E R R V P R A A E V P G A Q G Q Q G P R G R
CAGGGAGCCATGCTGGCTGCCAAGAGAGAAGGGTCCCCAGAGCCGCTGAGGTCCCCGGAGCCCAAGGCCAACAGGGACCCAGAGGCAGA

Gene : NYNS01b
Segment# : 3
Offset : 31
1st Codon : 1
A E V P G A Q G Q Q G P R G R E E A P R G V R M A A R L Q G
GCCGAAGTGCCTGCGCTCAGGACAGCAAGGCCCTAGGGGAAGGGAAGAGGCTCCAGAGGCGTCAGGATGGCCGCTAGGCTCCAGGGA

Gene : NYNS01b
Segment# : 4
Offset : 46
1st Codon : 1
E E A P R G V R M A A R L Q G A A
GAGGAAGCCCTAGGGGAGTGAGAATGGCTGCCAGACTGCAAGGCGCTGCC

Gene : LAGE1
Segment# : 1
Offset : 1
1st Codon : 1
A A M Q A E G Q G T G G S T G D A D G P G G P G I P D G P G
GCCGCTATGCAAGCCGAAGGCCAAGGCACAGGCGGAAGCACAGGCGATGCCGCTGGCCGACCCGGAATCCCTGACGGACCCGGA

Gene : LAGE1
Segment# : 2
Offset : 16

Figure 27 (Cont)

194/216

1st Codon : 1
D A D G P G G P G I P D G P G G N A G G P G E A G A T G G R
G A G C T G A C G G A C C C G G A G G C C T G G C A T T C C G A T G G C C T G G C G A A A C G C T G G C G G A C C C G G A G G C T G G C G T A C C G G A G G C A G A

Gene : LAGE1
Segment# : 3
Offset : 31
1st Codon : 1
G N A G G P G E A G A T G G R G P R G A G A A R A S G P R G
G G C A A T G C C G G A G G C C T G G C G A A G C C G G A G C C A G G C G G A A G G G G A C C C A G A G G C G T G G C G T G C C A G A G C C T C C G G C C T A G G G G A

Gene : LAGE1
Segment# : 4
Offset : 46
1st Codon : 1
G P R G A G A A R A S G P R G G A P R G P H G G A A S A Q D
G G C C C T A G G G A G C C G G A G C C G T A G G G C T A G C G G A C C C A G A G G C G G A G C C C T A G G G G A C C C A T G G C G G A G C C G T A G C G C T C A G G A T

Gene : LAGE1
Segment# : 5
Offset : 61
1st Codon : 1
G A P R G P H G G A A S A Q D G R C P C G A R R P D S R L L
G G C G C T C C C A G A G C C C T C A C G G A G G C G C T G C C T C C G C C A A G A C G G A A G G T G T C C C T G T G G C G T A G G A G A C C C G A T A G C A G A C T G C T C

Gene : LAGE1
Segment# : 6
Offset : 76
1st Codon : 1
G R C P C G A R R P D S R L L Q L H I T M P F S S P M E A E
G G C A G A T G C C C T T G C G G A G C C A G A A G G C C T G A C T C C A G G C T C C T G C A A T G C A T A T C A A T G C C T T T C T C A G C C C T A T G G A A G C C G A A

Gene : LAGE1
Segment# : 7
Offset : 91
1st Codon : 1
Q L H I T M P F S S P M E A E L V R R I L S R D A A P L P R
C A G C T C C A C A T T A C C A T G C C C T T T A G C T C C C C C A T G G A G C T G A G C T C G T G A G A A G G A T T C T G T C C A G G A T G C C G T C C C C T C C C C A G A

Gene : LAGE1
Segment# : 8
Offset : 106
1st Codon : 1
L V R R I L S R D A A P L P R P G A V L K D F T V S G N L L
T C G T C A G G A G A A T C C T C A G C A G A G C T G C C C C T C T G C C T A G G C C T G G C G C T G T G C T C A A G G A T T C A C A G T G T C C G G C A A T C T G C T C

Gene : LAGE1
Segment# : 9
Offset : 121
1st Codon : 1
P G A V L K D F T V S G N L L F I R L T A A D H R Q L Q L S
C C C G A G C C G T C T G A A A G A C T T T A C C G T C A G C G G A A C C T C C T G T T T A T C A G A C T G A C A G C C G C T G A C C A T A G G C A A C T G C A A C T G T C C

Gene : LAGE1
Segment# : 10
Offset : 136
1st Codon : 1
F I R L T A A D H R Q L Q L S I S S C L Q Q L S L L M W I T
T T C A T T A G G C T C A C C G C T G C G A T C A G A C A G C T C A G C T C A G C A T T A G C T C C T G C C T C C A G C A A C T G T C C C T G C T A T G T G G A T C A C A

Gene : LAGE1
Segment# : 11
Offset : 151
1st Codon : 1
I S S C L Q Q L S L L M W I T Q C F L P V F L A Q A P S G Q
A T C T C C A G C T G T C T G C A A C A G C T C A G C C T C C T G A T G T G G A T T A C C C A A T G C T T T C T G C C T G T G T T C T G G C T C A G G C T C C C T C C G G C C A A

Gene : LAGE1
Segment# : 12
Offset : 166
1st Codon : 1
Q C F L P V F L A Q A P S G Q R R A A

Figure 27 (Cont)

195/216

CAGTGTTCCTCCCCGTCTTCCTGCCCCAAGCCCCCTAGCGGACAGAGAAGGGCTGCC

Segments in scrambled order:

MAGE-1 #15

A P E E E I W E E L S V M E V Y D G R E H S A Y G E P R K L
GCCCTGAGGAAGAGATTTGGGAAGAGCTCAGCGTCATGGAAGTGATGACGGAAGGAACACTCCGCCTATGGCGAAGCCAGAAAGCTC

MAGE-1 #4

E E V P T A G S T D P P Q S P Q G A S A F P T T I N F T R Q
GAGGAAGTGCCCTACCGCTGGCTCCACCGATCCCCCTCAGTCCCCCAAGGCGCTAGCGCTTCCCTACCAATCAATTTCAAGGCAA

PRAME #10

T V W S G N R A S L Y S F P E P E A A Q P M T K K R K V D G
ACCGTCTGGTCCGGCAATAGGGCTAGCCTCTACTCTCTCCCTGAGCCTGAGGCTGCCAACCCTGACCAAAAAGAGAAAGGTGACGGGA

MAGE-3 #14

Q I M P K A G L L I I V L A I I A R E G D C A P E E K I W E
CAGATTATGCCTAAGGCTGGCTCCTGATTATCGTCTGGCTATCATTGCCAGAGAGGAGACTGTGCCCTGAGGAAAAGATTGGGAA

PRAME #9

L Q V L D L R K N S H Q D F W T V W S G N R A S L Y S F P E
CTGCAAGTGCTCGACCTCAGGAAAACTCCACCAAGACTTTTGACAGTGTTGGAGCGGAAACAGAGCCTCCCTGTATAGCTTTCCCGAA

PRAME #8

L D V L L A Q E V R P R R W K L Q V L D L R K N S H Q D F W
CTGGATGTGCTCCTGGCTCAGGAAGTGAGACCCAGAGGTGGAAGCTCCAGGTCTGGATCTGAGAAAGAATAGCCATCAGGATTTCTGG

NYNS01b #2

Q G A M L A A Q E R R V P R A A E V P G A Q G Q Q G P R G R
CAGGGAGCCATGTGGCTGCCAAGAGAGAAGGGTCCCCAGAGCGCTGAGGTCCCCGAGCCCAAGGCCAACAGGGACCCAGAGGCAGA

PRAME #24

Q S P S V S Q L S V L S L S G V M L T D V S P E P L Q A L L
CAGTCCCCCTCCGTGTCCAGCTCAGCGTCTGTCCCTGTCCGGCGTCATGCTACCGATGTGTCCCCGAACCCCTCCAGGCTCTGCTC

MAGE-1 #17

L T Q D L V Q E K Y L E Y R Q V P D S D P A R Y E F L W G P
CTGACACAGGATCTGGTCCAGGAAAAGTATCTGGAATACAGACAGGTCCCCGATAGCGATCCCGCTAGGTATGAGTTTCTGTGGGGCCCT

MAGE-1 #6

R Q P S E G S S S R E E E G P S T S C I L E S L F R A V I T
AGGCAACCTCCGAGGGAAGCTCCAGCAGAGAGGAAGAGGACCCCTCCACCTCCTGCATTCTGGAAGCCTCTTCAGAGCCGTCATCACA

BAGE #1

A A M A A R A V F L A L S A Q L L Q A R L M K E E S P V V S
GCCGCTATGGCTGCCAGAGCCGCTCTCTCGCCCTCAGCGCTCAGCTCCTGCAAGCCAGACTGATGAAGGAAGAGTCCCCCGTCTGTCTC

PRAME #34

T F Y D P E P I L C P C F M P N A A
ACCTTTTACGATCCCGAACCATCTCTGTGTCCCTGTTTCATGCCCAATGCCGCT

MAGE-3 #12

I E L M E V D P I G H L Y I F A T C L G L S Y D G L L G D N
ATCGAATGATGGAGGTGACCCCTATCGGACACCTCTACATTTTCGCTACCTGTCTGGGACTGTCTACGATGGCCTCCTGGGAGACAAT

GAGE-1 #2

R R Y V E P P E M I G P M R P E Q F S D E V E P A T P E E G
AGGAGATACGTGAGCCTCCCGAAATGATTGGCCCTATGAGACCCGAACAGTTTAGCGATGAGGTGAGCCTGCCACACCCGAAGAGGGA

TRP2IN2 #2

E A G G F F P W L K V Y Y Y R F V I G L R V W Q W E V I S C
GAGGCTGGCGGATTCTTTCCCTGGCTGAAAGTGATTACTATAGGTTTGTGATTGGCCTCAGGGTCTGGCAATGGGAAGTGATTAGCTGT

PRAME #1

A A M E R R R R L W G S I Q S R Y I S M S V N T S P R R L V E
GCCGCTATGGAAGGAGAAGGCTCTGGGGAAGCATTAGTCCAGGTATATCTCCATGTCCGTGTGGACCTCCCCAGAGGCTCGTGGA

TRP2IN2 #1

A A L M E T H L S S K R Y T E E A G G F F P W L K V Y Y Y R
GCCGCTCTGATGGAGACACCTCAGCTCCAAGAGATACAGAGGAAGCCGGAGGCTTTTCCCTGGCTCAAGGTCTACTATTACAGA

Figure 27 (Cont)

196/216

MAGE-1 #1

A A M S L E Q R S L H C K P E E A L E A Q Q E A L G L V C V
GCCGCTATGTCCTGGAACAGAGAAGCCTCCACTGTAAGCCTGAGGAAGCCCTCGAGGCTCAGCAAGAGGCTCTGGGACTGGTCTGCGTC

MAGE-1 #3

Q A A T S S S S P L V L G T L E E V P T A G S T D P P Q S P
CAGGCTGCCACAAGCTCCAGCTCCCCCTCGTGCTCGGCACACTGGAAGAGGTCCCCACAGCCGGAAGCACAGACCCCTCCCCAAGCCCT

PRAME #4

A L E L L P R E L F P P L F M A A F D G R H S Q T L K A M V
GCCCTCGAGCTCCTGCCCTAGGGAAGTGTTCCTCCCTCTGTTTATGGCTGCCCTTGACGGAAGGCATAGCCAAACCCCTCAAGGCTATGGTC

MAGE-3 #16

E L S V L E V F E G R E D S I L G D P K K L L T Q H F V Q E
GAGCTCAGCGTCTCGAAGTGTGAGGGAAGGGAAGACTCCATCCTCGGCGATCCCAAAAGCTCCTGACACAGCATTTGCTCCAGGAA

MAGE-1 #11

E S L Q L V F G I D V K E A D P T G H S Y V L V T C L G L S
GAGTCCCTGCAACTGGTCTTCGGAATCGATGTGAAAGAGGCTGACCCCTACCGGACACTCCTACGTCCTGGTCACCTGCTCTGGGACTGTCC

MAGE-3 #5

P D P P Q S P Q G A S S L P T T M N Y P L W S Q S Y E D S S
CCCGATCCCCCTCAGTCCCCCAAGGCGTAGCTCCCTGCCCTACCAATGAATTACCCTCTGTGGAGCCAAAGCTATGAGGATAGCTCC

LAGE1 #1

A A M Q A E G Q G T G G S T G D A D G P G G P G I P D G P G
GCCGCTATGCAAGCCGAAGGCCAAGGCACAGGCGGAAGCACAGGCGATGCCGATGGCCCTGGCGGACCCGGAATCCCTGACGGACCCGGA

NYNS01a #12

Q C F L P V F L A Q P P S G Q R R A A
CAGTGTTCCTCCCGTCTTCCTCGCCCAACCCCTAGCGGACAGAGAAGGGCTGCC

gp100In4 #2

T W G E G L P S Q P I I H T C V Y F F L P D H L S F G R P F
ACCTGGGGCGAAGGCCCTCCCTCCAGCCTATCATTCACATGCGTCTACTTTTCTCCCGATCACCTCAGCTTTGGCAGACCCCTTT

MAGE-1 #7

S T S C I L E S L F R A V I T K K V A D L V G F L L L K Y R
AGCACAAGCTGTATCCTCGAGTCCCTGTTTAGGGCTGTGATTACCAAAAGGTGCGCGATCTGGTGGCTTTCTGCTCCTGAAATACAGA

NYNS01a #1

A A M Q A E G R G T G G S T G D A D G P G G P G I P D G P G
GCCGCTATGCAAGCCGAAGGCAGAGGCACAGGCGGAAGCACAGGCGATGCCGATGGCCCTGGCGGACCCGGAATCCCTGACGGACCCGGA

GAGE-1 #7

D G P D G Q E M D P P N P E E V K T P E E E M R S H Y V A Q
GACGAGCCCGATGGCCAAGAGATGGACCCCTCCCAATCCGGAAGAGGTCAAGACACCCGAAGAGGAAATGAGAAGCCATTACGTGCCCCAA

NYNS01a #11

I S S C L Q Q L S L L M W I T Q C F L P V F L A Q P P S G Q
ATCTCCAGCTGTCTGCAACAGCTCAGCCTCCTGATGTGGATTACCCAATGCTTTCTGCCTGTGTTTCTGGCTCAGCCTCCCTCCGSCCAA

PRAME #26

E R A S A T L Q D L V F D E C G I T D D Q L L A L L P S L S
GAGAGAGCCTCCGCCACACTGCAAGACCTCGTGTGACGAATGCGGAATCACAGACGATCAGCTCCTGGCTCTGCTCCCTCCCTGTCTC

MAGE-3 #17

L G D P K K L L T Q H F V Q E N Y L E Y R Q V P G S D P A C
CTGGGAGACCTTAAGAACTGCTCACCCAACTTTGTGCAAGAGAATTACCTCGAGTATAGGCAAGTGCTGGCTCCGACCTGCCTGT

MAGE-1 #2

E A L E A Q Q E A L G L V C V Q A A T S S S S P L V L G T L
GAGGCTCTGGAAGCCCAACAGGAAGCCCTCGGCCTCGTGTGTGTGCAAGCCGCTACCTCCAGCTCCAGCCCTCTGGTCTCTGGGAACCCCTC

NYNS01a #7

E F Y L A M P F A T P M E A E L A R R S L A Q D A P P L P V
GAGTTTTACCTCGCATGCCCTTTGCCACACCCATGGAGGCTGAGCTCGCCAGAAGGTCCCTGGCTCAGGATGCCCTCCCTCCCTCCCTGTC

NYNS01b #4

E E A P R G V R M A A R L Q G A A
GAGGAAGCCCTAGGGGAGTGAGAATGGCTGCCAGACTGCAAGGCGCTGCC

Figure 27 (Cont)

197/216

BAGE #3
W R L E P E D G T A L C F I F A A
TGGAGACTGGAACCCGAAGACGGAACCGCTCTGTGTTTCATTTTCGCTGCC

GAGE-1 #3
E Q F S D E V E P A T P E E G E P A T Q R Q D P A A A Q E G
GAGCAATTCTCCGACGAAGTGGAAACCCGCTACCCCTGAGGAAGGCGAACCCGCTACCCAAAGGCAAGACCTGCGCTGCCCAAGAGGGA

MAGE-3 #6
T M N Y P L W S Q S Y E D S S N Q E E E G P S T F P D L E S
ACCATGAACCTATCCCTCTGGTCCCAGTCTACGAAGACTCCAGCAATCAGGAAGAGGAGCCCTAGCACATTCCCTGACCTCGAGTCC

MAGE-3 #7
N Q E E E G P S T F P D L E S E F Q A A L S R K V A E L V H
AACCAAGAGGAAGAGGGACCTCCACCTTTCCCGATCTGGAAAGCGAATTCAGGCGCTCTGTCCAGGAAAGTGGCTGAGCTCGTGCAT

PRAME #13
V D L F L K E G A C D E L F S Y L I E K V K R K K N V L R L
GTGGATCTGTTTCTGAAGAGGGAGCCTGTGACGAAGTGTITAGCTATCTGATTGAGAAAGTGAAGGAAAGAAATGTGCTCAGGCTC

NYNS01a #10
T I R L T A A D H R Q L Q L S I S S C L Q Q L S L L M W I T
ACCATTAGGCTCACCGCTGCCGATCACAGACAGCTCCAGCTCAGCATTAGCTCCTGCCTCCAGCAACTGTCCCTGCTCATGTGGATCACA

MAGE-3 #1
A A M P L E Q R S Q H C K P E E G L E A R G E A L G L V G A
GCCGCTATGCTCTGGAACAGAGAAGCCAACTGTAAAGCCTGAGGAAGGCTCGAGGCTAGGGGAGAGGCTCTGGAGTGGTCCGGCT

NYNS01a #2
D A D G P G G P G I P D G P G G N A G G P G E A G A T G G R
GACGCTAGCGACCCGAGGCGCTGGCATTCCCGATGGCCCTGGCGGAAACGCTGGCGGACCCGGAGAGGCTGGCGCTACCGGAGGCAGA

MAGE-3 #19
Y E F L W G P R A L V E T S Y V K V L H H M V K I S G G P H
TACGAATTCCTCTGGGGACCCAGAGCCCTCGTGGAAACCTCTACGTCAGGCTCTGCATCACATGGTGAAATCTCCGGCGGACCCCAT

PRAME #23
I T N C R L S E G D V M H L S Q S P S V S Q L S V L S L S G
ATCAAACTGTAGGCTCAGCGAAGGCGATGTGATGCACCTCAGCCAAAGCCCTAGCGTCAGCCAACTGTCCGTGCTCAGCCTCAGCGGA

MAGE-3 #18
N Y L E Y R Q V P G S D P A C Y E F L W G P R A L V E T S Y
AACTATCTGGAATACAGACAGGTCCCGGAAGCGATCCCGCTGTCTATGAGTTCTGTGGGGCCCTAGGGCTCTGGTCCGAGACAAGCTAT

MAGE-3 #11
V I F S K A S S S L Q L V F G I E L M E V D P I G H L Y I F
GTGATTTTCTCCAAGGCTAGCTCCAGCTCCAGCTCGTGTGTTGGCATTGAGCTCATGGAAGTGGATCCCATGGCCATCTGTATATCTTT

PRAME #21
Q A L Y V D S L F F L R G R L D Q L L R H V M N P L E T L S
CAGGCTCTGTATGTGGATAGCCTCTTCTTTCTGAGAGGCAGACTGGATCAGCTCCTGAGACACGTCATGAATCCCTCCGAGACACTGTCC

PRAME #20
Y I A Q F T S Q F L S L Q C L Q A L Y V D S L F F L R G R L
TACATTGCCCAATTCAGAAGCCAATTCCTCAGCTCCAGTGTCTGCAAGCCCTCTACGTCGACTCCCTGTTTTCTCAGGGGAAGGCTC

PRAME #7
G Q H L H L E T F K A V L D G L D V L L A Q E V R P R R W K
GGCCAACACCTCCACCTCGAGACATTCAAAGCCGCTCTGGATGGCTCGACGCTCTGCTCGCCCAAGAGGTCAGGCTAGGAGATGGAAA

LAGE1 #10
F I R L T A A D H R Q L Q L S I S S C L Q Q L S L L M W I T
TTCATTAGGCTCACCGCTGCCGATCACAGACAGCTCCAGCTCAGCATTAGCTCCTGCCTCCAGCAACTGTCCCTGCTCATGTGGATCACA

PRAME #15
C C K K L K I F A M P M Q D I K M I L K M V Q L D S I E D L
TGCTGTAAGAAACTGAAAATCTTTGCCATGCCCATGAGGATATCAAATGATTCTGAAAATGGTCAGCTCGACTCCATCGAAGACCTC

NYNS01a #5
G A P R G P H G G A A S G L N G C C R C G A R G P E S R L L
GGCGCTCCAGAGGCCCTCACGAGGCGCTGCCCTCCGGCTCAACGGATGTGTAGGTGTGGCGCTAGGGGACCCGAAAGCAGACTGTCT

Figure 27 (Cont)

198/216

MAGE-1 #8

K K V A D L V G F L L L K Y R A R E P V T K A E M L E S V I
AAGAAAGTGGCTGACCTCGTGGGATTCCTCCTGCTCAAGTATAGGGCTAGGGAACCCGTCACCAAAGCCGAAATGCTCGAGTCCGTGATT

MAGE-1 #13

Y D G L L G D N Q I M P K T G F L I I V L V M I A M E G G H
TACGATGGCCTCCTGGGAGACAATCAGATTATGCCTAAGACAGGCTTCTGATTATCGTCTGGTCATGATTGCCATGGAGGGAGGCCAT

PRAME #29

S I S A L Q S L L Q H L I G L S N L T H V L Y P V P L E S Y
AGCATTAGCGCTCTGCAAAGCCTCCTGCAACACCTCATCGGACTGTCCAACCTCACCCATGTGCTCTACCTGTGCTCTGGAAGCTAT

MAGE-3 #15

I A R E G D C A P E E K I W E E L S V L E V F E G R E D S I
ATCGTAGGGAAGGCGATTGCGCTCCCGAAGAGAAAATCTGGGAGGAACCTGTCCGTGCTCGAGGCTTTCGAAGGCAGAGAGGATAGCATT

PRAME #22

D Q L L R H V M N P L E T L S I T N C R L S E G D V M H L S
GACCAACTGTCTAGGCATGTGATGAACCTCTGGAAACCTCAGCATTACCAATTGCAGACTGTCCGAGGGAGACGTATGCATCTGTCC

MAGE-1 #19

R A L A E T S Y V K V L E Y V I K V S A R V R F F P P S L R
AGCGCTCTGGCTGAGACAAGCTATGTGAAAGTGTCTCGAGTATGTGATTAAAGTCAGCGCTAGGGTCAGGTTTCTTTCCCTCCCTGAGA

PRAME #30

S N L T H V L Y P V P L E S Y E D I H G T L H L E R L A Y L
AGCAATCTGACACAGTCTGTATCCCGTCCCCCTCGAGTCTTACGAAGACATTACCGGAACCCCTCCACCTCGAGAGACTGGCTTACCTC

NYN501b #1

A A M L M A Q E A L A F L M A Q G A M L A A Q E R R V P R A
GCCGCTATGCTCATGGCTCAGGAAGCCCTCGCCTTCTGATGGCCCAAGGCGCTATGCTCGCCGCTCAGGAAGGAGAGTGCCTAGGGCT

MAGE-1 #10

K N Y K H C F P E I F G K A S E S L Q L V F G I D V K E A D
AAGAATTACAAACACTGTTTCCCTGAGATTTTCGGAAGGCTAGCGAAAGCCTCCAGCTCGTGTGTCGATTGACGTCAAGGAAGCCGAT

MAGE-3 #4

T L V E V T L G E V P A A E S P D P P Q S P Q G A S S L P T
ACCTCGTGGAAAGTGACACTGGGAGAGGTCCCGCTGCCGAAAGCCCTGACCTCCCAAGCCCTCAGGGAGCCTCCAGCCTCCCCACA

PRAME #32

H A R L R E L L C E L G R P S M V W L S A N P C P H C G D R
CACGCTAGGCTCAGGGAAGTGTCTGCGAACTGGGAAGGCCTAGCATGGTGTGGCTGTCCGCCAATCCCTGTCCCCATTGCGGAGACAGA

PRAME #25

V M L T D V S P E P L Q A L L E R A S A T L Q D L V F D E C
GTGATGCTGACAGACGTGAGCCCTGAGCCTCTGCAAGCCCTCCTGGAAAGGCTAGCGCTACCTCCAGGATCTGGTCTTCGATGAGTGT

GAGE-1 #5

E D E G A S A G Q G P K P E A D S Q E Q G H P Q T G C E C E
GAGGATGAGGGAGCCTCCGCCGACAGGGACCCAAACCCGAGCCGATAGCCAAGAGCAAGGCCATCCCCAAACCGGATGCCAATGCCAA

MAGE-3 #10

E M L G S V V G N W Q Y F P P V I F S K A S S S L Q L V F G
GAGATGCTGGGAAGCGTCGTGGGAACTGGCAGTATTTCTTTCCCGTCATCTTTAGCAAAGCCTCCAGCTCCCTGCAACTGGTCTTCGGA

GAGE-1 #1

A A M S W R G R S T Y R P R P R R Y V E P P E M I G P M R P
GCCGCTATGTCTGGAGAGGCAGAAGCACATACAGACCCAGACCCAGAAGGTATGTGGAACCCCTGAGATGATCGGACCCATGAGGCCT

PRAME #2

Y I S M S V W T S P R R L V E L A G Q S L L K D E A L A I A
TACATTAGCATGAGCGTCTGGACAAGCCCTAGGAGACTGGTGCAGCTCGCCGACAGTCCCTGCTCAAGGATGAGGCTCTGGCTATCGCT

MAGE-1 #16

Y D G R E H S A Y G E P R K L L T Q D L V Q E K Y L E Y R Q
TACGATGGCAGAGACATAGCGCTTACGGAGAGCCTAGGAAACTGCTACCCAAGACCTCGTGCAAGAGAAATACCTCGAGTATAGGCAA

LAGE1 #12

Q C F L P V F L A Q A P S G Q R R A A
CAGTGTTCCTCCCGCTCTCTCGCCCAAGCCCTAGCGGACAGAGAAGGGCTGCC

Figure 27 (Cont)

199/216

MAGE-3 #20

V K V L H H M V K I S G G P H I S Y P P L H E W V L R E G E
GTGAAAGTGCTCCACCATATGGTCAAGATTAGCGGAGGCCCTCACATTAGCTATCCCCCTCTGCATGAGTGGGTGCTCAGGGAAGGCGAA

LAGE1 #7

Q L H I T M P F S S P M E A E L V R R I L S R D A A P L P R
CAGCTCCACATTACCATGCCCTTTAGCTCCCCCATGGAGGCTGAGCTCGTGAGAAGGATTCTGTCCAGGGATGCCGCTCCCCCTCCCCAGA

NYNS01a #9

P G V L L K E F T V S G N I L T I R L T A A D H R Q L Q L S
CCCGAGTGCTCCTGAAAGAGTTTACCGTCAGCGGAAACATTCTGACAATCAGACTGACAGCCGCTGACCATAGGCAACTGCAACTGTCC

PRAME #16

K M I L K M V Q L D S I E D L E V T C T W K L P T L A K F S
AAGATGATCCTCAAGATGGTGAAGCTGATAGCAATGAGGATCTGGAAGTGACATGCACATGGAACTGCCCTACCCCTCGCCAAATTTCTCC

MAGE-1 #14

F L I I V L V M I A M E G G H A P E E E I W E E L S V M E V
TTCCTCATCATTGTGCTCGTGATGATCGCTATGGAAGGCGGACACGCTCCCGAAGAGGAAATCTGGGAGGAAGTGTCCGTGATGAGGTC

PRAME #17

E V T C T W K L P T L A K F S P Y L G Q M I N L R R L L L S
GAGGTACCTGTACCTGGAAGCTCCCCACACTGGCTAAGTTTAGCCCTTACCTCGGCCAAATGATTAACTCAGGAGACTGCTCCTGTCC

MAGE-3 #2

E G L E A R G E A L G L V G A Q A P A T E E Q E A A S S S S
GAGGGACTGGAAGCCAGAGGCGAAGCCCTCGGCCTCGTGGGAGCCCAAGCCCTGCGCACAGAGGAACAGGAAGCCGCTAGCTCCAGCTCC

MAGE-3 #21

I S Y P P L H E W V L R E G E E A A
ATCTCTACCTCCCTCCACGAATGGGTCTGAGAGAGGGAGAGGAAGCCGCT

PRAME #19

H I H A S S Y I S P E K E E Q Y I A Q F T S Q F L S L Q C L
CACATTACGCTAGCTCCTACATTAGCCCTGAGAAAGAGGAACAGTATATCGCTCAGTTTACCTCCAGTTTCTGTCCCTGCAATGCCTC

NYNS01a #3

G N A G G P G E A G A T G G R G P R G A G A A R A S G P G G
GGCAATGCCGGAGGCCCTGCGGAAGCCGAGCCACAGGCGGAAGGGGACCCAGAGGCGCTGGCGCTGCCAGAGCCTCCGGCCCTGGCGGA

NYNS01a #4

G P R G A G A A R A S G P G G G A P R G P H G G A A S G L N
GGCCCTAGGGGAGCCCGAGCCGCTAGGGCTAGCGGACCCGGAGGCGGAGCCCTAGGGGACCCCATGGCGGAGCCGCTAGCGGACTGAAT

MAGE-1 #5

Q G A S A F P T T I N F T R Q R Q P S E G S S S R E E E G P
CAGGAGGCTCCGCTTTCCACAAACCATTAACTTTACCAGACAGAGACAGCTAGCGAAGGCTCCAGCTCCAGGGAAGAGGAAGGCCCT

NYNS01a #8

L A R R S L A Q D A P P L P V P G V L L K E F T V S G N I L
CTGGCTAGGAGAAGCCTCGCCCAAGACGCTCCCCCTCTGCCTGTGCTGGGCTCTGCTCAAGGAATTACAGTGTCCGGCAATATCCTC

PRAME #5

A A P D G R H S Q T L K A M V Q A W P F T C L P L G V L M K
GCCGCTTTCGATGGCAGACACTCCAGACACTGAAAGCCATGGTGCAAGCCTGGCCCTTTACCTGTCTGCCTCTGGGAGTGCTCATGAAA

MAGE-1 #20

I K V S A R V R F F F P S L R E A A L R E E E E G V A A
ATCAAAGTGTCGCCAGAGTGAGATTCTTTTCCCTAGCCTCAGGGAAGCCGCTCTGAGAGAGGAAGAGGAAGGCGTCCGCCGCT

PRAME #27

G I T D D Q L L A L L P S L S H C S Q L T T L S F Y G N S I
GGCATTACCGATGACCAACTGCTCGCCCTCCTGCCTAGCCTCAGCCATGTGCTCCAGCTCACCACACTGTCTCTATGGCAATAGCAIT

GAGE-1 #8

V K T P E E E M R S H Y V A Q T G I L W L L M N N C F L N L
GTGAAAACCCCTGAGGAAGAGATGAGGTCCCACTATGTGGCTCAGACAGGCATTCTGTGGCTGCTCATGAATAACTGTTTCTCAACCTC

LAGE1 #11

I S S C L Q Q L S L L M W I T Q C F L P V P L A Q A P S G Q
ATCTCCAGCTGTCTGCAACAGCTCAGCCTCCTGATGTGGATTACCCAATGCTTCTGCTGTGTTTCTGGCTCAGGCTCCCTCCGGCCAA

Figure 27 (Cont)

200/216

PRAME #14
Y L I E K V K R K K N V L R L C C K K L K I F A M P M Q D I
TACCTCATCGAAAAGGTCAAGAGAAAAGAAACGTCCTGAGACTGTGTGCAAAAAGCTCAAGATTTCGCTATGCCTATGCAAGACATT

MAGE-1 #9
A R E P V T K A E M L E S V I K N Y K H C F P E I F G K A S
GCCAGAGAGCCTGTGACAAAGGCTGAGATGCTGGAAAGCGTCATCAAAACTATAAGCATTGCTTTCCGAAATCTTTGGCAAAGCCTCC

LAGE1 #8
L V R R I L S R D A A P L P R P G A V L K D F T V S G N L L
CTGGTCAGGAGAATCCTCAGCAGAGACGCTGCCCTCTGCCTAGGCCTGGCGCTGTGCTCAAGGATTTCACAGTGTCCGGCAATCTGCTC

PRAME #28
H C S Q L T T L S F Y G N S I S I S A L Q S L L Q H L I G L
CACTGTAGCCAACCTGACAACCTCAGCTTTTACGGAACTCCATCTCCATCTCCGCCCTCCAGTCCCTGCTCCAGCATCTGATTGGCCTC

PRAME #33
M V W L S A N P C P H C G D R T F Y D P E P I L C P C F M P
ATGGTCTGGCTCAGCGCTAACCTTGCCCTCACTGTGGCGATAGGACATTCTATGACCCTGAGCCTATCCTCTGCCCTTGCTTTATGCCT

gp100In4 #1
A A S W S Q K R S F V Y V W K T W G E G L P S Q P I I H T C
GCCGCTAGCTGGAGCCAAAAGAGAAGCTTTGTGTATGTGTGGAAGACATGGGAGAGGGACTGCCTAGCCAACCCATTATCCATACCTGT

BAGE #2
L L Q A R L M K E E S P V V S W R L E P E D G T A L C F I F
CTGCTCCAGGCTAGGCTCATGAAGAGGAAGCCCTGTGGTCAGCTGGAGGCTCGAGCCTGAGGATGGCACAGCCCTCTGCTTTATCTTT

gp100In4 #3
V Y F F L P D H L S F G R P F H L N F C D F L A A
GTGTATTTCTTTCTGCCTGACCATCTGTCTTCGGAAGGCCTTTCCATCTGAATTTCTGTGACTTTCTGGCTGCC

PRAME #18
P Y L G Q M I N L R R L L L S H I H A S S Y I S P E K E R Q
CCCTATCTGGGACAGATGATCAATCTGAGAAGGCTCCTGCTCAGCCATATCCATGCTCCAGCTATATCTCCCCGAAAAGGAAGAGCAA

MAGE-3 #3
Q A P A T E E Q E A A S S S S T L V E V T L G E V P A A E S
CAGGCTCCCGCTACCGAAGAGCAAGAGGCTGCCCTCCAGCTCCAGCACACTGGTCGAGGTACCCCTCGGCGAAGTGCTGCCGCTGAGTCC

PRAME #6
Q A W P F T C L P L G V L M K G Q H L H L E T F K A V L D G
CAGGCTTGCCCTTTACATGCTCCCTCCCGCTCGGCTCTGATGAAGGGACAGCATCTGCATCTGGAACCTTTAAGGCTGTGCTCGACGGA

PRAME #12
L S T E A E Q P F I P V E V L V D L P L K E G A C D E L F S
CTGTCCACCGAAGCCGAACAGCCTTTTATTCCGTCGAGGTCTGCTGACCTCTTCTCAAGGAAGGCGCTTGCGATGAGCTCTTCTCC

NYNS01b #3
A E V P G A Q G Q Q G P R G R E E A P R G V R M A A R L Q G
GCCGAAGTGCTGGCGCTCAGGGACAGCAAGGCCCTAGGGGAAGGGAAGAGGCTCCAGAGGCGTCAGGATGGCCGCTAGGCTCCAGGGA

LAGE1 #5
G A P R G P H G G A A S A Q D G R C P C G A R R P D S R L L
GGCGCTCCAGAGGCCCTCACGGAGGCGCTGCCCTCCGCCAAGACGGAAGGTGTCCCTGTGGCGCTAGGAGACCCGATAGCAGACTGCTC

LAGE1 #4
G P R G A G A A R A S G P R G G A P R G P H G G A A S A Q D
GGCCCTAGGGGAGCCGAGCCGCTAGGGCTAGCGGACCCAGAGGCGGAGCCCTAGGGGACCCATGGCGGAGCCGCTAGCGCTCAGGAT

PRAME #3
L A G Q S L L K D E A L A I A A L E L L P R E L F P P L F M
CTGGCTGGCCAAAGCCTCTGAAAGACGAAGCCCTCGCCATTGCGCTCTGGAAGTGTCTCCAGAGAGCTCTTCCCTCCCTCTTCATG

GAGE-1 #4
E P A T Q R Q D P A A A Q E G E D E G A S A G Q G P K P E A
GAGCCTGCCACACAGAGACAGGATCCCGCTGCGCTCAGGAAGCGAAGACGAAGGCGCTAGCGCTGGCCAAGGCCCTAAGCCTGAGGCT

PRAME #11
P E A A Q P M T K K R K V D G L S T E A E Q P F I P V E V L
CCCGAAGCCGCTCAGCCTATGACAAAGAAAAGGAAAGTGGATGGCCTCAGCACAGAGGCTGAGCAACCCCTTTATCCCTGTGGAAGTGCTC

Figure 27 (Cont)

201/216

LAGE1 #6

G R C P C G A R R P D S R L L Q L H I T M P F S S P M E A E
GGCAGATGCCCTTGGAGCCAGAAGCCCTGACTCCAGGCTCCTGCAATGCATATCAATGCCTTTCTCCAGCCCTATGGAAGCCGAA

LAGE1 #9

P G A V L K D F T V S G N L L F I R L T A A D H R Q L Q L S
CCCGAGCCGCTCTGAAAGACTTTACCGTCAGCGGAAACCTCTGTTTATCAGACTGACAGCGCTGACCATAGGCAACTGCAACTGTCC

PRAME #31

E D I H G T L H L E R L A Y L H A R L R E L L C E L G R P S
GAGGATATCCATGGCACACTGCATCTGGAAAGGCTCGCCTATCTGCATGCCAGACTGAGAGAGCTCCTGTGTGAGCTCGGCAGACCCCTCC

GAGE-1 #6

D S Q E Q G H P Q T G C R C E D G P D G Q E M D P P N P E E
GACTCCAGGAACAGGGACACCTCAGACAGGCTGTGAGTGTGAGGATGGCCCTGACGGACAGGAAATGGATCCCCCTAACCCCTGAGGAA

TRP2IN2 #3

F V I G L R V W Q W E V I S C K L I K R A T T R Q P A A
TTCGTATCGGACTGAGAGTGTGGCAGTGGGAGGTCTCTCTGCAAACTGATTAAGAGAGCCACAACCAGACAGCCTGCCGCT

LAGE1 #2

D A D G P G G P G I P D G P G G N A G G P G E A G A T G G R
GACGCTGACGGACCCGAGGCCCTGGCATTCCCGATGGCCCTGGCGGAAACGCTGGCGGACCCGAGAGGCTGGCGCTACCCGAGGCAGA

MAGE-1 #12

P T G H S Y V L V T C L G L S Y D G L L G D N Q I M P K T G
CCACAGGCCATAGCTATGTGCTCGTGACATGCCTCGGCCCTCAGCTATGACGGACTGCTCGGCGATAACCAAAATCATGCCCAAACCGGA

MAGE-3 #9

F L L L K Y R A R E P V T K A E M L G S V V G N W Q Y F F P
TTCCTCTGCTCAAGTATAGGCTAGGGAACCCGTCACCAAGCCGAAATGCTCGGCTCCGTGGTGGCAATTGGCAATACTTTTTCCTT

GAGE-1 #9

T G I L W L L M N N C F L N L S P R K P A A
ACCGAATCCTCTGGCTCCTGATGAACAATGCTTTCTGAATCTGTCCCCAGAAAGCCTGCCGCT

MAGE-3 #8

E F Q A A L S R K V A E L V H F L L L K Y R A R E P V T K A
GAGTTTCAGGCTGCCCTCAGCAGAAAGTGGCCGAACTGGTCCACTTTCTGCTCCTGAAATACAGAGCCAGAGAGCCTGTGACAAAGGCT

MAGE-1 #18

V P D S D P A R Y E F L W G P R A L A E T S Y V K V L E Y V
GTGCTGACTCCGACCTGCCAGATACGAATTCCTCTGGGGACCCAGAGCCCTCGCCGAAACCTCCTACGTCAAGGTCTCGGAATACGTC

NYSOla #6

G C C R C G A R G P E S R L L E F Y L A M P P A T P M E A E
GGCTGTTGAGATGCGGAGCCAGAGGCCCTGAGTCCAGGCTCCTGGAATCTATCTGGCTATGCCTTTGCTACCCCTATGGAAGCCGAA

MAGE-3 #13

A T C L G L S Y D G L L G D N Q I M P K A G L L I I V L A I
GCCACATGCCTCGGCCCTCAGCTATGACGGACTGCTCGGCGATAACCAAAATCATGCCCAAAGCCGGAGTGTCTCATTTGTGCTCGCCATT

LAGE1 #3

G N A G G P G E A G A T G G R G P R G A G A A R A S G P R G
GGCAATGCCGAGGCCCTGGCGAAGCCGAGCCACAGGCGGAAGGGGACCCAGAGGCGCTGGCGCTGCCAGAGCCTCCGCGCCTAGGGGA

Artificial Protein:

APEEIIWEELSVMEVYDGREHSAYGEPRKLEEVPTAGSTDPPQSPQASAPPTTINFTRQTVWSGNRASLYSPPEPEAAQPMTKKRKVDGQIMPKAGL
LIIVLAIAREGDCAPEEKIWEIQVLDLRKNSHQDFWTVWSGNRASLYSPPELDVLLAQEVPRRWKIQVLDLRKNSHQDFWQAMLAQERRVPRAA
EVPGAQGGQGRGRQSPSVLSVLSLGVMLTDVSPPEPLQALLTQDLVQEKYLEYRQVPDSDPARYEFLWGPGRQPSSESSSREEBGPSTSCILESL
FRAVITAAMAAARAVFLALSQALLQARLMKESFPVSTFYDPEPILCPCFMPNAAIEMVEDPIGHLYIFATCLGLSYDGLLDNRRYVEPEMIGPMR
PEQFSDEVEPATPEEGEAGGFPPWLKVYYRVFVIGLRVQWQEVISCAAMERRRLWGSIQSRYISMSVNTSPRRLVEAALMETHLSSKRYTEAGGFPF
WLKVYYRAAMSLEQRSLHCKPBEALQAQEAALGLVCVQAATSSSSPLVLGTLEEVPTAGSTDPPQSPAELLLPRELFPPLFMAAFDGRHSQTLKAMV
ELSVLEVFEGRSDSILGDPKLLTQHFPVQESLQLVFGIDVKEADPTGHSYLVVTCGLSPDPQSPQGASSLPTTMNYPLWSQSYEDSSAAMQAEQG
GTGSGTGADGPGGPGIPDGPQGCFLPVFLAQPPSGQRRRAATWEGELPSQPIIHTCVYFPLPDHLSFGRPPSTSCILESLFRAVITKKVADLVGFLLL
KYRAAMQAEGRGTGSGTGADGPGGPGIPDGPQGDGPDGQEMDPNPNPEVKTPEEEMRSHYVAQISSCLQLSLMMITQCFLPVFLAQPPSGQERASA
TLQDLVFDECGITDDQLLALLPSLSLGDPIKLLTQHFVQENYLEYRQVPGSDPACAEALQAQEAALGLVCVQAATSSSSPLVLGTLEFYLAMPFATPME
ABLARRSLAQDAPPLPVBEAPRGVRMAARLQGAANRLEPEDGTALCFIFAAEQFSDEVEPATPEEGEPATQRQDPAQAQEGTMYPLWSQSYEDSSNQ
EEGPPSTPDLESNQEEGPPSTPDLESFQAALSRLKVAELVHVDLFLKEGACDELFSYLIBKVRKKNVLRILTIRLTAADHRQLQLSISCLQQLSL
LWMTAAMPLEQRSHQCKPREGLEARGEALGLVGADADGPGGPGIPDGPQGNAGGPGCAGATGGRYEFLWGPALVETSYVVLHMHVKISGGPHITN
CRLSEGDVMHLSQSPSVLSVLSLGNLYEYRQVPGSDPACYEFLWGPALVETSYVIFSKASSSLQLVFGIELMEVDPIGHLYIFQALYVDSLFPFL

Figure 27 (Cont)

202/216

RGRLDQLLRHVMNPLETISYIAQFISQFLSLQCIQALYVDSLFFLRGRIGQHLHLETFFKAVLDGLDVLVLAQEVPRPRWKFIIRLTAADHRQLQLSISSC
LQQLSLSLMNITCKKLLKIPAMPMQDITMILKMLVQDLSIEDLAGPRPHGGGAASGLNGCCRCGARGPESRLLKPKKVAIDLVGFLLLKKYRAREPVTKAEMLE
SVYIDGLGDNQIMPKTGLFIIVLVMIAEMGGSHISALQSLHLGLSLNTHLVYVPVLESYIAREBGDCAPEKKEWELSVLEVFEGRSDITDQLLR
HVMNPLETISITNCRLSEGDVHLSRALAETS YVKVLEYVIVKVSARVRFPPFSRLSNLTHLVYVPVLESYEDITHGLHLERLAYLAAMLMAQEAFL
MAQCGMLAAQCRHVRTPRAPHYKHCFFPEI PGKASESLQVLPGDIDVKEADTLVBVYTLGEVPAAESPDPPQSGOASSLPTHARLRLELCELGRPSMVVLSA
NPPCHGADRVMLTVSPPEYLALLERASITLQDLVFDECEDEGASADGQPEADSQEGQHPTQCECEBMSGLSVGNVWQYFFPVLISFKASSQQLLVF
GAAMSWRGRSTYRPRRYPVEPPEMIGPMRPYISMSVMTVSPRRLVELAGQSLKDLDEALAIYDGRHSAYGEPRKLLTDQLVQEKYLEYRQSCQLVFP
LAQAPSGORRAAVKVLHHMVKISGGPHISYPPHLHFWLREGEQLHITMPPSSPMEABLVRRIILSRDAAPLPRPGVLLKEFTVSGNIIITRLTAADHRQ
LQLSKMLKMLVQDLSIEDLEVTCTWKLP LTKAFESFLIIVLVMIAEMGGHAPKEEIRWELSVMEVEVTTCKWLPTLAKFSPYLGQMINLRLLLSGLE
ARBAIGLVGAQA PATEQEAASSSISYPLHBEWLREGEAAHIAHSSYISPEKEBQYIAQFISQFLSLQCLNAGGPGEGAGATGGRGPRGAGAAR
ASGPGGGPRGAGAARASGPGGAPRGPHGGAASGLNQASAPFTTINFTRQRPQSEGSSSREEBGPLARRSLAQDAPPLVPVGVLLKEFTVSGNIIIA
FDGRHSQTLLKAMVQNPFTCLPLGVMLKTVKSARVRFPPFSRLRAAREEBEGVAAGITDDQLLALLPSLHSCQSQTLTISFYGNSIVKTPPEEMRSHY
VAHQIWLWLLMNNCFNLISLQCLSLMNITQCFLVPVLAQAPSQYLIIEKVKKIRLNLCKKLIKIPAMPMQDIAREPVTKAEMLESYIKNYKH
CFPEIFGKASLVRRRIILSRDAAPLPRPGAVLKDFTVSGNLLHCSQTLTISFYGNSISISALQSLHQLILGLMVLSANPCPHCGDRTYDPEILPCPF
MLAASHVSKRSFVYVWKTNBGLPSQPIHTCLLQARLMKEBSPVVSWRLEPEDGTALCFIVYFPLPHLSFGPRFHLNFCDFLAEPYLGQMINLR
LHSHIAHSSYISPEKEBQAPATEBEQAASSSTLVEVTLGEVPAAESQAWPTCLPLGVLMKGQHLHLETFFKAVLDGLSTRAEQPPIVPEVLGDLF
LKEGACDELPSAEVPGAQOQCGPRGREAPRGVMAARLQGGAPRGPHGGAASQDGRCPGARSRLLRPRGAGAARGPRGAPRGPHGGAAS
AQDLAQSLKDEALAIALKELLPRELPLFPLMEPATQRQDPAQAQEGEDBGASAGQGPKPAEPAQAQPMTKKRVKVDGLSTREBQPFIPVEVLGRCP
GARRPDSRLQLHITMPPSPMEAREPGAVLKDFTVSGNLIIRLTAADHRQLQLSIEDITHGLHLERLAYLHARLRLELCELGRPSDQEGQHPTQGC
CEDGPDQEGEDPPNPEEFVIGLRVQWEVISCKLIRATTRQPAADAGDGGPGPIPDGPGNAGGPGEGAAGTGRPTGHSYLVLTCLGSLYDGLGDN
QIMPKTGFLLKKYRAREPVTKAEMLSVGVGNQYFFFTGILLWLLMNNCFNLNLSPRKPAABPQAALSRKVAELVHFLLLKKYRAREPVTKAEPDSDPAR
YIFNGPRALAEYSYVKVLEYVGCRCGARGPESRLLLEFYLAMPFATPMEARATCLGSLYDGLGDNQIMPKAGLLITVLAIGNAGGPGEGATGGRGP
RGAGAARASGPRG

Artificial DNA:

GCCCTGAGGAAGAGATTGGGAAGAGCTCAGCGTCATGGAAGTGATGACGGAAGGGAACACTCCGCTTATGGCGAACCAGAAAGCTCGAGGAAGT
 GCCTACCGCTGCTCACCAGCTCCCCCTCAGTCCGCCCAAGCGGCTAGCGCTTTCCCTACCACAATCAATTTCACAGGCAAAACCGTCTGGTTCGGCA
 ATAGGCGTAGCTCTACTCTTCCCTGAGCTCAGGCTCGGCAACCCATGACCAAAAGAGAAGGTGCAGCGACAGATTATGCCATAAGGCTGGCTCT
 CTGATTATCGTCTGGCTATCATTGCCAGAGAGGGAGACTGTGCCCCGTAGGAAAAGATTGGGAAGTCGAAGTGTGCAGCTCAGGAAAGACTCCCA
 CAAAGACTTTGGACAGTGGGAGCGGAAAACAGAGCTCCCTCTGTATAGCTTTCCCGAATCTGGATGTGCTCCTGCTCAGGAAGTGAGACCCAGAAGGT
 GGAAGCTCCAGGTCTGGATCTGAAAGAAATAGCCATCAGGATTCTGGCAGAGGACCTCTGGCTGCCAAGAGAGAAGGTTCCCCAGAGCCGCT
 GAGGTTCGCCGAGCCCAAGGCCAACAGGAACCCAGGACAGGACAGTCCGCCCTCGTGTCCAGCTCAGGCTCCTGTCTCCGTTCGGGCTCATGCTCAC
 CGATGTGTCCCCGAAACCCCTCAGGCTCTGCTCTGCACACAGATCTGGTCCAGGAAAAGTATCTGGAATACAGACAGGTCCCCGATAGCGATCCC
 CTAGGTATGAGTTTCTGTGGGCCCCTAGGCAACCTCCGAGGGAAGCTCCAGCAGAGGAGAGAGGACCTCCACCTCTGCAATTCTGGAAGAGCTC
 TTAGAGGCGGTACATCAAGCCGCTATGGCTGCCAGAGCCGCTTCTCTCGCTCAGGCTCAGCTCTCTGCAAGCCAGATGATGAAGGAAGAGTCCCC
 CGTGTGTGCCACTTTTAGCATCCGAAACCACTTCTGTGTCCCTGTTTCATGCCCAATGCCGCTATCGAACTGATGGAGTTCGACCTATCGGACACC
 TCTACATTTCTCGCTACCTGTCTGGGACTGTCTACGATTGCCTCTCGGGAAGCAATAGGAGATACGTCCAGCTCTCGGAATAGTTGGCCCTATGAGA
 CCGGAACAGTTTAGGCAATGAGTCTGAGCTGCCACCCGAAAGGAGGAGGCTGGCGAGTTCTTCTCGGTCCAGAGTGATTACTATAGTTTGT
 GATTGGCTCAGGCTCTGGCAATGGGAAGTGATTAGCTGTGCCGCTATGGAAGGAGAAGGCTCTGGGGAAGCATTAGTCCAGGTATATCTCCATGT
 CCGTGTGACCTCCCCAGAAAGGCTGGGAAGCGGCTCTGATGGAGACACACTCAGCTCACAAGATATACAGAGGAAGCCGAGGCTTTTCCCT
 TGGCTCAAGGTCTACTATTACAGAGCCGTATGTCTCTGGAACAGAGAAGCTCCATCTGAAGCTTAGGAAAGCCCTCGAGGCTCAGCAAGAGGCTCT
 GGGACTGGTCTGCGTCCAGGCTGCCAAGCTCCAGCTCCCCCTCTGTCTCGGCACACTGGAAGAGGTCCCCACCGGGAAGCAGAGACCTCCCC
 AAAGCGTCTGCCCTCGAGCTCTCGCTTAGGGAAGTTTCCCCCTCTGTTTATGCTGCTTTGACGGAAGCATAGCCAAACCTCAAGGCTATGGTC
 GAGCTCAGCGCTCTGGGAAGTTTGAAGGAAGGAAGACTCCATCTCGCGCATCCCAAAGCTCTGACAGCAGACTTTCGCTCCAGGAAGAGTCCCT
 GCAACTGGTCTTCGGAATCGATGTGAAAGAGGTGACCTTACCAGGACCTCAGCTCCTGCTCAGTCTCTGCGAAGTCTGCGGACTTCCCGATCAGT
 CCCCCAAGGCGCTAGCTCCCTGCCCTACCACAATGATTACCTCTGTGGAGCCAAAGCTCCAGCGACCCGAGATGTCTGCCCTCTGCAAGAGGCCAA
 GGCACAGGCGGAAGCAGGCGATGCCATGGCCCTGGCGGACCCGGAATCCCTGACGGACCCGAGCAGTGTCTCCCTCCCGTCTCTCTCGCCCAACC
 CCTAGCGGACAGAGAAGGGCTGCCACTGGGGCGAAGGCCCTCCCTCCAGCTATCATTCACATCGCTCTACTTTTCTCCCGATCACCTCTCA
 GCTTGTGACAGACCTTTAGCACAGCTGTATCTCTGAGTCCGTTTATGGGCTGTGATTACAAAAGGTGCGCGATCTGGTCCGCTTTCTGTCTCTG
 AATAACAGAGCCGCTATGCAAGCCGAAGGCGAGGACAGGCGAAGCAGGCGATGCCGATGGCCCTGGCGGAACCCGAATCTCTGAGAGCCCGG
 AGCGGACCGATGCGCAAGAGATGAGACCTCCCAATCCGAAGAGCTCAAGACAACCGAAGAGGAATGAGAAGCAATAGCTGCGCCAACTCTCA
 GCTGTCTGCAACAGCTCAGCTCCTCTGATGTGGAATTACCAATGCTTTCTGCTGTGTTTCTGGCTCAGCTCCCTCCGCGCAAGAGAGAGCTCCGCC
 ACATCTCAAGACTCTGTTTGAAGATTGCGGAATCAGACAGACTCAGCTCTGGCTCTGCTCCCTCCCTGCTCCCTGGGAGACCTTAAGAAACTCTG
 CACCAACACTTTGTGCAAGAGAAATTACTCTGAGTATAGCAAGTGCCTGCTCCAGCCCTGCTCTGAGGCTCTGGAAGCCCAAGGAAGCCCTCG
 GCCTGTGTGTGTGCAAGCCGCTACCTCCAGCTCCAGCCCTCTGGTCTGGGAACCCCTCGAGTTTATCTCTCGCATGCTCCCTTGCCACACCCATGGAG
 GCTGAGCTCGCCAGAGGCTCCGTGCTCAGGATGCCCTCCCTCCCGTCTGAGGAAGCCCTTAGGGAGTGAGAATGGCTGCGCAGACTGCAAGGCGC
 TGGCTGAGACTGGAACCCGAAAGCGAAGCCGCTCTGTGTTTCAATTTCTCGTCCGAGCAATTTCTCCGAGGAAGTGAACCCGCTACCCCTAGGAAG
 GCGAACCCGCTACCCAAGGCAAGACCTGCGCTGCCCCAAGAGGGAACCATGAATATCTCCCTCTGGTCTCAGCTCTACGAGACTCCAGCAATCAG
 GAGGAGAGAGGCGCTAGCACATCTCCGACCTCGAGTCCAACCAAGAGGAAGAGGACCTCCACCTTTCCGATCTGGAAGAGGAATCCAAGCCGC
 TCTGTCCAGGAAGGCTGGCTGAGCTCTGTCATGTGATCTGTTTCTGAAAGAGGAGGCTGTGACGAACTGTTTAGTCTTGTATGAGAAAGTGAAGA
 GGAAGAAGATGTGCTCAGGCTCACATTAGGCTCAGGCTCCGATCAGACAGACTCAGCTCAGATATTAGTCTCTGCTCCGACACTGTCCTGT
 CTCATTGTGATCAGACAGATATGCTCTGTGAAACAGAGAAGCCAACTGTAAGCCTGAGGAAGGCTCGAGGCTAGGGGAGAGGCTCTGGGACTGGT
 CGCGCTGACGCTGACGGACCCGAGGCTGGCATTTCCGATGGCCCTCGGGAACAGCTGCGGCAACCGGAGAGGCTGGCGCTACCGGAGGAGAT
 ACGAATTCTCTTGGGGACCAAGACCCCTCTGGGAACCTCTCATGCTCAGGCTCTGCATACATGTGTGAAATCTCCGCGGACCCCATACAAAC
 TGTAGGCTCAGCGAAGGCGATGTGATGCACTCAGCCAAAGCCCTAGCGTCAGCCAACTGTCCGTGCTCAGCTCAGCGGAAACTATCTGGAATACAG
 ACAGGTCCTCCGAGAGCATCCCGCTGTGATGTAGTTTCTGTGGGGCCCTAGGCTCTGGTGCAGACAGCTATGTGATTTCTCCAGGCTAGCTCCA
 GCTCTCAGCTCTGTGTTGGCATGAGCTCATGGAAGTGATGCCATTGGCCACTCTGATATFTCTCAGGCTCTGTATGTGATAGGCTCTTCTTCTG
 AGAGGCAGACTGGATCAGCTCCTGAGACACGTCATGAATCCCCCTCGAGACACTGCTACATTGCCCCAATTCAGAGCAATCTCTCAGCCCTCAGTG
 TCTGCAAGCCCTCTACGCTGCACTCCCTGTTTTTCTCAGGGGAAGGCTCGGCCAAACCTCCACTCGAGACATTCAAGAGCCGCTCTGGAATGGCCTGC
 ACCTCTGCTCTGCCCAAGAGGTCAAGCTTAGGATGGAATCTATTAGGCTCACCGCTCCGATCAGACAGCTCCAGCTCAGCATTAGTCTCTCTGC
 CTCAGCAACTCTCCCTGTCTCATGTGGATCATAGCTGTGAAGAACTGAAATCTTTGCAATGCCCATCGAGATACAAATGATTCTGAAATGTT

Figure 27 (Cont)

203/216

CCAGCTCGACTCCATCGAAGACCTCGGCGCTCCAGAGGCCCTCAGGAGCGCTGCTCCGGCTCAACGGATGCTGTAGGTGTGGCGCTAGGGGAC
CCGAAAGCAGACTGCTCAAGAAAGTGGCTGACCTCGTGGGATTCCTCTGCTCAAGTATAGGGCTAGGGAAACCGCTACCAAAGCCGAAATGCTCGAG
TCCGTGATTATCATGATGGCTCTCGGAGACAATCAGATTATGCTTAAGACAGGCTTTCTGATTATCGTCTGCTCATGATTGCGATGGAGGGAGGCCA
TAGCATTAGCGCTCTGCAAGCCCTCTGCAACACCTCATCGGACTGTCCAACCTCACCATGTGCTCTACCTCTGTGCTCTGGAAGCTATATCGCTA
GGGAAGCGGATGCTCGCTCCCGAAGAGAAAATCTGGGAGGAATGCTCCGTGCTCGAGGTCTTGAAGGCAGAGAGGATAGCATGACCAACTGCTCAGG
CATGTGATGAACCTCTGGAACCCCTCAGCATTACCAATTCAGAGCTGTCCGAGGGAGACGTATGCTATGCTGCTCAGGGCTCTGGCTGAGACAAGCTA
TGTGAAGGTGCTCGAGTATGTGATTAAGGTGAGCGCTAGGGTCTAGGTTTTTCTTTCCCTCCCTGAGAAGCAATCTGACACAGCTCTGTATCCCGTCC
CCCTCGAGTCCCTACGAAGACATTACCGAACCTCCACCTCGAGAGACTGGCTTACCTCGCGCTATGCTCATGGCTCAGGAAGCCCTCGCTTTCTG
ATGGCCCAAGGCGCTATGCTCGCGCTCAGGAAGGAGAGTGCTTAGGGCTAAGAATTAACAACACTGTTTCCCTGAGATTTTGGAAAGGCTAGCGA
AAGCTTCAGCTCTGTGTTGGCATGTAGCTCAAGGAAGCCGATACCTCGTGGAGTGACACTGGGAGAGGTCCCGCTCCGGAAGCCCTGACCTC
CCCAAGCCCTCAGGGAGCCCTCAGCCCTCCCAACACACGCTAGGCTCAGGAACTGCTCTGCGAATGGAAGGCTAGCATGTGTGGCTGTCCGCT
AATCCCTGTCCCATTTGCGGAGACAGAGTGATGTGACAGAGCTCAGCCCTGAGCTCTGCAAGCCCTCTGGAAGGGCTAGCGCTACCTCCAGGA
TCTGGTCTTCGATGAGTGTGAGGATGAGGGAGCCCTCGCGCGGACAGGGAACCAACCCGAGGCGATAGCCAGAGCAAGGCCATCCCAACCCGAT
GGGAATGCGAAGAGATGCTGGGAAGCGTGTGGGAACCTGGCAGTATTTCTTCCGTCTCTTTAGCAAAGCCCTCAGCTCCCTGCAACTGGTCTTC
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TAGCATGAGCGCTGGAAGAGCCCTAGGAGACTGGTGGAGCTCGCGGACAGTCCCTGCTCAAGGATGAGGCTCTGGCTATCGCTTAGCATGGCAGAG
AGCATAGCGCTTACGGAGAGCTTAGGAACCTGCTCAACCAAGACCTCGTGCAAGAGAAATACCTCGAGTATAGGCAACAGTGTTCCTCCCGCTTC
TCGCGCAAGCCCTCAGGAGAGAGGCTGCGGTGAAGGTGCTCCACCATATGGTCAAGATTAGCGGAGGCCCTCACATTAGCTATCCCGCTCT
GCATGAGTGGGTCTCAGGAAGGCGAACAGCTCCACATTACCATGCCCTTTAGCTCCCGCATGGAGCTGAGCTGTGAGAAGGATTCTGTCCAGG
ATGCGCTCCCTCCCGAGACCCGAGTGCTCTGAAAGAGTTTACCCTCAGCGGAAACATTCTGACAAATCAGACTGACAGCCGCTGACCATAGGCA
CTGCAACTGTCCAAGATGATCTCAAGATGGTGCAACTGGATAGCACTGAGGATCTGGAAGTGACATGCATGGAACTGCTCACTCCGCAAAAT
CTCCTTCTCTCATCATTTGTGCTGTGATGATGCTATGGAAGCGGACACGCTCCGGAAGAGAAATCTGGGAGGAAGTGTCCGTGATGGAGGTGAGG
TCACCTGTACTGGAAGCTCCCACTGGCTAAGTTTAGCCCTTACCTCGGCAAAATGATTAACTCAGGAGACTGCTCTGTCCGAGGAGCTAGGA
GCCAGAGGCGAAGCCCTCGGCTCGTGGAGCCCAAGCCCTGCGACAGAGGAACAGGAAGCCCTAGCTCCAGCTCCATCTCTACCTCCCTCCCA
CGAATGGGTCTGAGAGAGGAGAGGAGCCGCTCACTTACGCTAGCTCTTACATTAGCCCTGAGAAAGAGGAACAGTATATCGCTCAGTTTACCT
CCCAGTTTCTGTCTCTGCAATGCTCGGCAATGCGGAGGCCCTGGGAGGCGGAGCCACAGCGGAAGGGGACCCAGAGGCGCTGGCGCTGCGCA
GCCTCCGCGCTGGCGGAGGCCCTAGGGAGCGGCTAGGGCTAGCGGACCGGAGCGGAGCCCTAGGGGACCCCATGGCGGAGCCGCTAG
CGGACTGAATCAGGGAGCCCTCGGCTTTCCCAACCATTAACCTTACCAGACAGAGACAGCTAGCGAAGGCTCCAGCTCCAGGGAAGAGGAGGCC
CTCTGGCTAGGAGAGCCCTCGGCAAGAGCGCTCCCGCTGTGCTGTGCTGCGCTCTGCTCAAGGAATTACAGTGTCCGCAATATCTCGCGCT
TTGATGTCAGACACTCCAGACACTGAAGCCATGGTGCAAGCGGCTTACCTGTCTGCTCTGGAGTGTCTCATGAAATCAAGTGTCTGCGC
CAGAGTGAGATTCTTTTCCCTAGCCCTCAGGGAAGCCGCTCTGAGAGAGGAAGAGGCGCTCGCGCTGCGCTTACCGATGACCAACTGCTCGCC
TCCTGCTAGCTCAGCCATTGCTCCAGCTCACCACACTGCTCTTATGGAATAGCATTTGTGAACCCCTGAGGAAGAGATGAGTCCCACTAT
GTGGCTCAGACAGGCTCTGTGGCTGCTCATGAATAACTGTTTCTCAACTCATCTCCAGCTGTCTGCAACAGCTCAGCTCTCTGATGTGGATTAC
CCAATGCTTTCTGCTCTGTGTTCTGGCTCAGGCTCCCTCGGCAAACTCAGCTCATCGAAAGGTCAAGAGAAAGAAAACGCTCTGAGACTGTTTGA
AAAAGCTCAAGATTTTCTGCTATGCTCTATGCAAGACATTGCGAGAGAGCTGTGACAAAGGCTGAGATGCTGGAAGCGCTCATCAAAACATATAGCAT
TGCTTTCCGCAAACTTTTGGCAAGCCCTCCCTGGTCAAGGAGAACTCTCAGCAGAGAGCGCTGCGCCCTGCTTAGGCTGGCGCTGTGCTCAAGGATTT
CAGAGTGTCCGCAAACTGCTCCACTGTAGCCAACTGCAACCCCTCAGCTTTTACGGAACCTCCATCTCCATCTCCGCTCCAGTCCCTGCTCCAGC
ATCTGATTGGGCTCATGCTGTGCTCAGGCTAACCCCTGCGCTCACTGTGGCGATAGGACATTCTATGACCTGAGCTATCTCTGCGCTGTCTTT
ATGCTCGCGCTGCTAGCTGAGCCAAAGAGAGGCTTTGTGTATGTGTGGAAGACATGGGAGAGGAGTGTCTAGCCAAACCTATTCATACCTGTCT
GCTCCAGCTAGGCTCAGTCAAGAGGAAAGCCCTGTGGTCAAGTGTGAGGCTCAGGCTGAGGATGGCAAGCCCTCTGCTTTATCTTTGTGTTTCT
TTCTGCTGACCATCTGTCTTGGGAAGCCCTTTCCATCTGAATTTCTGTGACTTTCTGGCTGCCCCCTATCTGGACAGATGATCAATCTGAGAAGG
CTCTGCTCAGCCATATCCATGCTCCAGCTATATCTCCCGGAAAGGAGAGCAACAGGCTCCCGCTACCGAAGAGCAAGAGGCTGCTCCAGCTC
CAGCACACTGGTGGAGGTCACCTCGGCGAAGTGCTGCGCTGAGTCCAGGCTTGGCTTTACATGCTCCCTCGGCGTCTGATGAAGGGAC
AGCATCTGCTATGGAACCTTTAAGGCTGTGCTCGACGAGTGTCCACGAAGCCGAACAGGCTTTTATTCCCGTGGAGGCTCTGGTGGACCTCTTC
CTCAAGGAAGGCGCTTGGATGAGCTTTCTCGCGGAAGTGCTTGGCGCTCAGGACAGCAAGGCTAGGGGAAGGGAAGAGGCTCCAGAGGCGT
CAGGATGGCGCTAGGCTCCAGGGAGGCGCTCCAGAGGCCCTCAGGAGGCGCTGCTCCGCTCAAGAGCGAAGGTGTCTCTGTGGCGCTAGGAGAC
CCGATAGCAGACTGCTCGGCTTAGGGAGCCGAGCGCTAGGGCTAGCGGACCAGAGGCGGAGCCCTAGGGGACCCCATGGCGGAGCGCTAGC
GCTCAGGATCTGGCTGGCCAAAGCCCTCTGAAAGACGAAGCCCTCGCCATTGCGCTCTGGAACCTGCTCCCAAGAGAGCTCTTCTCTCCCTCTCAT
GGAGCTGCCACACAGAGACAGGATCCGCTGCGCTCAGGAAGGCGAAGAGCGCTAGCGTGGCAAGGCCCTAAGCTGTGGCTCTCCGAAG
CCGCTCAGCTATGACAAAGAAAAGGAAGTGGATGGCTCAGCACAGAGGCTGAGCAACCTTTATCCCTGTGGAAGTGTCTGGCAGATGCTTGC
GGAGCTCAGAAAGCCCTGACTCCAGGCTCTGCAACTGCAATATCAAAAGCTTTCTCAGGCTTATGGAAGCCGAACCCGAGGCGCTCTGAAAGACTT
TACCGTCAAGCAAACTCTCTGTTATCAGACTGACAGCGCTGACATAGGCAACTGCACTGTCCGAGGATATCCATGGCACACTGCACTGGA
GGCTCGCTATCTGATGCTGAGAGAGCTCTGTGTGAGCTCGGAGAGCTCCGACTCCAGGAACAGGACACCTCAGACAGGCTGTGAG
TGTGAGGATGGCCCTGAGCGGACAGGAATGGATCCCTTAACTCAGGAATTCGTCTATCGGACTGAGAGTGTGGCAGTGGGAGGTCTCTCTGCAA
ACTGATTAAGAGAGCCACAACAGACAGCTTCCGCTGAGCTGACGAGCCGAGGCGCTGGCATTCGCGATGGCCCTGGCGGAACGCTGGCGGAC
CCGAGAGGCTGGCGTACCGAGGCGAGCCCAAGGCCATAGCTATGTGCTGTGACATGCTCGGCTCAGCTATGACGAGCTGCTCGGCGATAC
CAATCATGCCCAAAACCGGATTCCTCTGCTCAAGTATAGGGCTAGGGAACCGCTACCAAGCCGAATGCTCGGCTCGTGGTGGCAATTGGCA
ATACTTTTCCCTACCGAATCTCTGGCTCTGATGAACAATGCTTTCTGAATCTGTCCCGCAAAAGCCCTGCGCTGAGTTTTCAGGCTGCCCTCA
GCAGAAAGGTGCGCAACTGGTCTCACTTTCTGCTCTGAAATACAGAGCCAGAGAGGCTGTGACAAAGGCTGTGCTGACTCCGACTGCGAGATAC
GAATTCCTCTGGGAGCCAGAGCCCTCGCGCAAACTCTACGTCAAGGCTCTGGAATACGTGCGCTGTGTCAGATGCGGAGCCAGAGGCTGAGTC
CAGGCTCTGGAATTTCTATCTGGCTATGCTTTGCTACCCCTATGGAAGCCGAAGCCACATGCTCGGCTCAGCTATGACGAGCTGCTCGCGGATA
ACCAATCATGCCCAAGCCGAGCTCATCATTTGTGCTCGCAATGCGGAGGCCCTGGCGAAGCCGAGCCACAGGCGGAAGGGGACCC
AGAGGCGCTGGCGCTGCCAGAGCTCCGCGCTTAGGGG

Figure 27 (Cont)

204/216

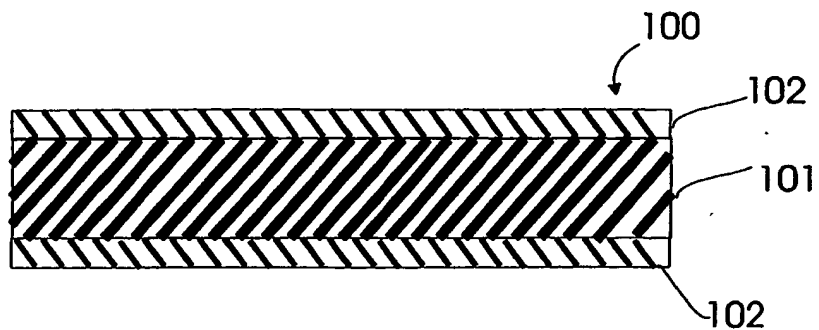


FIGURE 28

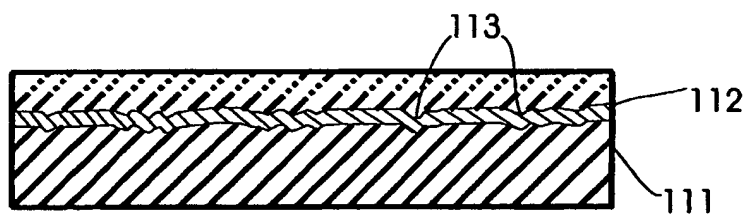


FIGURE 29

205/216

Cassettes for construction of a full-length HIV Savine**Cassette A1**

ggatccaccatGACAGGCCCTTGACAAAACGTCAGCACCGTGCAATGCACACACGGAATCAGACCCGTCGTGTCCA
CCCAACTGCTCCTGAATGGCTCCCTGAGAAGCCTCTACAATACCGTCGCCACACTGTGGTGCGTCCACCAAAGGAT
TGACGTCAGGGACACAAAGGAAGCCCTCGACAAAATCGAACTCGGCGATGGCGGAGGCGCTGAAAGGCAAGGCACC
TCCAGCTCCTTCAACTTTCCACAAATCACACTGTGGCAAAGGCCTCTGGTCACCGAACCCCTTCAGAAAAAGAATC
CCGATATGGTGATTACAGTACATGGACGATCTGTATGTGGGAAGCGATCTGGAATCGGACAGCATTTTACCAC
ACCCGATAAGAAACACCAAAAGGAACCACCATTCCTCTGGATGGGATACGAACTGCATCCCGATAGGTGGACCGTC
CAGCCTCTTAATTTCCCTCAGATTACCCTCTGGCAGCGTCCCCTCTGACAATCAAAATCGGCGGACAGCTCATAG
AGGCTCTGCTCGACACAGGCTCCTATGGCAGAAAGAAACGTAGGCAACGTAGACGCGCTCCTCAGAGCAGCAAGGA
TCACCAATACCTTATCTCTGAGCAACCCCTCTCCTTCTTTAGGGAAAACCTGGCTTTCCAGCAAGGTAAAGCCAGA
GAGTTTTCCAGCGAACAGACAAGAGCCAATAGCTCCGCCTCCAGGAAGAGCCCCCAAATCTCCGGCGAAAGCTCCG
TCATTCTGGGATCTGGCACCAAAAACGCGCTACTAGAAGAATCGAAGTGAAAGATACCAAGAGGCTTTTGATAA
GATTGAGGAGGTGCAAAAGAAAAGCGAGCAAAAGACACAACAGGCTGCCGCTAAAGCCGGATACGTCACCGATAGG
GGAAGGCAAAAGATTATCTCCCTGACAGAGACAACCAATCAGAAAACCGAACTGCATGCCATTCAAGAAGCCACTA
CCACACTGTTTTGCGCCAGCGATGCCAAAGCCTATGAGACAGAGGTCCACAATGTGTGGGCCACACACGCTTGCGT
CCCCGCTGACGATACAGTGCTGGAGGAGATGAACCTCCCCGGAATGGAAGCCTAAGATGATTGGCGGAATCGGC
GGATTCAATTAAGGTGAGAAAAATCGGACCCGAAAACCTTACAATACCCCAATCTTCGCTATCAAGAAAAAGGACT
CCACCAATGAGGAAAGCTCGTGATTTCAGAGTTAGGATTATCAATATCCTCTACCAAAGCAATCCCTATCCTAG
CTCCGAAGGCTCCAGGCAAACCAGAAAGAATAGGAGAAGGAGATGGGGAGGCGAACGGGGTAGGGATAGGTCCGTG
AGACTGGTCAACGGATTCTTAGCCCTCGCTGGGACGATCTGAGAAACCTCTGCCTCTTCGAAAACCTCTGGGTCA
CCGTCTACTATGGCGTCCCGTCTGGAGAGAGGCTGCCACAACCCCTCTTCTGTGCCTCCGACGCTAAGGCTTACGC
TGCCATGGCTGGCAGAAGCGGCGGCACAGACGAAGAGCTCCTGAGGGCTATCAGAATCATTAACATTCTGTATCAG
TCCAACCCCTACCTTCCGCTAGTATGAGAATCAGAACCTGGAACAGCCTGGTCAAGCATCACATGCACATCTCCA
AGAAAGCCAAAGGCTGGTTCTATAGGCATCACTTTGAGGAGTCCGAGCTCGTGAATCAGATTATCGAAAAGCTCAT
CAAAAAGGAAAAGGTCTACCTATCATGGGTACCAGCCCACAAGGGAATCGGACAAACCAAGAGCTCCAGAAACAG
ATTATCAAAATCCAAAACCTTAGGGTCTACTATAGGGATAGCAGAGACCCCTATCTGGAAGGGACCCAAAAGCTTTG
AGGAAATCTGGAACAATATGACATGGATTGAGTGGGAGAGAGAGATTAGCAATTACACAAGCCAAATCTATAAGAT
TCTGAAACCCGAACCCACAGCCCCTCCGCTGAGAATTTAGATTGCGGTGAGGAACTACACCCCTCCCAAAAGCAA
GAGCAAAAGGATAAGGAGCAATACGATCAGATTCTTATTGAGATTGCGGCAAGAAAGCTATTGGTACGGTGCTCG
TGGGACCTACCCCTGTGAATATCATTGGCAGAATTTACGAAACCTATGGCGATACCTGGGAGGGCGTCGAGGCTCT
GATCAGAATCCTCCAGCAACTGATGTTTATCCATTTAGAAATCGGATGTTTTCATTGCCAAGTGTTTCTCACC
AAAGGTCTCGGCATTAGCCACGGAAGGAAAAGAGAAAACAGAGAAGGGGAGCTCCCCAAGCTGCCATGGACCCCG
TGGACCCCAAGCTGGAGCCTTGGAACACCCCTGGCTCCAGCCTAAGACAGCCTGTTACAAATGCTATTGCAAAAA
GTGCCCTAGCGAAGAGACAACCCCTAGCCAGAAACAGGAACAGAAAGACAAAGAACTCTACCCCTTTAGCCAGC
CTCAAGTCCCTGTTTGGCAATGACAATTTCAATATGTGGAAGAATGACATGGTGGAACAGATGCAAGAAGACATTA
TCTTACTATGGGACCAAGCCTCAAGCCTTGCGTCAAGCTCGACGTCGGCGATGCCTATTTCTCCGTGCCTCTGGA
TAAAAACTTCAGAAAGTATACCGCTTTCACAATCCCTAGCACAAACAATGAGCAACTGAAAGGCGAAGCCATCCAT
GGCCAAGTGAATTGCTCACCAGGCATTTGGCAACTGGATTGCACACACCTGGAGGGAAAGATTATCCCTAAGGTCA
AGCAATGGCCTCTGACAGAGGAAAAGATTAAGGCTCTGACTGAGATTTGCAAAGAGATGGAGGAAGAGGGAAAGAT
TAGCATGGATGACCTTACGTCGGCTCCGACCTGG

FIGURE 30

206/216

AGATTGGCCAACATAGGACCAAAATCGAAGAGCTCAGGGAACACCTCTGAAATGGGGACTCACCGAAACCACAAA
CCAAAAGACTGAGCTCCAAGCTATCCATCTGGCTCTGCAAGACTCCGGCTTAGAGGTCAACATTGTGACAGACATT
CCCGCTGAGACTGGTCAAGAGACCGCCTTTTTCATTCTGAAACTGGCTGGCAGATGGCCTGTGAAAGTCATTACA
CAGACAATGGCAGGACAAAGATTGAGGAACTGAGACCGCATCTGCTCAAATGGGGCTTCACAACCCCTGACAAAAA
GCATCAGAAAGAGCCTCCCTTTCTGTCTAGTGTCAAGAACTGACAGAGGATAAGTGGAACGAACCCAGAAAAATC
AAGAGACGCAGAGAAAAATCACACAATGAATGGCCATACTGCCACAGAGTCCCAGAATCAGCAAGACAGAAACGAAA
AGGAACTGCTGGAGCTCGACAAATGGGCAAGCCTCTGGAATTGGTTTAACATTACCGACACCGGAAATAGCTCCAA
AGTGTCCCAGAATTACCCTATCGTCCAGAATGTCCAAGGCCAAATGGTCCACCAACCCCTCTCCCCAGACTCATC
GGACTGAGAATCGTTTTTCGCTGTGCTCAGCATTATCAATAGGGTCAGGCAAGGCTATAGCCCTCTGTCTTCCAAA
CCCTCCCCCTCATCCATCTGCAATACTTTGACTGTTTTCGCTGACTCCACCATTAGGAGAGCCATCTTGGGACACAT
AGTGAGAAGGAGATGCGAATACGCTGTGGGACTCGGAGCCATGTTCTTGGCTTTCTGGGTGCCGTGGCTCCACC
ATGGGCGCTGCCTCCATGACACTGACAGTGCAAGCCTATGACCTAGCAAAGACCTCATTGCTGAGATTGAGAAAC
AGGGCCAGGGTCAGTGGACATTTAGATTTCCTCAAGAGCCTTTCAAAAACGGAACCGTCCTGGTCGGCCCTACACC
CGTCAACATCATCGGAAGGAACATGCTGACACAGCTTGGCCGCACTCTCAACTTTCCATTAGCAAAGGCAGCCCT
GCTATCTTTCAGTCCAGCATGCCACAGATTCTGGAGCCTTTTAGGATAAAAAACCCCTGAGATGGTCATCTATCAGT
ATCCTAGCCCTCTGACATTGCGATGGTGTTCCTCAAACTGGTCCCCGTGGACCCAGCGAAGTGGAAGAGATCAACAA
GGGCGAAAAACAATTGCCCCCTGTTTAGGAAATACACAGCCTTTACCATTCCCTCCATCAATAACGAAACCCCTGGC
ATTAGGTATCAGTATAACGTCTGCTCAGGGATGGGGAAGCACAATGGGAGCCGCCAGCATGACCCTCACCGTCC
AGGCTAGGCTACTGCTCAGCGGAATCGTCCAGCAACAGAGCAATCTGCTGGAGGAGAATAGGGAAATCCTCAGAGA
GCCTGTGCATGGCGTCTACTACGATCCCTCCAAGGATCTGGTCTGAAATCCAAAAGCAAGGCAGAGAGGAACTG
TCCACCATGGTGGATATGGGAACTACGACCTCGGAGTGGACAATAACCTCGCCGCTATTAGAATCCTGCAACAGC
TCATGTTTCACTTTAGGATTGGCTGCCAGCACTCCAGGATTGGCATCATCCGTGAGAGAAGGGCCAGAGCTCC
CAGGAAAAAGGGATGCTGGAAGTGTGGCAGAGAGGGACACCAGATGAAGGATTGCACTGAGAGACAGGCTAACTTT
CTGGGAAAGGATGCCAGACTGGTTATCAAAACCTATTGGGGACTGCATACCCGTGAGAGAGACTGGCACCTCGGCC
ATGGCGTCAGCATTGAGTGGAGGATAAGGGAAAGGGCTGAGGATAGCGGCAACGAAAGCGAAGCGACACAGAAGA
GCTCAGCACATTGGTGGACATGGGCAATTACGATCTGTCTAGCCCTGCCCCAGGGGACCCGATAGGCTGGAGAGA
ATCGAAGAGGAAGGCGGAGAGCAAGGCAGAGGCAGAAGCGTCAGGCTCGTGAATGGCAGAGAGGTGAGGAAGTCA
ATGAGGGAGAGAATAACTGTCTGCTTCACCCCTATCAGTCAACATGGCATGGAAGACGAAGAGAGAGAGGTCAATAG
CGATATCAAAGTGGTCCCCAGAAGGAAAGCCAAAATCATTAGGGATTACGGAAAGCAAATGGCTGGCGATGACTGT
GTGGCCAGCTTCTCTTCCGAGCAAACAGGGGCTAACTCTCTACAAGCAGAAAGCTGGGAGACGGAGGCGGAGCCG
ACAGACAGGGAACAAGCTCCAGCTGTTTCAATTGCGGCAAAGAGGGACACATTGCCAAAACTGTAGGGCCCCCTCG
CAAGAAAGGTTGTTGGAATGCGGAAAGGAAGGCCATCAAATGAAAGACTGTACCGAAAGGCAAGCCAATTTCTCTC
GGCAAAATCTGGCCCTCCAACAAAGGCAGACCCGGAACCTTTCTCAAAGCAAATGGCTCTGGTATATCAAAATCT
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CCGAGACCTCGATAAACATGGCGCTATTACAAGCTCCAATACCGCTGCCAATAACGCTGACTGTGTCTGGCTGAAG
GCTGTGCCATGACACCCCTGGAGATCATCGCTATCGTCGCCTTTATCGTCGCCCTCATCATAGCCATTGTGGTCT
GGACAATCGTCTACATTGAGTATGTCGACTgaagatctgaattc

Figure 30 (Cont)

207/216

A2 fragment

ggatccaccATGACAGGCCCTTGACACAAACGTGAGCTCCGTGCAATGCACACACGGAATCAAACCCGTCTGTGTCCA
CCCAACTGCTCCTGAATGGCTCCCTGAAAAGCCTCTACAATACCGTCGCCACACTGTGGTGTGTCCACCAAAGGAT
TGAGGTCAAGGACACAAAGGAAGCCCCTGACAAAATCGAACTCGGCGATGGCGGAGGCGCTGAAAGGCAAGGCACC
TCCAGCTCCATCAACTTTCCACAAATCACACTGTGGCAAAGGCCCTCTGGTCACCGAACCCCTTCAGAAAAGAGAATC
CCGAAATGGTGAATTTACCAGTACATGGACGATCTGTATGTGGGAAGCGATCTGGAAATCGGACAGCATTTTACCAC
ACCCGATAAGAAACACCAAAGGAACCACCATTCCTCTGGATGGGATACGAACTGCATCCCGATAGGTGGACCGTC
CAGCCTTTTAATTTCCCTCAGATTACCCCTCTGGCAGCGTCCCCTCGTGACAATCAAATCGGCGGACAGCTCATAG
AGGCTCTGCTCGACACAGGCTCCTATGGCAGAAAGAAACGTAGGCAACGTAGACGCGCTCCTCAGAGCAGAAAGGA
TCACCAATACCCCTATCTCTGAGCAACCCCTCTCCTTCTTTAGGGAAAACCTGGCTTTCCAGCAAGGTAAAGCCAGA
GAGTTTTCAGCGAACAGACAGGAGCCAATAGCTCCGCCCTCAGGAAGAGCCCCCAAATCTCCGGCGAAAGCTCCG
TCATTCTGGGATCTGGCACCAAAAACGCCGCTACTAGAAGAATCGATGTGAGAGATACCAAAGAGGCTCTGGATAA
GATTGAGGAGGAGCAAAAACAAAGCAAGCAAAAGACACAACAGGCTGCCGCTAAAGCCGGATACGTACCGATAGG
GGAAGGCAAAAGATTATCTCCCTGACAGAGACAACCAATCAGAAAACCGAACTGCATGCCATTCAAGAAGCCGATA
CCACACTGTTTTGCGCCAGCGATGCCAAAGCCTATGACACAGAGGTCCACAATGTGTGGGCCACACACGCTTGCGT
CCCCGCTGACGATACAGTGTCTGGAGGAGATGAACCTCCCCGAAAATGGAAGCCTAAGATGATTGGCGGAATCGGC
GGATTCAATTAAGGTGAGAAAGATCGGACCCGAAAACCCCTTACAATACCCCAATCTTCGCTATCAAGAAAAGAACT
CCACCAATGGAGAAAAGCTCGTGGATTTCAGAATTAGGATTATCAAATCCTCTACCAAAGCAATCCCTATCCTAG
CTCCGAAGGCACCAGGCAAACAGAAAGAATAGGAGAAGGGGATGGGAGGCGAACAGGGTAGGGATAGGTCCGTG
AGACTGGTCAACGGATTCTTAGCCCTCGCCTGGGACGATCTGAGAAGCCTCTGCCTCTTCGACAACCTCTGGGTCA
CCGTCTACTATGGCGTCCCCGTCTGGAGAGAGGCTAACACAACCCCTCTCTGTGCCTCCGACGCTAAGGCTTACGC
TGCCATGGCTGGCAGCAGCGGCAGCACAGACGAAGAGCTCCTGAAGGCTGTCAGAATCATTAAAGATTCTGTATCAG
TCCAACCCCTTACCCCTTCGCTAGTATGAAAATCAGAACCTGGAAGAGCCTGGTCAAGCATCACATGTACATCTCCA
AGAAAGCCAATGGCTGGTTCTATAGGCATCACTTTGAGGAGTCCGAGGTCGTGAATCAGATTATCGAAAAGCTTAT
CAAAAAGGAAAAGGTCTACCTATCATGGGTACCAGCCACAAGGGAAATCGGACGAACCAAAGAGCTCCAGAAAACAG
ATTATCAAATCCAAAACCTTTAGGGTCTACTATAGGGATAGCAGAGACCCTATCTGGAAGGGACCCAAAAGCCTTG
AGGAAATCTGGAACAATATGACATGGATTCACTGGGAGAGAGAGATTAGCAATTACACAAACCTAATCTATAAGAT
TCTGAGACCCGAACCCACAGCCCTCCCGCTGAGAATTTGGATTTCGGTGAGGAACTACACCCTCCCAAAAGCAA
GAGCCAAAGGATAAGGAGCAATACGATCAGATTATTATTGAGATTTGCGGCAAGAAAGCTATTGGTACAGTGTCTCG
TGGGACCTACCCCTGTGAATATCATTGGCAGAAATTTACGAAACCTATGGCGATACCTGGGAGGGCGTCGAGGCTCT
GATCAGAATCCTCCAGCAACTGATGTTTATCCATTTAGAATCGGATGTTTTATTGCCAAGTGTGTTTTCTCACC
AAAGGTCTCGGCATTAGCCACGGAAGGAAAAAGAGAAAAACAGAGAAGGCGAGCTCCCCAAGCTGCCATGGACCCCG
TGGACCCCAACCTGGAGCCTTGGAACACCCCTGGCTCCAGCCTAAGACAGCCTGTAACAAATGCTATTGCAAAAA
GTGCCCTAGCGAAGAGACAACCCCTAGCCAGAAACAGGAACAGAAAGACAAAGAACTCTACCCCCCTTTAGCCAGC
CTCAAGTCCCTGTTTGGCAATGACAATTTCAATATGTGGAAGAATAACATGGTGGAACAGATGCAAGAAGACATTA
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TAAAAACTTCAGAAAGTATACCGCTTTACAATCCCTAGCACAAACAATGAGCAACTGAAAGGCGAAGCCATGCAT
GGCCAAGTGAATTGCTCACCAGGCATTTGGCACTGGATTGCACACACCTGGAGGGAAAGATTATCCCTAAGGTCA
AGCAATGGCCTCAGACAGAGGAAAAGATTAAAGCTCTGACTGAGATTTGCACAGAGATGGAGCAAGAGGGAAAGAT
TAGCATGGATGACCTCTACGTCCGCTCCGACCTGGAGATTGGCCAACATAGGACCAAATCGAAGAGCTCAGGGCA

Figure 30 (Cont)

208/216

CACCTCCTGAGATGGGGACTCACCGACACCACAAACAAAAGACTGAGCTCCACGCTATCCATCTGGCTCTGCAAG
ACTCCGGCTTAGAGGTCAACATTGTGACAGACATTCGCCGCTGAGACTGGTCAAGAGACCACCTATTTCAATTCTGAA
ACTGGCTGGCAGATGGCCTGTGAGAATCATTCACACAGACAATGGCAGGACAAAGATTGAGGAACTGAGACCGCAT
CTGCTCAAATGGGGCTTCAACCCCTGACAAAAAGCGTCAGAAAGAGCCTCCCTTTCTGTCTAGTGTCAAGAAAC
TGACAGAGGATAAGTGGAAACAAACCCAGAAAAATCAAGGGACACAGAGAAAATCACACAATGAATGGCCATGCTGC
CACAGAGTCCCAGAATCAGCAAGACAGAAACGAAAAGGAACTGCTGGAGCTCGACAAATGGGCAAGCCTCTGGAAT
TGGTTTAACATTACCGACACCGGAAGTAGCTCCAAGTGTCCAGAATTACCTTATCGTCCAGAATCTCCAAGGCC
AAATGGTCCACCAACCCATCTCCCCAGACTCGTCGGACTGAGAATCATTTTCGCTGTGCTCAGCATTATCAATAG
GGTCAGGCAAGGCTATAGCCCTCTGTCTTCCAAACCCCTCACCTCATCCATCTGTATTACTTTGACTGTTTCGCT
GACTCCACCATTAGGAGAGCCATCCTTGGACACAGAGTGAGCAGGAGATGCGAATACGCTGTGGGAATCGGAGCCA
TGTTCCCTTGGCTTTCTGGGTGCCGCTGGCTCCACCATGGGCGCTGCCTCCATCACACTGACAGTGCAAGCCTATGA
CCCTAGCAAAGACCTCATTGCTGAGATTAGAAAACAGGCTCAGGATCAGTGGACATATCAGATTTTCCAAGAGCCT
TTCAAAAACGGAACCGTCTGGTGGGCCCTACACCCGTCAACATCATCGGAAGGAACCTGCTGACACAGATAGGCT
GCACCTCAACTTTCCATTAGCAAAGGCAGCCCTGCTATCTTTCAGTCCAGCATGACACAGATTCTGGAGCCTTT
TAGGAAACAAAACCTGACATGGTCATCTATCAGTATCCTAGCCCTCTGACATTCCGATGGTGTTCAAACTGGTC
CCCGTGGACCCAGCGAAGTGAAGAGACCAACAAGGGCGAAAACAATTGCCTCCTGTTTAGGAAATACACAGCCT
TTACCATTCCCTCCACCAATAACGAAACCCCTGGCATTAGGTATCAGTATAACGTCCTGCCTCAGGGATGGGGAAG
CACAATGGGAGCCGCCAGCATGACCTCACCGTCCAGGCTAGGCAACTGCTCAGCGGAATCGTCCAGCAACAGAAC
AATCTGCTGGAGGAGAATAGGGAATCCTCAAAGAGCCTGTGCATGGCGTCTACTACGATCCCTCCAAGGATCTGA
TCGCTGAAATCCAAAGCAAGGCACAGAGGAACTGTCCGCCTTGGTGGATATGGGAAACTACCACCTCGGAGTGG
CAATAACCTCGCCCTATTAGAACTCTGCAACAGCTCATGTTCACTTTAGGATTGGCTGCCAGCACTCCAGG
ATTGGCATCATCCGTGAGAGAAGGGCCAGAGCTCCAGGAAAAGGGATGCTGGAAGTGTGGCAAAGAGGGACACC
AGATGAAGGATTGCACTGAGAGACAGGCTAACTTTCTGGGAAAGGATGCCAGACTGGTTATCAAAACCTATTGGGG
ACTGCATACCGGTGAGAGAGACTGGCACCTCGGCCATGGCGTCAGCATTGAGTGGAGGACAAGGGAAAGGGCTGAG
GATAGCGGCAACGAAAGCGAAGGCGACAGAGAAGAGCTCAGCACAAATGGTGGACATGGGCAATTACGATCTGTCTA
GCCCTGCCCCCAGGGGACCCGATAGGCTGGAGAGAATCGAAGAGGAAGGCGGAGAGCAAGACAGAGACAGAAGCGT
CAGGCTCGTGAATGGCAGTGAGGCGGAGGAAGTCAATAAGGGAGAGAATAACTGTCTGCTCCACCCTATGAGTCAA
CATGGCATGGAAGACGAAGACAGAGAGGTCAATAGCGATATCAAAGTGGTCCCAGAAAGGAAAGCCAAATCATT
GGGATTACGGAAAGCAAATGGCTGACGATGACTGTGTGGCCGGCTTCTCTTCCGAGCAACAAGGGCTAACTCCCC
TGCAAGCAGAAAGCTGGGAGACGGAGGCGGAGCCGACAGACAGGGAACAAGCTCCAGCTGTTTCAATTGCGGCAAA
GAGGGACACATTGCCAAAAGCTGTAGGGCCCCCTCGCAAGAAAGGTTGTTGGAATGCGGAAGGGAAGGCCATCAAA
TGAAAGACTGTACCGAAAGGCAAGCCAATTTCTCGGCAAAATCTGGCCCTCCAAAAAGGCAGACCCGGAAACTT
TCTCAAAGCAAATGGCTCTGGTATATCAAAATCTTTATCATGATCGTCGGTGGACTGATTGGCCTCAGGATTATC
TTTGCCGTCTGTCCATCATTAACGGGGCCGTGAGCCGAGACCTCGATAAACATGGCGCTATTACAAGCTCCAATA
CCGCTGCCAATAACCTGACTGTGTCTGGCTGGAGGCTGCTGCCATGACACCCCTGGAGATCATCGCTATCGTCGC
CCTTATCGTCGCCCTCATCATAGCCATTGTGGTCTGGACAATCGTCTACATTGAGTATGTGCGActgaagatctgaa
ttc

Figure 30 (Cont)

209/216

B1 fragment

ggatccaccATGCTCGAGAATATGCTCACCCAAATCGGATGCACACTGAATTTCCCTATCTCCCCATTGAGACAG
TGCCTGTGAAACTGAAACCCGGAATGGATGGCGCCGCCACCTTTAGGCCTGGCGGAGGCAATATCAAAGACAATTG
GAGAAGCGAACTGTATAAGTATAAGGTCGTGAAGATTAAGCCTCTGGGAATCACATGGATTCCCGAATGGGAGTTC
GTCAACACACCCCCACTGGTCAAGCTATGGTATCAGCTGGAGAAAGACCCTATCGTTGGCGTTGAGCCTCAGGATC
TCAACACGATGCTGAATCTTGTTAGGAGGCCATCAGGCCGCTATGCAAATGCTGAAAGAGACAATCAATGAGGAAGC
CTCTGTCTGTTTCTGGATGGCATTGACAAAAGCTCAAGAGGAACATGAAAAGTATCACTCCAACCTGGAGGACAATG
GCCAACGACTTTAATCTGATGAAGCATCTCGTCTGGGCCTCTAGGGAGCTGGAGAGATTGCTCTGAATCCCAGCC
TGCTGGAGACATCCGAAGGCTGTCAGCAAATTGCTGAGGAAGAGATTATCATTAGGTCCGAGAATTTACAAAACAA
TGTCAAAACCATTATCGTCCAACCTCAACGAAAGCGTCGAGATTAACATGGGCGCTAGGGCTAGTGTCTCAGAGGC
GGCAAGCTGGACGCCCTGGGAAAAGATTAGGCTCAGGCCCTGGCGGAAAGAAAAGTATAGGCTCAAGGAGAAGGGAG
GCCTGGAGGGACTGGTTTACTCCAAAAGAGGCAAGACATTCTGGATCTGTGGGTGTATAACACACAGGGATTAC
TAGATGGGGAACCATGATCCTCGGCTTGTTGATTATCTGTAGCGCCAGCGAGAATCTGTGGGTGACAGTGTATTAC
GGAGTGCCTGTGTGGAGGAGACAGCTCCTGTCCGGCATTGTGCAACAACAAAATAACCTCCTGAGGGCTATCGAAG
CCCAACAGCATCTGCTCCAGCTCACCGTCTGGGTGAGGCATTTCCCCAGGCCTTGGCTCCACGGCCTGGGACAGTA
CATCTATGAGACATACGGAGACACATGGGCGGGAGTGGAAGCCCTCACAGCCCTCATCACACCCAAAAGATTAGG
CCTCCCTCCCATCCGTGAAAAGCTCACCGAAGACAGATGGAATGAGCCTCAAAGACATATAGCGCTGGCGAAA
GGATTATCGATATCATTGCATCCGACATTCAGACTAAGGAACTGCAAAAGCAAATCCTAAAGATTGAGAAATTCGC
TGTGTTTATCCATAACTTTAAGAGGAAGGGAGGCATTGGCGGCTACTCCGCCGGAGAGAGAATCATTGACATTATC
GCCACCGATATCATTCCCGTGGGCGAAATCTATAAGAGATGGATCATTCTGGGACTCAACAAAATCGTGAGAATGT
ATCTACCCGTCAGCATTCTGGATATCAGAGTGAGACAGGGATACTCCCCCTCAGCTTTCAGACACTGTGCCCCG
TCCCAGAGGCCCTGACAGACTCGGAGGCATTGAGGAAGAGTCCAGCCAGGACCATCAGTATCCCATTTCCGAAACAG
CCTCTGCCTCAGACAAGGGGAGACAATCCCAAGACCTAAGGAAAGCAAAAGGCTAGTGGAGGGGTGAGTCCA
TGAATAAGGAACTGAAAAGATTATCGGACAGGTCAGGGACCAGGCTGAGCACCTGAAAACCGCTGTGCAAATGGC
TGCCATGCAGATGCTCAAGGATACCATTAACGAAGAGGCTGCCGAGTGGGACAGAGTCCATCCCGTCCATGCCGGG
CCCGTTCCCCCTCTCACCGAGATTTGTAAAGAAATGAAAAAGAAGGCAAAATCTCCAAGATTGGCCCTGAGAATC
CCTATAACACACCCCATCTTTGCCATTCAAGTGAGAGAGCAAGCCGAACACCTCAAGACAGCCGTCCAGATGGCAGT
CTTCATTACAAATTTCAAAGGAGAGGCGGAATCGGAGGCAAAAGAAAGATAGCACAAAGTGGAGGAACTGGTA
GACTTTAGGGAGCTCAACAAACGTACACAGGATTTCTGGGAGGTCCAGCTCGGCTTTTGGCTCTGGCTGGGATG
ACCTCAGGAGCCTGTGTCTGTTTCTAGCTATCACAGACTGAGAGACTTTATCCTCATCGTTGCCAGAATCTGCCGACA
TAGCAGAATCGGCATCACTAGGCAACGTAGAGGTAGGAACGGCGCCTCCAGTTCGCTGCCCCCAAAATCTCCTTC
GACCCCATTTCCCATTCATTATGCGCTCCCGTGGCTTCGCTATCCTCAAGTGTAAAGATAAGAACTTCAATGGCG
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CCTCGCCGATCAGCCTAGCCTCTATCCTCCCTTAGCTTCCCTGAAAAGCCTCTTCGGAAACGATCCCTTATCCCAA
GCCGCTAGAAGGGCTATCCTCGGCCATATAGTCAGGAGAAGGTGTGAGTATCAGTCCGGACACAATAAGGTCCGGCT
CCCTGCAATACCTCGCACTCAGTCAACCCACAACCGCTTGCTACAAGTGTACTGTAAGAAATGTTGCTTCCACTG
TCAGGTCTGCTTCTGAAGAAGGGACTGGGAATCAGGGATTACGGAAAGCAAATGGCTGGCGATGACTGTGTGGCC
AGCAGGCAAGACGAAGACGCAGCCAAGTACCATAGCAATTGGAGAACCATTGGCAATGAGTTTAACCTCCCCCTA
TCGTCCCTAAGGAAATCGTCGCAAATTGCAATAAGTGTAAAGAAATGGAACTGCTGGAGGAACTGAAACA
TGAAGCCGTGAGACACTTTCCAGACCCCTGGCTGCATGGCCTCGGTCAACACGATATCATTAGCCTCTGGGATCAG

Figure 30 (Cont)

210/216

TCCCTGAAACCCCTGTGTGAAACTGACACCCCTCTGCGTCACCCTCAACTGTACCAATGCCAATCTGATGAAGAGAT
ACTCCACCCCAAGTGGACCCCCGATCTGGCTGACCAACTGATTACCTCCACTATTTGATTGCTTTGCCGATAGCGC
AATCCATCCCATCGGCCAACACGGAATGGAGGATGAGGATAGGGAAGTGCTGAAATGGAAATTCGATAGCCATCTG
GCTCTCAGGCATATCGCTTCTAGTCCTATCGATACCGTCCCCGTCAAGCTCAAGCCTGGCATGGACGGACCCAAAG
TGAAACACTGGCCCCCTACCGAAGAGAAAATCAAAGCCATTGGCCCTAGCAACAAGGGAAGGCTGGCAATTTCCC
GCAGTCCAGGCCTGAGCCTACCGCACCCCCAGCCGAGAGCTTTAGATTCCGCATTAGCAAAAAGGCTAAGGGATGG
TTTTACAGACACCATTACGATAGCCGACACCCTAAGGTCAGCTCCGAGGTCCACATTCCCCTCGGCATGATGACCG
CTTGCCAAGGCGTCGGCGGACCCAGTCACAAAGCCAGGGTACTGGCAGAGGCTATATCCCAGGTGAACAACGCTAA
CATTCCTCCCATTGTGGCCAAAGAGATTGTGGCAAAGTGTGACAAATGCCAGCTCAAGAGTGAGGCTATTACGGA
CAGGTGAAGTGTAGCCCTTCCGAGGGAACAAGACAGACTAGGAAGAACAGACGTAGAAGGTGGCGTGGCAGGCAAA
GGCAAATCCACTCCATCTCCGAGAGGATTCTGGGACAGATGAGGGAACCCAGAGGCTCCGACATTGCCGGTACTAC
AAGCACACTGCAAGAGCAAATCGCATGGATGACAAGCAATCCCCCTAGCATTCAACAAGAGTTTGGCATTCCCCTAT
AACCCTCAGTCCCAGGGCGTCGTGGAAAGCATGAACAAAGAGCTAAAGAAAATCATTGGCAGACAGGAGATCCTCG
ATCTCTGGGTCTACCATACCCCAAGGCTATTTCCCTGACTGGCAGAATTACACACCCGACCCGGAGTCAGATACCC
TAGCAGAGAAAGACAGAGACAGATTCAATCTATTAAAGCAATGGATTCTCAGCAACTGCCTCGGCAGATCCGCTGAG
CCTGTGCCTCTGCAACTGTATAAGACACTGAGAGCCGAACAGGCTACCCCAAGAGGTCAAGAATTGGATGACCGAGA
CACTGCTCGTGCAAAACGCTAACCCCTGACTGTGAGAGAGTGTATCTGGCTTGGGTCCCCGCTCATAAAGGCATTGG
CGGAAACGAACAGGTGGACAACTGGTCAGCGCTGGCATTAGGAAAACAGACCCTAACCCCTCAGGAAATCCATCTG
GAAACGTCACCGAGAACTTTAACATGTGGAAAAACGATATGGTGGAGCAAATGCATGAGGCTGGCTATGCCATTCT
TGAAATGCAATAACAAAAGGTTCAACGGAAGTGGACCCAGTAAGAATGTGTCCACCGTCCAGTGTACCCATGGCCT
AGAGCTCAAGAATAGCGCTATCTCCCTGCTCAACGCTACCGCTATCGCTGTGGCTGGGTGGACCGATAGGGTTATC
GAAGTGGTTAGTCCCGGCATCCCAAAGTGTCCAGCGAAGTGCATATCCCTCTGGGAGACGCTAGGCTCATCATT
GGACATACTGGGGCCTCCACACAGGCGCTGCTATGGGCGGTAAATGGTCCAAGTGTCCCTCGTCCGATGGCCCGC
AGTGAGAGAGAGAATCAGACAGACACCCCTGCCGCTGAGGGAGTGCTCAAGACCGCAAGTACTCTAGGAAGAGG
GGTGCCCATACCAATGACGTCAAGCAACTGACAGAGGCTGTGCAAAAGATTGCCACAGAGTCTAGCTGGGAGGGTC
TGAAATACTGGGGGAATCTGCTCCAGTACTGGGGCCAGGAAGTGAATACTCCGCCGTGAGCCTCTGAATGCCAC
AGCCATTGAGCTGCTGAGAAAGAAAGCTGGACCGTCAACGATATCCAAAAGCTCGTGGGAAAGCTCAACTGGGCA
TCCCAGATTTACCCGGAAGAGCCATTGAGGCTCAGCAACACATGCTGCAACTGACAGTGTGGGGCATTAAAGCAAC
TGCAAGCCAGAGTGCTCGCCATTGAGAGATACCTCGCCCTCCAGGATAGCGGATTGGAAGTGAATATCGTCACCGA
TAGCCAATACGCTCTAGGCATCATTCAGGCTCAGCCTGACAAAAGCGAAAGGGAAATCTCCAATATACCAATCAG
ATTTACAAGATCCTCACCGAATCTCAAATCAACAGGATAGGAATGAGAAAGACCTCCTGGCTCCCAAAAGGCTA
AGAGAAGGGTCGTGCAAAAGGGAAGCGTGCCGTGGCATTGGCGCTATGTTTCTCGGATTCTCGGCGCTGCCAA
ACCCAAAATGATCGGAGGCATTGGAGGCTTTATCAAAGTCAGGCAGTATGACCAAATCCTTATCGAAATCTGTGGA
AACAAAGGCTATCTCTACCATAGGCTCAGGGATTTCAATCTGATCGTCGCTAGGATTGTGGAAGTGTCTGGCCGTA
GCTCCCTGAAAGGCCTCCAGAGAGGCACACTGAATGCCCTGGGTGAAAGTGATTGAGGAAAAGGGATTAGTCCCGA
AGTGATTCCCATGTTTTCCGCTCTGTCCGAGGGAGCCACACTCGAGtgaagatctgaattc

Figure 30 (Cont)

211/216

B2 fragment

ggatccaccATGCTCGAGAATATGCTCACCCAAATCGGATGCACACTGAATTTCCCTATCTCCCCATTGACACAG
TGCCTGTGAAACTGAAACCCGGAATGGATGGCGCGCCATCTTTAGGCCTGGCGGAGGCAATATGAAAGACAATTG
GAGAAGCGAACTGTATAAGTATAAGGTCGTGAAGATTAAGCCTCTGGGAATCACATGGATTCCCGAATGGGAGTTC
GTCAACACACCCCCACTGGTCAAGCTATGGTATCAGCTGGAGAAAGAGCCTATCGTTGGCGCTGAGCCTCAGGATC
TCAACACGATGCCGAATACTGTAGGAGGCCATCAGGCTGCTATGCAAATGCTGAAAGACACAATCAATGAGGAAGC
CGCTGTCTCTGTTTCTGGATGGCATTAAACAAAGCTCAAGAGGAACATGAGAAGTATCACTCCAACCTGGAGGACAATG
GCCAACGACTTTTAATCTGATGAAGCATCTCGTCTGGGCCCTCTAGGGAGCTGGAGAGATTCTGCTCTGAATCCCGGCC
TGCTGGAGACATCCGAAGGCTGTAAAGCAAATTGCTGAGGAAGAGATTATCATTAGGTCCGAGAATTTACAAAACAA
TGTCAAAACCATTTATCGTCCACCTCAACGAAAGCGTCGAGATTAACATGGGCGCTAGGGCAAGTGTCCTCAGCGGC
GGCAAGCTGGACGCTGGGAAAAGATTAGGCTCAGGCTGGCGGCAAGAAAAAGTATAGGCTCAAGGAGAAGGGAG
GCCTGGACGGACTGATTTACTCCCAAAAGAGGCAAGACATTCTGGATCTGTGGGTGTATAACACACAGGGATTAC
TAGATGGGGAACCTTGATCCTCGGCTTGGTGATTATCTGTAGCGCCAGCGAGAATCTGTGGGTGACAGTGTATTAC
GGAGTGCCTGTGTGGAGGAGACAGCTCCTGTCCGGCATTGTGCAACAGCAAATAACCTCCTGAGGGCTATCGAAG
CCCAACAGCATCTGCTCCAGCTCACCGTCTGGGTGAGGCATTTCCCCAGGCCTTGGCTCCACAGCCTGGGACAGTA
CATCTATGAGACATACGGAGACACATGGTTCGGGAGTGGAAGCCCTCAAAGCCCTCATCAAACCCAAAAAGATTAAAG
CCTCCCTCCCATCCGTGAAAAAGCTCACCGAAGACAAATGGAATAAGCCTCAAAGACATATAGCGCTGGCGAAA
GGATTGTGATATCATTGCAACCGACATTGAGCTAAGGAAGTCAAAACCAAATCATAAAGATTGAGAATTTTCGC
TGTGTTTATCCATAACTTTAAGAGGAAGGGAGGCATTGGCGGCTACTCCGCCGAGAGAGAATCATTGACATTATC
GCCAGCGATATCGTTCCCGTGGGCGATATCTATAAGAGATGGATCATTCTGGGACTCAACAAAATCGTGAGAATGT
ATTCACCCGTCAGCATTCTGGATATCAGAGTGAGACAGGGATACTCCCCCTCAGCTTTCAGACACTGATGCCCGC
TCCAGAGGCCCTGACAGACTCGAACGCATTGAGGAAGAGTCCAGGCAGGACCATCAGTATCCCATTTCCGAACAG
CCTCTGTCTCAGACAAGGGGAGACAATCCACAGACCCTAAGGAAAGCAAAAGGCTAGTGGAGTGGTTCGAGTCCA
TGAATAAGGAACTGAAAAAGATTATCGGACAGGTCAGGGACCAGGCTGAGCACCTGAAAACCGCTGTGCAAATGGC
TGCCATGCAGATGCTCAAGGATACCATTAACGAAGAGGCTGCCGAGTGGGACAGAATCCATCCCGTCCATGCCGGA
CCCATTGCCCCCTCTCACCGAGATTTGTAAAGAAATGGAAAAAGAGGCAAAATCTCCAGGATTGGCCCTGAGAATC
CCTATAACACACCCGCTCTTTGCCATTCAAGTGAGAGACCAAGCCGAACACCTCAAGACAGCCGTCAGATGGCAGT
CTTCATTCACAATTTCAAAGGAAAGGCGGAATCGGAGGCAAAAAGAAAGATAGCACAAAGTGGAGGAAACTGGTT
GACTTTAGGGAGCTCAACAAACGTACACAGGATTTCTGGGAGGTCAGCTCGGCTTTTCGGCTCTGGCTTGGGATG
ACCTCAGGAGCCTGTGTCTGTTTCTAGCTATCACAGACTGAGAGACTTTATCCTCATCGTTGCCAGAACCTGCCGACA
TAGCAGAAATCGGCATCACTAGGCAACGTAGAGGTAGGAACGGCTCCTCCAGGTCCGCTGCCCCCAAATCTCCTTC
GACCCCATTTCCATTCACTATTGCGCTCCCGCTGGCTTCGCTATCCTCAAGTGTAACAATAAGACATTCAATGGCG
AAAAGGATTGGCATCTGGGACAGGGAGTGTCCATCGAATGGAGAAAGAAAGCTATAGCACACAGGTGGACCCTGA
CCTCGCCGATCAGCCTAGCCTCTATCCTCCCTTAGCTTCCCTGAAAAGCCTCTTCGGAAACGATCCCTCATCCAA
GCCGCTAGAAGGGCTATCCTCGGCCAAATAGTCAGGAGAAGGTGTGAGTATCAGTCCGGACACAATAAGGTCCGGCT
CCCTGCAATACCTTGCCTCAGCCAACCCAAAACCGCTTGCTACAAGTGTTACTGTAAAGAAATGTTGCTACCACTG
TCAGGTCTGCTTCTGAAAGAGGGACTGGGAATCAGGGATTACGGAAAGCAAATCGCTGGCGCTGACTGTGTGGCC
AGCAGGCAAGACGAAGACGCAGCCAAGTACCATAGCAATTGGAGAACCATGGCCAGTGAGTTTAACCTCCCCCTA
TCGTGCTAAGGAAATCGTCGCAAGTTGTGATAAGTGTAACGAATGGACACTGGAACCTGCTGGAGGAACTGAAACA
TGAAGCCGTGAGACACTTTCCAGACCCCTGGCTGCATGGCTCGGTCAACACGATATCATTAGCCTCTGGGATCAG

Figure 30 (Cont)

212/216

TCCCTGAAACCCTGTGTGAAACTGACACCCCTCTGCGTCACCTCAACTGTACCAATGCCAATCTGCTGAAGAGCT
ACTCCACCCAAGTGGACCCCGATCTGGCTGACCATCTGATTACCTCCACTATTTTCGATTGCTTTTCCGATAGCGC
AATCCATCCCATGGGCTTACACGGAATGGAGGATGAGGAAAGGGAAGTGCTGAAATGGAAATTCGATAGCCATCTG
GCTCTCAGGCATATCGCTTCTAGTCTATCGATACCGTCCCCGTCAAGCTCAAGCCTGGCATGGACGGACCCAAAG
TGAAACAGTGGCCCCCTCACCGAAGAGAAAATCAAAGCCATTTGGCCTAGCAACAAGGGAGGGCTGGCAATTTCTT
GCAGTCCAGGCCTGAGCCTACCGCACCCCGAGCGAGAACTTTAGATTTCGGCATTAGCAAAAAGGCTAAGGGATGG
TTTTACAGACACCATTACGAAAGCCAACCCCTAAGGTGAGCTCCGAGGTCCACATTCCCCTCAGCATGATGACCG
CTTGCCAAGGCGTCGGCGGACCCAGTCAAAAGCCAGGGTACTGGCAGAGGCTATGTCCCAGGTGAACAACGCTAA
CATTCCTCCCATTGTGCCCAAAGAGATTGTGGCAAACCTGTGACAAATGCCAGCTCAAGGGTGAGGCTATGCACGGA
CAGGTGGACTGTAGCCCTTCCGAGGGATCAAGACAGGCTAGGAAGAACAGACGTAGAAGGTGGCGTGAGAGGCAAA
GGCAAATCCGCGCCATCTCCGAGTGGATTCTGGGACAGATAAGGGAACCCAGAGGCTCCGACATTGCCGGTACCAC
AAGCACACTGCAAGAGCAAATCGCATGGATGACAAACAATCCCCCTGGCATTAAAGCAAGAGTTTGGCATTCCCTAT
AACCTCAGTCCCAGGCGCTCGTGGAAAGCATGAACAAAGAGCTCAAGAAAATCATTGGCAGACAGGAGATCCTCG
ATCTCTGGGTCTACAATACCCAAGGCTTTTTCCCTGACTGGCAGAATTACACACCCGACCCGGAATCAGATACCC
TAGCAGAGCAAGACAGAGACAGATTCTATGCTATTAGCGAAAGGATTCTCAGCAACTTCTCAGGACACCCGCTGAG
CCTGTGCCTCTGCAACTGTATAAGACACTGAGAGCCGAACAGGCTACCCAAGAGGTCAAGAATTGGATGACCGACA
CACTGCTCGTGCAAAACGCAAACCCCTGACTGTGAGAAAGTGTATCTGGCTTGGGTCCCCGCTCATAAAGGCATTGG
CGGAAACGAACAGGTGGACAAACTGGTCAGCGCTGGCATTAGGAAAACAGACCCTAACCTCAGGAAATCGATCTG
GAAAACGTACCGAGAACTTTAATCATGTGGAAAAACAATATGGTGGAGCAAATGCAAGAGGCTGGCTATGCCATTCT
TGAAATGCAATAACAAAAAGTTCAACGGAAGTGGACCCCTGTAAGAATGTGTCCACCGTCCAGTGTACCCATGGCCT
AGAGCTCAAGAAATAGCGCTGTCTCCCTGTCTCAACGCTACCGCTATCGCTGTGGCTGAGTGGACCGATAGGGTTATC
GAAGTGGTTTCACTCCAGCATCCCAAAGTGTCCAGCGAAGTGCATATCCCTCTGGGAGACGCTAGGCTCGTCATTA
AGACATACTGGGCGCTCCACACAGGCGCTGCTATGGGCGGTAAATGGTCCAAGTGTCTCCCTCGTCCGATGGCCCGC
AGTGAGAGAGAGAATCAGACAGACACCCCTGCCGCTGAGGGAGTGCTCAAGACCGGCAAGTACTCCAGGATGAGG
AGTGCCCATACCAATGACGTCAAGCAACTGACAGAGGTTGTGCAAAAGATTGCCACAGAGTCTAGCTGGGAGGGTC
TGAAATACTTGTGGAATCTGCTCCTGTACTGGGCGCTGGAAGTGAAGAACTCCGCCGTGAGCCTCCTGAATGCCAC
AGCCATTGTGCTGCCTGAGAAAGAGGCTGGACCGTCAACGATATCCAAAGCTCGTGGGAAAGCTCAACTGGGCA
TCCAGATTTACGCCGGAAGAGCCATTGAGGCTCAGCAACACTTGCTGCAACTGACAGTGTGGGGCATTAAAGCAAC
TGCAAGCCAGAGTGCTCGCCATTGAGAGATACCTCGCCCTCCAGGATAGCGGATCGGAAGTGAATATCGTCACCGA
TAGCCAATACGCTCTAGGCATCATTAGGCTCAGCCTGACAAAAGCGAAAGGGAATCTCCAACATATACCAATCAG
ATTTACAAGATCCTCACCGAATCTCAAAATCAACAGGATAGGAATGAGCAAGAACTCCTGGCTCCACAAAGGCTA
AGAGAAGGGTCGTGCAAGGGGAAAGCGTGCCGTGGCATTGGCGCTATGTTTTTCGATTCTCGGCGCTGCCAA
ACCCAAAATGATCGGAGGCATTGGAGGCTTTATCAAAGTCAGGCAGTATGACCAAAATCCTTATCGAAATCTGTGGA
CAGAAGGCTATCTCCTACCATAGGCTCAGGGATTTATTCTGATCGTCGCTAGGATTGTGGAAGTGTCTGGCCATA
GCTCCCTGAGAGGCCTCCGGAGAGGCACACTGAATGCCTGGGTGAAAGTGGTTGAGGAAAAGGGATTCAATCCCGA
AGTGATTCCCATGTTTACCGCTCTGTCCGAGGAGCCACACTCGAGtgaagatctgaattc

Figure 30 (Cont)

213/216

C1 fragment

ggatccaccATGCTCGAGAGCAACACACCCGCTAATAATGCCGATTGCGCGTGGCTGAAAGCCCAGGAAGAGGAAG
AAGTGGGATTTCTGTGAGACCCCAAGTGCTAGAGCTTGGAGGGCTATCCTCAACATTCCCAGGAGGATTAGGCA
AGGCTTTGAGAGAGCCCTCCTAGCCGCCGAATGGGACAGGGTTACCCCTGTGCACGCTGGCCCTGTGCTCCCGC
CAAATGAGAGAGCCAGAGGAAGCGATATCGCTGGCACAAACCCTCAGGCCCATGACATATAAGGCCGCTATTGACC
TCAGCTTGTTCCTGAAAGAGAAAGGCGGACTGGAAGGCCTCATCTATAGCAAGAAAGCTGCTATGGAACAGGCTCC
CGAAGACCAAAGCCCTCAGAGAGAGCCTTACAATGAGTGGACCCTGGAGCTCCTGGAAGAGCTCAAGAAAGAGGCT
CAAGGCCAATGGACCTACCAAATCTTTCAGGAACCCCTTAAAGAATCTGAAAACCGGAAAGTATTCCAGAATGAGAA
GCGCTCACACAACTGGATGACAGAAACCCCTCCTGGTCCAGAATGCCAATCCCGATTGCAAGTCCATCCTCAGGGC
TCTGGGAACCGGAGCCACACTGGAAGAGCCTGAGGTTCATCCCTATGTTCTCAGCCCTCAGCGAAGGCGCTACCCCC
CAAGACCTGAATACGATGCTCAACATCGTCAGCGGACACCAATCCACCCTCCAGGAACAGATTGGCTGGATGACAA
ATAACCCCTCCCATCCCTGTGCGGAGAGATTTACAAAAGGTGGATTATCCTCGGCCCTGACTAGAATCCCCCATCCCGC
CGCCCTCAAGAAAAAGAAAAGCGTCACCGTCTGGATGTGGGAGACGCTTACTTCAGCGTCCCCCTCGACGAAGAC
CAAAAGGAAACCTGGGAGGCTTGGTGGACGGAATACTGGCAGGCTACCTGGATTCTTGAGTGGGAGTTTGTGAATA
CCCCTCCCCTCGTGTTCCTCGGATTGGCATAACTATACCCCTGGCCCTGGCATAAGGTATCCCCTCACCTTTGGATG
GTGCTTTAAGCTCGTGCTGTGGACCCCAAACGTGGTACCAACTGGAAGGAACCCATTGTGCGAGCCGAAACC
TTTTACGTGGACGGAGCCGCAACAGAGAGACAAAGCTCGGCCAAAACGTCCAGGGACAGATGGTGCATCAGGCTA
TTAGCCCCCAGGACCCCTCAACGCTTGGGTCAAGGTCTGGAAGAGAAAGCCTTTAACGAAACCGAAGTGCATAACGT
CTGGGCTACCCATGCCTGTGTGCGTACCGATCCCAATCCCAGAGATTCTCCTGGAGAATGTGACAGAGCTCAAG
GATCAGAACTCCTCGGCATTGGGGATGCTCCGGCAAAATCATTGCAACCACTGTGCCTTGGAAACAGCTCCT
GGTCCAACCAAGCTGGCCATAACAAAGTGGGAAGCCTCCAGTATCTGGCTCTGACGGCTCTGATTAAGCCTAAGAA
AATCAAACCCCTCTGCCTAGCGTTAAGACAATCATTGTGCATCTGAATGAGTCCGTGGAAATCAATTGCACAAGG
CCTAACATAACACAAGGAAAGCCGCGCTAGTGAAGTACGGAATAAGTCCAAACAGAAAACCCAGCAAGCTGCCG
CCGATACAGGCGACTCCAGCCAGGTCAGCCAAAATATCCCATTTGTGTCAAACCTTACCTCCACCACTGTGAAAGC
CGCTTGTGTGGTGGGCCAATATCAAACAGGAGTTTGGAAATCCCTTACAATCCCCAAAGCCAAACATTTCTATGTGGAT
GGCGCTGCCAATAGGGAACCCAACTGGGAAAGCGGGCTATGTGACAGACAAAGGCAGACAGAAAGTCATTAGCG
GAATCTGGCAGCTCGACTGTACCCATCTGGAAGGCAAAGTCATTCTGGTAGCCGTCCACGTCCGCTCCGGCTACAT
TGAGGCTGAGGTGGCAATGAGCAAGTGGATAAGCTCGTGAGTTCCGGAATCAGAAAGGTGCTATTCTCGACGGA
ATCAATAAGGCTCAGGAAGAGCACGAAGTCAGGGAAAGGATTAGGCGAACCCTCCCGCTGCTGAAGGCGTCGGCG
CTGTCTCCCAGGATCTGGATAAGTACGGAGCCCTCACCTCCACAAGCGGAACCCAAAGTCCCAGGGAACCTGAAAC
TGGCGTCCGCAACCCCTCAGATTTTGGGAGAGTCCAGCGTTGTCTCGGCTCCGGCTCCATCGTCATCTGGGGTAAA
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TTACTGTGCCCCCTCTAGCTGGATGGGCTATGAGCTCCACCCTGACAGATGGACAGTGCAACCCATCGTGCTCCCC
GAAAAGGACTCCTGGACAGTGAATGACATTGAGAAATCAATTCTGAGAGCCCTCGGCCCAGGCGCTTCCCTGGAGG
AAATGATGACAGCATGTGAGGAGTGGGAGGCCCTGGCCATAAGGCTAGAGTGTATTACAGAGACTCCAGGGACCC
CATTTGGAAAGGCCCTGCCAACTGCTCTGGAAAGGCGAAGGCGCTGTGGTCATCCAAGACATTAAGATTGGAGGC
CAACTGATAGAAGCCCTCCTGGATACAGGAGCCGATGACACCGTCTGGAAGATATGAATCTGCCCTGGCAAGTGGG
GAATCAAACAGCTCCAGGCTAGGGTCTGGCTATCGAGAGGTATCTGAAAGATCAACAGTTTCTGGGACTCTGGGG
CTGTAGCGGAAAGGCTGCTATGGAACAGATGGCAAGTGTATCGTCTGGCAAGTGGACAGGATGAAGATTAGG

Figure 30 (Cont)

214/216

ACATGGAATAGCCTCGTGAAACACCATATGTATATATCTGTACCACAACCGTCCCCTGGAAGTCCACCTGGAGCA
ATAAGTCCTTCGAAGAGATTTGGAATAACATGACCTGGATTCAATGGCTGATTCTCGCTATCGTCGTGTGGACCAT
TGTGTATATCGAATACAAGAACTGCTCAGGCAAAGGAGAATCGATAGGCTCATCAAAAGGCTCAACCCTGGCCTC
CTGGAACCGCTGAGGGATGTAAACAGATCCTGGAACAGCTCCAGCCCGCCCTCCAGACAGGCACCGAAGAGCTCT
CTAGTAGAAAGCTCCTGAAACAGAGAAAGATTGACAGACTGATTGAGAGAATCAGAGAGAGAGCCGAAGACTCCGG
CAATGAGTCCGAGGGAGACACACCCGGAATCAGATACCAATACAATGTGCTCCCCAAGGCTGGAAGGGCTCCCCA
CCCATTTTCCAAAGCTCCATGACCCAAATCCTCATGATGCAAAGGGGAAACTTTAAGGGACAGAAAAGGATTATCA
AGTGCTTCAACTGTGGAAGGAAGGCCATCTCGCTAGGAATTGCAGACCTCCCCTAGAGAGACTGAACCTGGATTG
CTCCGAGGATAGCGACACCTCCGGCACACAGCAAAGCCAAGGCACAGAGACAGAAGTGGGACTCGTGGCTGTGCAT
GTGGCCAGCGGATATATCGAAGCCGAAGTGATCCCTGCCGAAACTGGACAGGAAACCGCTTACTTTATCCTCAAGA
TTAAGCCTGTGGTCAGCACACAGCTCCTGCTCAACGGTAGCCTCGCTGAAGAGGAAATCATTATCAGAAGCGAAAA
CTTTACCGATAACAACTGGTCGGCAAACCTGAATTGGGCTTCCCAAATCTACGCTGGCATCAAAGTGAAGCAACTG
TGTAAGCTCCTGAGAGGCACCAAAGCCCTCACTCCTCTGTGTGTGACACTGAATTGCACAAACGCTAACCTCATCA
ATGTGAATGCTGCTCAAAACAGAGGCGATAACCTACCGGTCCCGAAGAGTCCAAGAAAGAGGTCCGCTCCAAGAC
AGAGACAGACCCCTTGTGACGCCGCCCTAGCTCCAACCTTCTGGGAAGGTCTGCCGAACCCGTCCCCCTCCAGCCC
CCCCCTCTGGAAGGCTCCACCTCGACTGTAGCGAAGACTGTGGCGAACTGGATAAGTGGGCCTCCTGTGGAAGT
GGTTCAATATACCAACTGGCTGTGGTACATTAAGATTTTCATTATGATTGTGGGAGGCAATAAGATTGTGAGGAT
GTACTCACCTGTCTCCATCCTCGACATTAAGCAAGGCCCTAAGGAACCTTCAGGGATTACGTGGACAGATTTCGCT
AAGCTCCTGTGGAAGGGAGAGGGAGCCGTCGTGATTGAGGACAACCTCCGACATTAAGGTCTGCGCCAGGAGAAAGG
CTAAGATTATCGAACTGAATAAGAGAACCCTAAGACTTTTGTGAAGTGCAACTGGGAATCCCTCACCTGCTGGACT
GAAGAAGAAAAAGTCAGTGACAGTGGCCGCTATGAGAGTGAAAGAGACACAGATGAAGTGGCCCAATCTGTGGAAG
TGGGGACAATGATTCTGGGACTGGTCATCATTTGCTCCGCTCCATTAAAGGTGAGACAGCTCTGCAAACCTGCTCA
GGGTACAAAGGCTCTGACAGAGATTGTGACACTGACAGAGGAAGCCGAACTGGAAGTCTCATATGGAAGTTGA
CTCCCGCCTCGCCCTGAGACATATCGCCAGGGAAGTGCATCCCGAGTTCTACAAAGACTGCGCTGCTGTGAGCTC
CTGGGACGCTCCAGCTCAAGGGACTGCAAAGGGGATGGGAAGGCCTCAAGTATTTGTGGAACCTCCTGCAGTATT
GGGCTCTAGCCTGGGGCAACTGCAACCTGCTCTGAAAACCGGATCAGAGGAAGTGAAGTCCCTGTATAACACAAT
CGTACCCTCTGGTGTGTGCATCAGGAGCTCTACAAATACAAAGTGGTCAAAATCAAACCCCTCGGCATTGCCCCCT
ACCAGAGCCAAAAGGAGAGTGGTCGAGAGAGAGAAAAGGCTCACCGAAATCGTCCCACTCACCGAAGAGGCTGAGC
TGGAGCTGGAGGAAAACAGAGAGATTCTGAGGGAACCCGTCCACGGAGTGATAGAGTGCTCGCCGAAGCCATGAG
CCAAGTCAACAATGCCAATCATGATGCAGAGAGGCAATTTCAAAGGCCTAAAGAGAATCATCAAACAAGAGGAA
GAGGAGGTGGCTTCCCCGTGAGCCCCAGGTCCCACTGAGACCTATGACCTACAAAGGAGCCGTGATCTGTCTCT
TCTTCAGACAGGGACCCAAAGAGCCTTTTCAGAGACTATGTGGATAGGTTTTTCAAACCCCTCAGGGCTGAGCAAGC
CTCACAGGAAGTGAAAAACTGGGAGAAAATCAGACTGAGACCTGGTGCCAAAAGAAATACAAAATGAAACACATT
GTGTGGGCCTCCAGGGAAGTGGAAGGTTTGCCCTCCAGTATGCCCTCGGCATCATCCTAGCCCAACCCGATAAGT
CCGAGTCCGAGCTCGTGAATCAGATTATCGAAGAGCTCATCAAGAAGATTGCCGTGCGCGGATGGACAGACAGAAT
CATTGAGGTGACCAAAGGGCTTGGAGAGCCATTCTGAATATCCCAGGAGAATCAGACAGACTAGACTCGCCGGA
AGGTGGCCCCGTGAGACAATCTATACCGATAACCGAAGCAATTTACAAGCGCTACCGTCAAGGCTGCCTGCTGGT
GGGCTGATGTGAAACAGCTCACCGCAGTCGTCCAGAAAATCGCTACCGAAAGCATTGTGATATGGGGAAAGACGCC
CAAGTTCAGACTGCCTATCGCTGCCGCCAGCAACGAGAATGGAGACCATGGCTGCTTgaagatctgaattc

Figure 30 (Cont)

215/216

C2 fragment

ggatccaccATGCTCGAGAGCAACACAGCCGCTAACAAATACCGATTGCGTGTGGCTGAAAGCCCAGGAAGAGGAAG
AAGTGGGATTTCTGTGAGACCCCAAGTGCCTAGAGCCGGGAGGGCTATCCTCAACATTCCCACGAGGATTAGGCA
AGGCCTTGAGAGAGCCCTCCTAGCCGCCGAATGGGATAGGATTACCCCTGTGCACGCTGGCCCTATCGCTCCCGGC
CAAATGAGAGAGCCCAGGGGAAGCGATATCGCTGGCACAACCCTCAGGCCCATGACATATAAGGCCGCTATTGACC
TCAGCTTGTTTTCTGAAAGAGAAAGGCGGACTGGATGGCCTCATCTATAGCAAGAAAGCTGCTATGGAACAGGCTCC
CGAAGACCAAAGCTCTCAGAGAGAGCCTTACAATGAGTGGACCTGGAGCTCCTGGAAGAGCTCAAGCACGAGGCT
CAAGGCCAATGGACCTTCCAAATCTTTCAGGAACCCCTTTAAGAACTTGAAAACCGGAAAGTATGCCAGAATGAGAG
GCGCTCACACAACTGGATGACAGATACCCTCCTGGTCCAGAATGCCAATCCCGATTGCAAGTCCATCCTCAAGGC
TCTGGGACCCGGAGCCTCACTGGAAGAGCCTGAGGTATCCCTATGTTCTCAGCCCTCAGCGAAGGCGCTACCCCC
CAAGACCTGAATATGATGCTCAACACCGTCCGGCGGACACCAATCCACCCTCCAGGAACAGATTGGCTGGATGACAA
ATAACCTCCCATCCCTGTGCGAGAGATTTACAAAAGGTGGATTATCCTCGGCCTGACTAGAATCCCCCATCCCGC
CGGCCTCAAGAAAAAGAAAAGCGTCACCGTCTGGATGTGGGAGACGCTTACTTCAGCGTCCCCCTCGACGAAGGC
CAAAGGGAAACCTGGGAGGCTTGGTGGATGGAATACTGGCAGGCTACCTGGATTCTTGAGGGGGAGTTTGTGAATA
CCCCCTCCCTCGTGTTCCTCGATTGGCAAACTATACCCCTGGCCCTGGCACAAGGTATCCCTCACCTTTGGATG
GTGCTTTAAGCTCGTGCTGTGACCCCAAACTGTGGTACCAACTGGAAAAGGACCCCATTTGTCGGAGTCGAAACC
TTTACGCGGACGAGCCGCCAACAGAGAGACAAAGCTCGGCCAAAACGTCCAGGGACAGATGGTGCATCAGCCTA
TTAGCCCCAGGACCTCAACGCTTGGGTCAAGGTATCGAAGAGAAAGGCTTTAGCGACACCGAAGTGCATAACGT
CTGGGCTACCCATGCTGTGTGCTTACCGATCCCAATCCCAAGAGATTCTCCTGGAGAATGTGACAGAGCTCAAG
GATCAGAAATCCTCGGCATTTGGGGATGCTCCGGCAAACTCATTGTCACAACCACTGTGCTTGGAAACAGCTCCT
GGTCCAACCCAGCTGGCCATAACAAAGTGGGAAGCCTCCAGTATCTGGCTCTGAAGGCTCTGATTACGCCTAAGAA
AATCAAAACCCCTCTGCCTAGCGTTAAGACAATCATTTGTCATCTGAATGAGTCCGTGGAAATCAATTGCACAAGG
CCTAACATAACACAAGGACAGCCGCCCTAGTGAAGTACAGAATAAGTCCAGACAGAAAACCCAGCAAGCCGCCG
CCGATACAGGCAGCTCCAGCAAGGTGAGCCAAAACCTATCCCATTTGTGTCCAACCTTTACCTCCACCACTGTGAAAGC
CGCTTGTTGGTGGGCCAATATCAACAGGAGTTTGGAAATCCCTTACAATCCCAAGCCGAACATTCTATGTGGAT
GGCGCTGCCAATAGGGAAACCAAACCTGGGAAAGGCTGGCTATGTGACAGACAGAGGCAGACAGAAAGTCGTTAGCG
GAATCTGGCAGCTCGACTGTACCCATCTGAAAGGCAAAGTCATTCTGGTAGCCGTCCACGTCGCCTCCGGCTACAT
TGAGGCTGAGGTCCGCAATGAGCAAGTGGATAAGCTCGTGATTTCGGAATCAGAAAGGTGCTATTCTCGACGGA
ATCGATAAGGCTCAGGAAGAGCACGAAGTCAGGGAAGGATTAGCGAGCCGCTCCCGCTGCTGAAGGCGTCGGCG
CTGTCTCCAGGATCTGGATAAGTACGGAGCCATCACCTCCACAAGCGGAACCCAACAGTCCAGGGAACTGAAAC
TGGCGTCCGCAACCCCTCAGATTTTGGGAGAGTCCAGCGCTGTCTCGGCTCCGCTCCATCGTCATCTGGGGTAAA
ACCCCTAAGTTTAAGCTCCCATTCAGAAAGAGACATGGGAAACCTGGTGGATGGACTATTGGCAAGCCGCTGCTT
ACAGACTGATCAGCTGTAACACAAGCGTTATCACACAGGCTTGCCCTAAGATTAGCTTTGAGCCTATCCCTATCCA
TTACTGTGCCCCCTCTAGCTGGATGGGCTATGAGCTCCACCCTGACAGATGGACAGTGCAACCCATCGTGCTCCCC
GAAAAGGAGTCTTGACAGTGAATGACATTGAGAAAACAATTCTGAAAGCCCTCGGCCCAGGCGCTACCCTGGAGG
AAAATATGACAGCATGTCAGGGAGTGGGAGGCCCTGGCCATAAGGCTAGAGTGTATTACAGAGACTCCAGGGACCC
CATTTGGAAGAGGCCCTGCCAACTGCTCTGGAAGGCGAAGGCGCTGTGGTCAATCAAGACATTAAGATTGGAGGC
CAACTGAAAGAAGCCCTCTGGATACAGGAGCCGATGACACCGTCTGGAAGATATCAATCTGCCTGGCAAGTGGG
GAATCAACAGCTCCAGGCTAGGGTCTGGCTATCGAGAGGTATCTGAAAGATCAACAGCTTCTGGGAATCTGGAG
CTGTAGCGGAAAGGCTGCTATGGAACAGATGGCAAGTGATGATCGTCTGGCAAGTGGACAGGATGAAGATTAGG

Figure 30 (Cont)

216/216

ACATGGAATAGCCTCGTGAAACACCATATGTATCTTATCTGTACCACAGCCGTCCCCTGGAAGTCCACCTGGAGCA
ATAAGTCCTTCGAAGAGATTTGGAATAACATGACCTGGATTGAATGGCTGATTATCGCTATCGTCGTGTGGACCAT
TGTGTTTATCGAATACAAGAACTGCTCAGGCAAAGGAAAATCGATAGGCTCATCGAAAGGCTCAACCCTGGCCTC
CTGGAAACCGCTGAGGGATGTAAACAGATCCTGGAACAGCTCCAGCCCGCCCTCAAGGCAGGCACCGAAGAGTCT
CTAGTAGAAAGCTCCTGAGACAGAGAAAGATTGACAGACTGATTGAGAGAATCAGAGAGAGAGCCGAAGACTCCGG
CAATGAGTCCGAGGGAGACACACCCGGAATCAGATACCAATACAATGTGCTCCCCAAGGCTGGAAGGGCTCCCCA
GCCATTTTCAAAGCTCCATGACCAAAATCCTCATGATGCAAAGGGGAACTTTAAGGGACAGAAAAGGATTATCA
AGTGCTTCAACTGTGGAAGGAAGGCCATCTCGCTAGGAATTGCAGACCTCCCCTGGAGAGACTGAACCTGGATTG
CTCCGAGGATAGCGACACCTCCGGCACACAGCAAAGCCAAGGCACAGAGACAGGAGTGGGACTCGTGGCTGTGCAT
GTGGCCAGCGGATATATCGAAGCCGAAGTGATCCCTGCCGAAACTGGACAGGAAACCGCTTACTTTCTCTCAAGA
TTAAGCCTGTGGTCAGCACACAGCTCCTGCTCAACGGTAGCCTCGCTGAAGAGGAAATCATTATCAGAAGCGAAAA
CTTTACCAATAACAACTGGTCGGCAAACCTGAATTGGGCTTCCCAAATCTACCCTGGCATCAAAGTGAGGCAACTG
TGTAAGCTCCTGAGAGGCACCAAAGCCCTCACCCCTCTGTGTGTGACACTGAATTGCACAAACGCTAACCTCATCA
ATGTGAATGCTGCTCAACCCAGAGGCGATAACCCTACCGATCCCAAAGAGTCTAAGAAAGAGGTGCGCTCCAAGGC
AGAGACAGACCCCTTTTGACGCCGCCCTAGCTCCACCTTTCTGGGAAGGTCTGTGCAACCCGTCCCCCTCCAGCTC
CCCCCTCTGGAAGGCTCCACCTCGACTGTAGCGAAGACAGTGACGAACCTGGATAAGTGGGCCTCCCTGTGGAAGT
GGTTCAATATCACCAACTGGCTGTGGTACATTAAGATTTTCATTATGATTGTGGGAGGCAATAAGATTGTGAGGAT
GTACCAACCTGTCTCCATCCTCGACATTAAGCAAGGCCCTAAGGAACCCCTCAGGGATTACGTGGACAGATTGCGT
AAGCTCCTGTGGAAGGGAGAGGGAGCCGTGCTGATTGAGGACAACTCCGACATTAAGGTCGTGCCAGGAGAAAGG
CTAAGATTATCGAACTGAATAAGAGAACCCAAGACTTTTGGGAAGCGCAACTGGGAATCCCTCACCATGCTGGACT
GAAAAAGAAAAAGTCCGTGACAGTGGCCGCTATGAGAGTGAAAGAGACACAGATGAACTGGCCCAATCTGTGGAAG
TGGGGCACAATGATTCTGGGACTGGTCATCAITTTGCTCCGCTCCATTAAGGTCAAACAGCTCTGCAAACCTGCTCA
GGGGTGCAAAGGCTCTGATAGACATTGTGCCACTGACAGAGGAAGCCGAACCTGGAACCTGCTCATATGGAAGTTTGA
CTCCACCTCGCCCTGAGACATATCGCCAGGGAAGTGCATCCCGAGTACTACAAAGACTGCGCTGCTGTGAGCTC
CTGGGACGCTCCAGCCTCAAGGAACTGCGAAGGGGATGGGAAGCCCTCAAGTATTTGTGGAACCTCCTGCAGTATT
GGGGCTCTAGCCTGGAGCAACTGCAATCTGCTCTGAAAACCGGATCAGAGGAACTGAGGTCCCTGTTTAAACACAGT
CGCTACCTCTGGTGTGTGCATCAGGAGCTCTACAAATACAAAGTGGTCAAATCGAACCCCTCGGCATTGCCCT
ACCAAAGCCAAAAGGAGAGTGGTCCAGAGAGAGAAAAGGCTCACCGATATCGTCACACTCACCGAAGAGGCTGAGC
TGGAGCTGGAGGAAAACAGAGAGATTCTGAAGGAACCCGTCCACGGAGTGATAGAGTGCTCGCCGAAGCCATGAG
CCAAGCCAACAATGCCAACATCATGATGCAGAGAGGCAATTTAGAGGCCCAAAGAGAATCATCAACAAGAGGAA
GAGGGGTTCGGCTTCCCCGTGAGGCTCAGGTCCCACTGAGACCTATGACCTACAAAGCAGCCATCGATCTGTCTT
TCTTCAAACAGGGACCCAAAGAGCCTTTAGAGACTATGTGGATAGGTTTTTCAAACCCCTCAGGCTGAGCAAGC
CTCACAGGAAGTGAAAACTGGGAGAAAATCAGACTGAGATCTGGTGGCAAAAAGAAAATACAACTGAAACACATT
GTGTGGGCCTCCAGGGAACGGAAGGTTTGCTCCAGTATGCCCTCGGCATCATCCTAGCCCAACCCGATAAGT
CCGAGTCCGAGCTCGTGAGTCAGATTATCGAAGAGCTCATCAAGAAGATTGCCGTGCGCGGATGGACAGACAGAGT
CATTGAGGTGCTCAAAGGGCTTGGAGAGCCATTCTGAATATCCCAGGAGAATCAGACAGACTAGACTCGCCGGA
AGGTGGCCCGTCAAGATAATCCATACCGATAACGGAAGCAATTTACAAGCACTGCCGTCAAGGCTGCTGTGGT
GGGCTGATGTGAAACAGCTCACCGAAGTCGTTAGAAAATCGCTACCGAAGCATTGTGATATGGGGAAAGACACC
CAAGTTCAGACAGCCTATCGCTGCCGCCAGCAACGAGAACATGGACGCCATGGCTGCTTgaagatctgaattc

Figure 30 (Cont)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU01/00622

A. CLASSIFICATION OF SUBJECT MATTER		
Int. Cl. ⁷ : C07K 19/00; C12Q 1/68; C07K 2/00, 14/005, 14/15, 14/20, 14/435; C12N 15/09		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED		
Minimum documentation searched (classification system followed by classification symbols) SEE ELECTRONIC DATABASES BELOW		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched SEE ELECTRONIC DATABASES BELOW		
Electronic data base consulted during the international search (name of data base and, where practicable, search terms used) CA WPIDS MEDLINE: Combinatorial protein/peptide/polypeptide; gene/DNA shuffling; domain swapping; vaccine; synthetic protein/peptide polypeptide		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 00/18906 A. MAXYGEN INC. 6/4/00	All
X	WO 99/41402 A. MAXYGEN INC. 19/8/99	All
X	WO 99/41369 A. MAXYGEN INC. 19/8/99	All
X	WO 99/41368 A. MAXYGEN INC. 19/8/99	All
X	Ryu DDY and Nam D-H. Recent progress in biotechnological engineering. Biotechnol Prog. Jan-Feb 2000. 16: 2-16.	All
X	Punnonen J. Molecular breeding of allergy vaccines and antiallergic cytokines. Int Arch Allergy Immunol. March 2000. 121: 173-182	All
<input checked="" type="checkbox"/> Further documents are listed in the continuation of Box C <input checked="" type="checkbox"/> See patent family annex		
* "A" "E" "L" "O" "P"	"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention "X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone "Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art "&" document member of the same patent family	
Date of the actual completion of the international search 1/8/01		Date of mailing of the international search report 7 August 2001
Name and mailing address of the ISA/AU AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustralia.gov.au Facsimile No. (02) 6285 3929		Authorized officer Gillian Allen Telephone No : (02) 6283 2266

INTERNATIONAL SEARCH REPORT

International application No.

PCT/AU01/00622

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Coward E. Shufflet: shuffling sequences while conserving the k-let counts. Bioinformatics. 1999. 15(12): 1058-59.	60-77
X	Crameri A et al. DNA shuffling of a family of genes from diverse species accelerates directed evolution. Nature. 1998. 391: 288-291.	1,3,4-14, 30-33,47
X	Giver L and Arnold H. Combinatorial protein design by <i>in vitro</i> recombination. Curr Opin Chem Biol. 1998. 2: 335-338	1,3,4-14, 30-33, 47
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X	Fisch I et al. A strategy of exon shuffling for making large peptide repertoires displayed on filamentous bacteriophage. Proc Nat Acad Sci USA. 1996. 93: 7761-66	1, 2, 4-14, 30-33, 47
X	Stemmer WPC. DNA shuffling by random fragmentation and reassembly: <i>in vitro</i> recombination for molecular evolution. Proc Nat Acad Sci USA. 1994. 91: 10747-751.	1-18, 30-33, 47
X	Stemmer WPC. Rapid evolution of a protein <i>in vitro</i> by DNA shuffling. Nature. 1994. 370: 389-391.	1, 2, 4-14, 30-33

INTERNATIONAL SEARCH REPORT
Information on patent family members

International application No.
PCT/AU01/00622

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member	
WO 00/18906 A.	AU 11990/00	WO 99/41369 A.	AU 26741/99
	EP 1117777		AU 26742/99
WO 99/41402 A.			AU32891/ 99
			AU 32910/99
	AU 26742/99		EP 1053312
	AU 32891/99		EP 1053343
	AU 32910/99		EP 1054973
	EP 1053312		EP 1056842
	EP 1053343		
	EP 1054973		
		WO 99/41368 A	AU 26741/99
			AU26742/99
			AU 32891/99
			EP 1053312
			EP 1053343
			EP 1056842
END OF ANNEX			